ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40L

TECHNICAL FIELD

Antibodies and fragments thereof that target CD40L, compositions comprising the same, and methods of using the same for treatment of diseases involving CD40L activity are provided.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 8, 2012, is named 20089600.txt and is 1,254,371 bytes in size.

BACKGROUND

CD40 ligand (CD40L), also known as CD154, gp39, TNF-related activation protein (TRAP), 5c8 antigen, or T-BAM, is a trimeric transmembrane protein of the tumor necrosis factor (TNF) superfamily of molecules. CD40L is primarily expressed on activated T cells, as well as on activated leukocytes, eosinophils, basophils, natural killer cells, mast cells, and non-immune cells such as platelets and activated endothelial cells. CD40L also exists in soluble form (sCD40L) that is produced by microsomal stimulus-dependent cleavage of the membrane-bound CD40L. Most of sCD40L in circulation (>90%) is platelet-derived.

CD40L binds CD40, a type I transmembrane glycoprotein belonging to the TNF receptor (TNFR) family. Although all monomeric, dimeric, and trimeric forms of sCD40L can bind to CD40, the trimeric form of sCD40L has the most potent biological activity through oligomerization of cell surface CD40, a common feature of TNFR family. The highest expression of CD40 has been observed on antigen presenting cells (APCs), such as B cells, macrophages, and dendritic cells, while lower expression of this receptor is noted on a variety of other cell types, including stromal cells and thymic epithelium. The CD40-CD40L interaction is essential for normal T-B cell interactions, including increased co-stimulation, T-cell priming, cytokine production, antibody-class switching and affinity maturation, and antibody and autoantibody production.

The crucial role of CD40-CD40L interactions in immune and inflammatory responses has made them a promising target for treatment of pathological immuno-inflammatory processes. Blockade of CD40-CD40L interactions by means of specific CD40L monoclonal antibodies (mAbs) successfully prevents allograft rejection in primates and treats autoimmune diseases and atherosclerosis in animal models. Montgomery et al., *Transplantation* 74: 1365-1369 (2002).

In humans, two different anti-CD40L mAb clones have been used in clinical trials for treatment of different autoimmune diseases. Maribel et al., *Mol. Immunol.* 45: 937-44 (2008). Monoclonal antibodies, however, can display unusually high incidence of thromboembolic (TE) complications, such as atherothrombotic central nervous system events, myocardial infarction, pulmonary embolism, and deep vein thrombosis. For example, the usefulness of the anti-CD40L mAb clone hu5c8 (anti-CD40L mAb, Biogen) is limited by an unusually high incidence of TE complications. TE by these antibodies is thought to result from the formation of higher-order immune complexes (IC) of the mAbs with membrane-bound CD40L on platelets, or sCD40L shed from platelets, that can ligate and thereby aggregate neighboring platelets via their FcgRIIa receptors, resulting in thrombi formation. The risk of thromboembolism has led to a halt in all ongoing clinical trials. Boumpas et al., *Arthritis & Rheumatism* 48: 719-727 (2003).

SUMMARY

In a first aspect, the invention provides an isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain is at least 95% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

In further aspects, the invention provides a nucleic acid encoding the antibody polypeptide of the invention, a vector comprising such a nucleic acid, and an isolated host cell comprising such a vector.

In additional aspects, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of the antibody polypeptide of the invention and a pharmaceutically acceptable carrier, as well as the use of an antibody polypeptide of the invention for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease.

The invention is as defined in the claims. However, the description which follows may refer to additional polypeptides and other subject matter outside the scope of the present claims. This description is retained for technical information.

Anti-CD40L antibody antagonists that are less likely to cause platelet aggregation and thus cause thromboembolism are still needed in a clinical setting. Novel antibody polypeptides that specifically bind human CD40L are provided. The antibody polypeptides advantageously do not cause platelet aggregation. The antibody polypeptides are useful in the treatment of diseases involving CD40L activation, including autoimmune diseases, transplant rejection, and allergic responses. The antibody polypeptides comprise a variable domain. Exemplary antibody polypeptides are in the form of a domain antibody (dAb) that contains a single variable domain. Alternatively, the dAbs can be bi-specific reagents that comprise a second variable domain that can bind another antigen, such as human serum albumin (HSA), for example.

An antibody polypeptide is provided comprising a first variable domain that specifically binds human CD40L, wherein the first variable domain comprises the amino acid sequence of one of the variable domains selected from the BMS2h lineage. Further provided is an isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain comprises: (a) a CDR1 region which differs from the CDR1 region of BMS2h-572-633 by up to three amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS2h-572-633 by up to three amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS2h-572-633 by up to three amino acids, (d) a FR1 region which differs from the FR1 region of BMS2h-572-633 by up to three amino acids, (e) a FR2 region which differs from the FR2 region of BMS2h-572-633 by up to three amino acids, (f) a FR3 region which differs from the FR3 region of BMS2h-572-633 by up to three amino acids, and (g) a FR4 region which differs from the FR4 region of BMS2h-572-633 by up to three amino acids; and wherein the antibody polypeptide inhibits binding of CD40L to CD40 with an EC50 of 100 pM to 100 nM. Also provided is an antibody polypeptide, wherein the amino acid sequence of the first variable domain comprises: (a) a CDR1 region which differs from the CDR1 region of BMS2h-572-633 by up to three amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS2h-572-633 by up to three amino acids, and (c) a CDR3 region which differs from the CDR3 region of BMS2h-572-633 by up to three amino acids. Alternatively, the amino acid sequence of the first variable domain can differ from the amino acid sequence of BMS2h-572-633 by up to and including 10 amino acids. Furthermore, the amino acid sequence of the first variable domain can differ from the amino acid sequence of BMS2h-572-633 by up to and including 5 amino acids. The amino acid sequence of the first variable domain can also differ from the amino acid sequence of BMS2h-572-633 by up to and including 2 amino acids. Alternatively, the first variable domain differs from the amino acid sequence of BMS2h-572-633 by 1 amino acid.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-572, wherein the amino acid sequence of the first variable domain further comprises: (a) a CDR1 region having a sequence Trp-X_1-Leu-Met-Gly (SEQ ID NO: 2), wherein X_1 is Glu or Gln; (b) a CDR2 region having a sequence Gly-Ile-Glu-Gly-Pro-Gly-Asp-Val-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (SEQ ID NO: 3); and (c) a CDR3 region having a sequence Lys-X_2-Y_2- Z_2-Ser-Asp-Tyr (SEQ ID NO: 4), wherein X_2 is Asp or Glu, Y_2 is Ala or Ser, and Z_2 is Lys, Asn, or Arg. Also provided is the antibody polypeptide, wherein the amino acid sequence of the first variable domain further comprises: (a) a FR1 region having a sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Asn (SEQ ID NO: 5); (b) a FR2 region having a sequence Trp-X_1-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser (SEQ ID NO: 6), wherein X_1 is Ala or Val; (c) a FR3 region having a sequence Arg-Thr-Phe-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Val-Lys-Val-Gly (SEQ ID NO: 7); and (d) a FR4 region having a sequence Arg-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 8). Alternatively, the first variable domain of the antibody polypeptide can comprise the amino acid sequence of BMS2h-572-633.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-719, comprising a first variable domain with the following consensus sequence: Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-X_1-Y_1-Tyr-Glu-Met-Z_1-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ser-Ile-Ser-Ser-Asp-Gly-Ser-Phe-Thr-Tyr-Tyr-Ala-A_1-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-B_1-Pro-Phe-Thr-Glu-C_1-Asp-Tyr-Trp-Gly-His-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 9), wherein X_1 is Lys or Asn; Y_1 is Arg, Lys, Ser, or Thr; Z_1 is Met or Gln; A_1 is Asp or Glu; B_1 is Asp or Glu; and C_1 is Phe, Met, or Leu.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-503, comprising a first variable domain with the following consensus sequence: Asp-Ile-Gln-Met-Thr-Gln-Ser-Pro-Ser-Ser-Leu-Ser-Ala-Ser-Val-Gly-Asp-Arg-Val-Thr-Ile-Thr-Cys-Arg-Ala-Ser-His- X_1-Ile-Gln-Arg-Tyr-Leu-Ser-Trp-Tyr-Gln-Gln-Lys-Pro-Gly-Lys-Ala-Pro-Lys-Leu-Leu-Ile-Leu-Trp-Gly-Ser-Gln-Leu-Gln-Ser-Gly-Val-Pro-Ser-Arg-Phe-Ser-Gly-Ser-Gly-Ser-Gly-Thr-Asp-Phe-Thr-Leu-Thr-Ile-Ser-Ser-Leu-Gln-Pro-Glu-Asp-Phe-Ala-Thr-Tyr-Tyr-Cys-Gly-Gln-Trp-Trp-Ala-Pro-Pro-Gln-Thr-Phe-Gly-Gln-Gly-Thr-Lys-Val-Glu-Ile-Lys-Arg (SEQ ID NO: 10), wherein X_1 is His or Asp.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-116, comprising a first variable domain with the following consensus sequence: Asp-Ile-Gln-Met-Thr-Gln-Ser-Pro-Ser-Ser-Leu-Ser-Ala- X_1-Val-Gly-Asp-Arg-Val-Thr-Ile-Thr-Cys-Arg-Ala-Ser-Gln-Pro-Ile-Gly-Pro-Asp-Leu-Leu-Trp-Tyr-Gln-Gln-Lys-Pro-Gly-Lys-Ala-Pro-Lys-Leu-Leu-Ile-Tyr-Gln-Thr-Ser-Ile-Leu-Arg-Ser-Gly-Val-Pro-Ser-Arg-Phe-Ser-Gly-Ser-Gly-Ser-Glu-Thr-Asp-Phe-Thr-Leu-Thr-Ile-Ser-Asn-Leu-Gln-Pro-Glu-Asp-Y_1-Ala-Z_1-Tyr-Tyr-Cys-Gln-Gln-Tyr-Trp-Ala-Phe-Pro-Val-Thr-Phe-Gly-A_1-Gly-Thr-Lys-Val-Val-Ile-Lys-Arg (SEQ ID NO: 11), wherein X_1 is Ser or Tyr; Y_1 is Leu or Phe; Z_1 is Thr or Lys; and A_1 is Lys, Arg, or Gln.

Also provided is an antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein the antibody polypeptide is a domain antibody (dAb). The antibody polypeptide can be a fusion polypeptide comprising the first variable domain and an Fc domain. Alternatively, the fusion polypeptide can comprise an IgG4 Fc domain. The fusion polypeptide also can comprise an IgG1 Fc domain. The fusion polypeptide can also comprise an IgG1 Fc domain. Alternatively, the fusion polypeptide can comprise a CT-Long domain. The fusion polypeptide can also comprise a CT-short domain. Alternatively, the fusion polypeptide can comprise a N297Q Long Fc domain. The fusion polypeptide can alternatively comprise a N297Q Short Fc domain.

Also provided is an antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, wherein the second antigen is an antigen other than human CD40L. The second antigen can be a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule. Alternatively, the second antigen can be serum albumin (SA).

Also provided is a nucleic acid encoding any of the antibody polypeptides provided herein. Further contemplated is a vector comprising the nucleic acid. An isolated host cell can comprise such vector.

A pharmaceutical composition is provided comprising a therapeutically-effective amount of the presently provided antibody polypeptide and a pharmaceutically acceptable carrier. The pharmaceutical composition can further comprise an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

A method of treating an immune disease in a patient in need of such treatment is provided comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition described herein. An exemplary method administers the pharmaceutical composition in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. The immune disease can be an autoimmune disease or a graft-related disease. Alternatively, the immune disease is a graft-related disease. Furthermore, the graft-related disease can comprise solid organ, tissue and/or cell transplant rejection. Alternatively, the graft-related disease is graft versus host disease (GVHD). The graft-related disease can further be an acute transplant rejection. Alternatively, the graft-related disease can be a chronic transplant rejection.

Also provided is the method of treating a graft-related disease, wherein the pharmaceutical composition is co-administered with a CTLA4 mutant molecule. The CTLA4 mutant molecule can be L104EA29Y-Ig (belatacept).

A method of treating an immune disease in a patient in need of such treatment is also provided comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition provided herein, wherein the immune disease is selected from the group consisting of selected from the group consisting of Addison’s disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn’s disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves’ disease, Guillain-Barre syndrome, Hashimoto’s disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren’s syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction. Alternatively, the immune disease can be myasthenia gravis, idiopathic thrombocytopenic purpura, or systemic sclerosis.

Also provided is a use of an isolated antibody polypeptide disclosed herein for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease. Further provided is a use of an isolated antibody polypeptide disclosed herein for preparation of a medicament for alleviating at least one symptom of an immune disease in a patient in need thereof.

Further provided herein is an isolated antibody polypeptide comprising a first variable domain, wherein said antibody polypeptide specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of BMS2h-572-633, and wherein the antibody polypeptide inhibits binding of CD40L to CD40 with an EC50 of 100pM to 100nM. In one aspect, the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS2h-572, BMS2h-719, BMS2h-503, and BMS2h-116. In another aspect, the first variable domain comprises an amino acid sequence at least 95% identical to BMS2h-572-6, BMS2h-572-608, BMS2h-572-614, BMS2h-572-619, BMS2h-572-633, BMS2h-572-634, BMS2h-572-635, BMS2h-719-2, BMS2h-719-202, BMS2h-719-203, BMS2h-719-213, BMS2h-719-214, BMS2h-719-215, BMS2h-719-218, BMS2h-719-225, BMS2h-503-1, BMS2h-503-2, BMS2h-116-1312, BMS2h-116-1313, or BMS2h-116-1320. In yet another aspect, the first variable domain comprises the amino acid sequence of BMS2h-572-6, BMS2h-572-608, BMS2h-572-614, BMS2h-572-619, BMS2h-572-633, BMS2h-572-634, BMS2h-572-635, BMS2h-719-2, BMS2h-719-202, BMS2h-719-203, BMS2h-719-213, BMS2h-719-214, BMS2h-719-215, BMS2h-719-218, BMS2h-719-225, BMS2h-503-1, BMS2h-503-2, BMS2h-116-1312, BMS2h-116-1313, or BMS2h-116-1320.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A depicts the domain antibody that comprises a V_H variable domain BMS2h-572-633 fused to a modified Fc tail from Abatacept IgG1.

FIG. 1B shows the amino acid sequence (SEQ ID NO: 1355) of the variable domain BMS2h-572-633. The Fc fusion protein is a dimer of molecular weight 77,984 Daltons, with each polypeptide chain consisting of 354 amino acids. The variable domain is fused by a linker to the mutated Fc construct of human IgG1, wherein three cysteine residues are substituted with serine, and one proline is substituted with a serine residue.

FIG. 2 depicts a working model for the CD40-40L pathway. The top panel demonstrates initial stages of an encounter between a T cell and an APC. The initial encounter driven by T cell receptor (TCR) engagement of pMHC complex (signal 1) coupled with an early CD28-CD80 interaction (signal 2) is sufficient for the cell surface expression of trimeric CD40L (bottom panel). Engagement of CD40 by CD40L results in numerous biological responses outlined in the grey box.

FIG. 3 provides sequences (SEQ ID NOS 1356-1361, respectively, in order of appearance) of various Fc domains. Linker regions are shown in boxes.

FIG. 4 shows examples of various Fc-formatted domain antibodies (SEQ ID NOS 1362-1365, respectively, in order of appearance). Linker regions are indicated by boxes.

FIG. 5 depicts SPR sensorgram data for the binding of 12.5-0.39nM BMS-986004 (2:1 dilution series) to biot-IZ-hCD40L captured on a streptavidin SPR sensor chip at 25°C. Colored lines show the double-referenced sensorgram data, and black lines show the 1:1 Langmuir fit to the data, with an avidity-influenced apparent Kd value of 0.11 nM.

FIG. 6 shows ITC data for titrations of 19 µM IZ-hCD40L into 2 µM BMS-986004 (black) or 18 µM BMS-986004 into 2 µM IZ-hCD40L (blue). The molar ratio (apparent stoichiometry) is defined per mole of IZ-hCD40L trimer and per mole of bivalent BMS-986004 Fc-dimer. Molar ratio values obtained as the equivalence points on the abscissa suggest more than one mole of BMS-986004 can bind per mole of IZ-hCD40L trimer; however, an exact structural model for the complex cannot be determined from the ITC data alone. Squares represent the integrated heat of binding data and solid lines represent the best fit to a "2 sets of sites model."

FIG. 7 shows in vivo efficacy of mouse CD40L surrogate dAb-Fc (KLH-induced antibody response.

FIG. 8 demonstrates that mouse dAb BMS-2m-126-24-Fc and antibody MR-1 inhibit TNBS-induced colitis in mice.

FIG. 9 shows that BMS-2m-126-24-Fc and CTLA4-Ig work synergistically to prolong the survival of cardiac allografts.

FIG. 10 provides a hypothetic model for anti-CD40 monoclonal antibody-mediated platelet aggregation.

FIG. 11A shows plasma concentration vs. time profile of BMS-986004 after IV dosing of 11 mg/kg in monkeys.

FIG. 11B demonstrates plasma concentration vs. time profiles of BMS-986003 after IV dosing of 2 mg/kg in monkeys.

FIG. 12 presents plasma concentrations vs. time profiles of BMS-986003 (after SC dosing at 0.2, 2 and 20 mg/kg in monkeys) and of 5c8 IgG1 (after IV dosing at 20 mg/kg in monkeys).

FIG. 13 shows plasma concentrations vs. time profiles of BMS-2m-126-24-CT after 1 mg/kg IV and SC dosing, and 10 mg/kg SC dosing to mice.

FIG. 14 demonstrates PK/PD modeling of BMS-986003 and 5c8-IgG1 plasma exposures and anti-KLH antibody response (IgG Titers).

FIG. 15 shows PK/PD modeling of BMS-986004 plasma exposures and *ex vivo* RO on peripheral blood mononuclear cells (PBMC).

FIG. 16 demonstrates that IV.3 blocks 5c8/sCD40L IC-mediated activation of platelets in human blood.

FIG. 17 shows the effect of Fc variants on platelet activation in human blood.

FIG. 18 demonstrates activation of platelets with 5c8-CT/sCD40L IC in blood from human donors genotyped for FcgRIIa polymorphism.

FIG. 19 diagrams platelet activation by various antibodies in blood from human donors.

FIG. 20 shows levels of platelet activation by various antibodies, including BMS-986003, in hFcgRIIa-expressing transgenic mice.

FIGS. 21, 22, 23, and 24 show is ClustalW2 alignments of representative domain antibody polypeptides from lineages BMS2h-572, BMS2h-719, BMS2h-503, and BMS2h-116, respectively. FIG. 21 discloses SEQ ID NOS 243, 251, 257, 262 and 274-276, respectively, in order of appearance, FIG. 22 discloses SEQ ID NOS 352, 354-355 and 357-361, respectively, in order of appearance, FIG. 23 discloses SEQ ID NOS 1087-1088, respectively, in order of appearance, and FIG. 24 discloses SEQ ID NOS 970-971 and 974, respectively, in order of appearance.

FIG. 25 shows SPR sensorgram data for binding experiments using monovalent dAbs BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and monovalent Fab fragment of 5c8, where the indicated molecules compete with each other for binding to CD40L (biotinylated IZ-hCD40L).

FIG. 26 shows SPR sensorgram data for experiments testing the binding of BMS2h-572-619-CT-long, BMS2h-572-633-CT-long, BMS2h-572-6-CT-long, BMS2h-719-202-CT-long, BMS2h-572-608-CT-long, BMS2h-572-634-CT-long, BMS2h-572-614-CT-long, BMS2h-572-635-CT-long, and 5c8-CT-long molecules to either CD40L monomer (upper 3 panels) or CD40L trimer (lower 3 panels).

DETAILED DESCRIPTION

Antibody polypeptides that specifically bind to human CD40L are provided. The antibody polypeptides do not activate platelets, and the antibody polypeptides are useful in the treatment of diseases involving CD40L activation, such as graft-related diseases and autoimmune diseases. The antibody polypeptides may be selected using a primary screen that utilizes cell binding assays, followed by one or more rounds of error-prone or degenerate oligonucleotide-directed affinity maturation. As a result, a genus of antibody polypeptides that specifically bind CD40L are provided.

A “lineage” is a set of related antibody polypeptides that were prepared from a common precursor by error-prone or degenerate oligonucleotide-directed affinity maturation, as disclosed in the examples below, and that are expected to bind CD40L. The nomenclature of the antibody polypeptides is used to designate the various lineages. The nomenclature “BMS2h-572,” for example, refers to antibody polypeptides of lineage 572, which were raised against human CD40L. “Lineage BMS2h-572” antibody polypeptides include BMS2h-572-1 through BMS2h-572-19, BMS2h-572-21 through BMS2h-572-24, BMS2h-572-601 through BMS2h-572-627, and BMS2h-572-630 through BMS2h-572-635.

Accordingly, in one aspect, an antibody polypeptide comprises a variable domain that specifically binds human CD40L, where the antibody polypeptide competes with the binding of any one of the domain antibodies (dAbs) listed in TABLE 1 or TABLE 3. For example, the antibody polypeptide may compete with a dAb selected from the 2h lineage. The dAb also may be selected from a lineage selected from the group consisting of BMS2h-116, BMS2h-503, BMS2h-572, and BMS2h-719, such as the dAb BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for instance. In another aspect, an antibody polypeptide specifically binds human CD40L as any one of the dAbs listed in TABLE 1 and TABLE 3. For example, the antibody polypeptide may comprise a variable domain that specifically binds human CD40L as the dAb BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for instance.

The antibody polypeptides may be a domain antibody containing a single variable domain. The antibody polypeptides also may comprise additional domains, such as an Fc domain. For instance, the antibody polypeptide may comprise a second variable domain that specifically binds human serum albumin (HSA). Such dual specific antibody polypeptides may have an increased half-life, for example.

As used herein, “specific binding” refers to the binding of an antigen by an antibody polypeptide with a dissociation constant (K_d) of about 1 μM or lower as measured, for example, by surface plasmon resonance (SPR). Suitable assay systems include the BIAcore^{TM} surface plasmon resonance system and BIAcore^{TM} kinetic evaluation software (e.g., version 2.1). The affinity or K_d for a specific binding interaction may be about 1 μM or lower, about 500 nM or lower or about 300 nM or lower.

The term “about” will be understood by persons of ordinary skill in the art and will vary to some extent on the context in which it is used. Generally, about encompasses a range of values that are plus/minus 10% of a referenced value.

In accordance with this detailed description, the following abbreviations and definitions apply. It must be noted that as used herein, the singular forms “a”, “an”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “an antibody” includes a plurality of such antibodies and reference to “the dosage” includes reference to one or more dosages and equivalents thereof known to those skilled in the art, and so forth.

1. CD40L and CD40L Activities

Antibody polypeptides are provided that bind human CD40L. CD40L is also known as CD154, gp39, TNF-related activation protein (TRAP), 5c8 antigen, or T-BAM. Relevant structural information for human CD40L can be found, for example, at UniProt Accession

Number P29965. “Human CD40L” refers to the CD40L comprising the following amino acid sequence:

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        10         20         30         40         50
60
MIETYNQTSP RSAATGLPIS MKIFMYLLTV FLITQMIGSA LFAVYLHRRL
DKIEDERNLH

        70         80         90        100        110
120
EDFVFMKTIQ RCNTGERSLS LLNCEEIKSQ FEGFVKDIML NKEETKKENS
FEMQKGDQNP

       130        140        150        160        170
180
QIAAHVISEA SSKTTSVLQW AEKGYYTMSN NLVTLENGKQ LTVKRQGLYY
IYAQVTFCSN

       190        200        210        220        230
240
REASSQAPFI ASLCLKSPGR FERILLRAAN THSSAKPCGQ QSIHLGGVFE
LQPGASVFVN

       250        260
VTDPSQVSHG TGFTSFGLLK L
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(SEQ ID NO: 1)

CD40L has also been sequenced in *Sus scrofa*, *Mus musculus*, *Canis familiaris*, *Bos ffini*, *Macaca mulatta*, *Aotus tivirgatus*, *Callithrix jacchus*, *Cercocebus torquatus atys*, *Macaca nemestrina*, *Rattus norvegicus*, *Gallus gallus*, *Felis catus*, and *Sus scrofa*.

Binding of the present antibody polypeptides to CD40L antagonizes CD40L activity. “CD40L activities” include, but are not limited to, costimulation and activation an APC in association with T cell receptor stimulation by MHC molecules on the APC, secretion of all immunoglobulin isotypes in the presence of cytokines, stimulation of B cell proliferation, cytokine production, antibody class switching and affinity maturation. For example, patients with X-linked hyper-IgM syndrome express functional CD40 on their B cells, but their activated T cells have a defective CD40L protein, resulting in its inability to activate B cells and induce immunoglobulin isotype switching. Aruffo *et al.*, *Cell* 72:291-300 (1993).

CD40L activities can be mediated by interaction with other molecules. “CD40 activities” include the functional interaction between CD40L and the following molecules: CD40 (CD40L receptor), α5β1 integrin, and αIIbβ3. For example, CD40L binds its receptor, CD40, which is expressed on a variety of APCs, such as B cells, macrophages, and dendritic cells, as well as on stromal cells, vascular endothelial cells, and platelets.

As used herein, the terms “activate,” “activates,” and “activated” refer to an increase in a given measurable CD40L activity by at least 10% relative to a reference, for example, at least 10%, 25%, 50%, 75%, or even 100%, or more. A CD40L activity is “antagonized” if the activity is reduced by at least 10%, and in an exemplary embodiment, at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, or even 100% (i.e., no detectable activity), relative to the absence of the antagonist. For example, an antibody polypeptide may antagonize some or all CD40L activity. In one embodiment, the antibody polypeptide does not activate B cell proliferation. In another embodiment, the antibody polypeptide does not activate cytokine secretion by T cells or dendritic cells (DCs), where the cytokine is at least one cytokine selected from the group consisting of IL-2, IL-6, IL-10, IL-12, IL-13, IL-17, IL-23, TNF-α, and IFN-γ.

2. Antibody Polypeptides

The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a dAb that contains a single variable domain. Antibody polypeptides may be full-length anti-CD40L immunoglobulin molecules comprising two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. In this embodiment, the amino terminal portion of each chain includes a variable domain (V_L or V_H) of about 100-120 amino acids. The complementarity determining regions (CDRs) contained therein are primarily responsible for antigen recognition, although framework residues can play a role in epitope binding. The carboxy-terminal “half” of each heavy chain defines a constant region (Fc) primarily responsible for effector function.

Antibody polypeptides also may be “fragments” comprising a portion of the full-length anti-CD40L immunoglobulin molecule that comprises a variable domain that specifically binds CD40L. Thus, the term “antibody polypeptides” includes an antigen-binding heavy chain, light chain, heavy chain-light chain dimer, Fab fragment, $F(ab')_2$ fragment, Fv fragment, single chain Fv (scFv), and dAb, for example. The term “antibody polypeptides” thus includes polypeptides made by recombinant engineering and expression, as well as monoclonal antibodies produced by natural recombination and secretion by hybridoma cell clones.

Light chains are classified as kappa (κ) or lambda (λ), and are characterized by a particular constant region, C_L, as known in the art. Heavy chains are classified as γ, μ, α, δ, or ε, and define the isotype of an antibody as IgG, IgM, IgA, IgD, or IgE, respectively. The heavy chain constant region is comprised of three domains (CH1, CH2, and CH3) for IgG, IgD, and IgA; and four domains (CH1, CH2, CH3, and CH4) for IgM and IgE. Anti-CD40L antibodies may have a heavy chain constant region selected from any of the immunoglobulin classes (IgA, IgD, IgG, IgM, and IgE).

Each light chain variable domain (V_L) and heavy chain variable domain (V_H) is composed of three CDRs and four framework regions (FRs), arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The three CDRs of the light chain are referred to as “LCDR1, LCDR2, and LCDR3” and the three CDRs of the heavy chain are referred to as “HCDR1, HCDR2, and HCDR3.”

As used herein, the term “Fc domain” refers to the constant region antibody sequences comprising CH2 and CH3 constant domains as delimited according to Kabat et al., *Sequences of Immunological Interest,* 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The Fc domain may be derived from an IgG1 or an IgG4 Fc region, for example.

A variable domain may be fused to an Fc domain. Examples of various Fc-formatted domain antibodies and their potency are provided in TABLE 6. FIG. 3 provides sequences of various Fc domains provided herein. Linker regions are shown in boxes. As used in TABLE 6, “Fc” indicates that the dAb is fused to a human IgG1 short Fc. “CT Long Fc,” also called CT-L2, refers to the Fc from CTLA4. The underlined **S** are cysteine-to-serine point mutations made to eliminate the disulfides in the Fc hinge. “CT Short,” also called CT-S1, is shorter than CT Long by 7 amino acids. “N297Q Long Fc,” also referred to as N297Q-L4, is the Fc domain of human IgG1 with a N297Q mutation made to eliminate the N-linked carbohydrate in the Fc. “N297Q Short Fc,” also called N297Q-S3, is short than N297Q Long Fc by 7 amino acids, and is a human IgG1 with a N297Q point mutation made to eliminate the N-linked carbohydrate in the Fc domain. “CT-Fc SP5” is the CT Long Fc, where SP5 refers to the octeonectin signal peptide used for secretion from the mammalian expression host. Cleavage site is indicated by “^”. FIG. 4 further provides examples of various Fc domain formats.

When a variable domain is fused to an Fc domain, the carboxyl terminus of the variable domain (either a V_L or V_H domain, including dAbs) may be linked or fused to the amino terminus of the Fc CH2 domain. Alternatively, the carboxyl terminus of the variable domain may be linked or fused to the amino terminus of a CH1 domain, which itself is fused to the Fc CH2 domain. The protein may comprise the hinge region between the CH1 and CH2 domains in whole or in part.

The CDRs contain most of the residues that form specific interactions with the antigen. In one embodiment, the variable domain of an antibody polypeptide comprises CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of one of the dAbs listed in TABLE 1 or TABLE 3 or that each differ from the CDR1, CDR2, and CDR3 regions by one, two, or three amino acids. For example, the antibody polypeptide may comprise CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for example.

A "domain antibody" (dAb) comprises a single variable (V_L or V_H) domain that is capable of specifically and monovalently binding an antigen, such as CD40L. For example, a dAb may have a V_{HH} structure, characteristic of a camelid dAb. A "V_H domain" as used herein is meant to include a V_{HH} structure. In another embodiment, the V_H domains (including all features and combination of features presented as embodiments herein) are other than V_{HH} domains. dAbs may form homo- or heterodimers in solution. While not limited by any particular theory, it is believed that the dAbs disclosed herein do not cause platelet aggregation, because the antibodies containing mutated Fc constructs do not bind FcγRIIa (also known as CD32a) on the platelet surface and do not activate platelets.

As used herein, the term "variable domain" refers to immunoglobulin variable domains defined by Kabat et al., *Sequences of Immunological Interest,* 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The numbering and positioning of CDR amino acid residues within the variable domains is in accordance with the well-known Kabat numbering convention.

The term "human," when applied to antibody polypeptides, means that the antibody polypeptide has a sequence, *e.g.*, framework regions and/or CH domains, derived from a human immunoglobulin. A sequence is "derived from" a human immunoglobulin coding sequence when the sequence is either: (a) isolated from a human individual or from a cell or cell line from a human individual; (b) isolated from a library of cloned human antibody gene sequences or of human antibody variable domain sequences; or (c) diversified by mutation and selection from one or more of the polypeptides above. An "isolated" compound as used herein means that the compound is removed from at least one component with which the compound is naturally associated with in nature.

Antibody polypeptides can be administered to human patients while largely avoiding the anti-antibody immune response often provoked by the administration of antibodies from other species, *e.g.*, mouse. For example, murine antibodies can be "humanized" by grafting murine CDRs onto a human variable domain FR, according to procedures well known in the art. Human antibodies as disclosed herein, however, can be produced without the need for genetic manipulation of a murine antibody sequence.

Variable domains may comprise one or more FR with the same amino acid sequence as a corresponding framework region encoded by a human germline antibody gene segment. For example, a domain antibody may comprise the V_H germline gene segments DP47, DP45, or DP38, the V_κ germline gene segment DPK9, the J_H segment JH4b, or the J_κ segment $J_\kappa1$.

Changes may be made to antibody polypeptide sequences while retaining the ability to bind CD40L specifically. Specifically, the antibody polypeptides (*e.g.*, a dAb) may comprise a variant variable domain that retains the function of specifically binding CD40L as the dAb BMS2h-572-633. In one embodiment, the variant variable domain may compete with BMS2h-572-633 for specific binding to CD40L. Error-prone affinity maturation, as disclosed in the examples below, provides one exemplary method for making and identifying antibody polypeptides with variant sequences that specifically bind CD40L.

For example, a variant variable domain may differ from one of the variable domains listed in TABLE 1 and TABLE 3 by up to 10 amino acids or any integral value between, where the variant variable domain specifically binds CD40L. Alternatively, the variant variable domain may have at least 90% sequence identity (*e.g.*, at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) relative to a sequence listed in the present Sequence Listing. Non-identical amino acid residues or amino acids that differ between two sequences may represent amino acid substitutions, additions, or deletions. Residues that differ between two sequences appear as non-identical positions, when the two sequences are aligned by any appropriate amino acid sequence alignment algorithm, such as BLAST.

In one embodiment, amino acid substitutions may be made to individual FR regions, such that a FR comprises 1, 2, 3, 4, or 5 amino acid differences relative to the amino acid sequence of the corresponding FR encoded by a human germline antibody gene segment. In another embodiment, the variant variable domain may contain one or two amino acid substitutions in a CDR. In other embodiments, amino acid substitutions to FR and CDR regions may be combined. Representative variable domains that specifically bind CD40L are listed in TABLE 1 and TABLE 3.

The information regarding the boundaries of the V_L or V_H domains of heavy and light chain genes may be used to design PCR primers to amplify the variable domain from a cloned heavy or light chain coding sequence encoding an antibody polypeptide known to bind CD40L. The amplified variable domain may be inserted into a suitable expression vector, *e.g.*, pHEN-1 (Hoogenboom et al. (1991) *Nucleic Acids Res.* 19:4133-4137) and expressed, either alone or as a fusion with another polypeptide sequence, using techniques well known in the art. Based on the disclosed amino acid and polynucleotide sequences, the fusion protein can be produced and purified using only ordinary skill in any suitable mammalian host cell line, such as CHO, 293, COS, NSO, and the like, followed by purification using one or a combination of methods, including protein A affinity chromatography, ion exchange, reverse phase techniques, or the like.

In one aspect, the antibody polypeptide is a "dual specific" antibody polypeptide comprising a first variable domain that specifically binds human CD40L. Dual specific antibody polypeptides comprise a second variable domain that specifically binds a second antigen that is other than human CD40L.

In another embodiment, the second antigen may be a cell surface molecule of an immune effector cell or a soluble molecule such as a cytokine, for example. Binding of the dual specificity antibody polypeptide could be used to antagonize CD40L and antagonize a biological activity of the second antigen. Cell surface molecules of immune effector cells include the cluster of differentiation (CD) molecules. Representative CD markers are listed on the Internet at hypertext transfer protocol http://en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation (last modified on August 8, 2012). Cell surface molecules of immune effector cells also include Major Histocompatibility Complex (MHC) Class II molecules. Antibodies against these cell surface molecules are known in the art and can be used a source of a variable domain to construct a dual specific antibody polypeptide.

In one embodiment, antibody polypeptides of a dual specific ligand may be linked by an "amino acid linker" or "linker." For example, a dAb may be fused to the N-terminus of an amino acid linker, and another dAb may be fused to the C-terminus of the linker. Although amino acid linkers can be any length and consist of any combination of amino acids, the linker length may be relatively short (*e.g.*, five or fewer amino acids) to reduce interactions between the linked domains. The amino acid composition of the linker also may be adjusted to reduce the number of amino acids with bulky side chains or amino acids likely to introduce secondary structure. Suitable amino acid linkers include, but are not limited to, those up to 3, 4, 5, 6, 7, 10, 15, 20, or 25 amino acids in length. Representative amino acid linker sequences include $(GGGGS)_n$ (SEQ ID NO: 12), where n may be any integer between 1 and 5. Other suitable linker sequences may be selected from the group consisting of AS, AST, TVAAPS (SEQ ID NO: 13), TVA, and ASTSGPS (SEQ ID NO: 14).

The binding of the second antigen can increase the *in vivo* half-life of the antibody polypeptide. For example, the second variable domain of the dual specific antibody polypeptide may specifically bind serum albumin (SA), *e.g.*, human serum albumin (HSA). The antibody polypeptide formatted to bind I can have an increased *in vivo* t-α ("alpha half-life") or t-β ("beta half-life") half-life relative to the same unformatted antibody polypeptide. The t-α and t-β half-lives measure how quickly a substance is distributed in and eliminated from the body. The linkage to I may be accomplished by fusion of the antibody polypeptide with a second variable domain capable of specifically binding I, for example. Anti-human serum albumin antibodies are well-known in the art. *See, e.g.*, Abcam®, Human Serum Albumin antibodies ab10241, ab2406, and ab8940, available on the Internet at hypertext transfer protocol www.abcam.com/index.html, or GenWay, ALB antibody, available on the Internet at hypertext transfer protocol www.genwaybio.com. Variable domains that specifically bind I can be obtained from any of these antibodies, and then fused to an antibody polypeptide of the disclosure using recombinant techniques that are well known in the art.

Alternatively, the linking of the antibody polypeptide to I can be accomplished by directly fusing the antibody polypeptide sequence to an I coding sequence using techniques well known to the skilled artisan. The I coding sequences can be obtained by PCR using primers derived from the cDNA sequence available at GenBank Accession No. NM000477, for example.

In one embodiment, the tα-half-life of the I-linked domain antibody composition is increased by 10% or more. In another embodiment, the tα-half-life of the I-linked domain antibody composition is in the range of 0.25 hours to 6 hours. In another embodiment, the tβ-half-life of the I-linked domain antibody composition is increased by 10% or more. In another embodiment, the tβ-half-life of the I-linked domain antibody composition is in the range of 12 to 48 hours.

In another embodiment, an antibody polypeptide may be formatted to increase its *in vivo* half-life by PEGylation. In one embodiment, the PEG is covalently linked. In another embodiment, the PEG is linked to the antibody polypeptide at a cysteine or lysine residue. In yet another embodiment, the PEG-linked antibody polypeptide has a hydrodynamic size of at least 24 kD. In yet another embodiment, the total PEG size is from 20 to 60 kD, inclusive. In yet another embodiment, the PEG-linked domain antibody has a hydrodynamic size of at least 200 kD.

PEGylation can be achieved using several PEG attachment moieties including, but not limited to N-hydroxylsuccinimide active ester, succinimidyl propionate, maleimide, vinyl sulfone, or thiol. A PEG polymer can be linked to an antibody polypeptide at either a predetermined position, or can be randomly linked to the domain antibody molecule. PEGylation can also be mediated through a peptide linker attached to a domain antibody. That is, the PEG moiety can be attached to a peptide linker fused to an antibody polypeptide, where the linker provides the site (e.g., a free cysteine or lysine) for PEG attachment. Methods of PEGylating antibodies are well known in the art, as disclosed in Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review," *Adv. Drug Deliv. Rev*. 54(4):531-45 (2002), for example.

Antibody polypeptides also may be designed to form a dimer, trimer, tetramer, or other multimer. Antibody polypeptides, e.g., dAbs, can be linked to form a multimer by several methods known in the art, including, but not limited to, expression of monomers as a fusion protein, linkage of two or more monomers via a peptide linker between monomers, or by chemically joining monomers after translation, either to each other directly, or through a linker by disulfide bonds, or by linkage to a di-, tri- or multivalent linking moiety (e.g., a multi-arm PEG). In one embodiment, the multimer can bind a single molecule of CD40.

3. Pharmaceutical Compositions and Methods of Treatment

A pharmaceutical composition comprises a therapeutically-effective amount of one or more antibody polypeptides and optionally a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers include, for example, water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof.

Pharmaceutically acceptable carriers can further comprise minor amounts of auxiliary substances, such as wetting or emulsifying agents, preservatives, or buffers that enhance the shelf-life or effectiveness of the fusion protein. The compositions can be formulated to provide quick, sustained, or delayed release of the active ingredient(s) after administration. Suitable pharmaceutical compositions and processes for preparing them are well known in the art. *See, e.g.,* Remington, THE SCIENCE AND PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005).

The pharmaceutical composition further may comprise an immuno-suppressive/immunomodulatory and/or anti-inflammatory agent. A method of treating an immune disease in a patient in need of such treatment may comprise administering to the patient a therapeutically effective amount of the pharmaceutical composition. Antagonizing CD40L-mediated T cell activation could inhibit undesired T cell responses occurring during autoimmunity, transplant rejection, or allergic responses, for example. Inhibiting CD40L-mediated T cell activation could moderate the progression and/or severity of these diseases.

As used herein, a "patient" means an animal, e.g. mammal, including humans. The patient may be diagnosed with an immune disease. "Treatment" or "treat" or "treating" refers to the process involving alleviating the progression or severity of a symptom, disorder, condition, or disease. An "immune disease" refers to any disease associated with the development of an immune reaction in an individual, including a cellular and/or a humoral immune reaction. Examples of immune diseases include, but are not limited to graft-related disease, inflammation, allergy, and autoimmune disease. The autoimmune disease may be selected from the group consisting of systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, diabetes, psoriasis, scleroderma, atherosclerosis, inflammatory bowel disease, and ulcerative colitis.

Diseases that can be treated by administering the pharmaceutical composition may be selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products (*e.g.*, Factor VII in hemophiliacs), systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, and vasculitis. Autoimmune-mediated conditions include, but are not limited to, conditions in which the tissue affected is the primary target, and in some cases, the secondary target. Such conditions include, but are not limited to, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus' phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

Preferred indications for administration of the present pharmaceutical compositions are, for example, immune thrombocytopenic purpura, systemic sclerosis, myasthenia gravis, allograft rejection, and graft-versus-host disease.

The pharmaceutical composition may be administered alone or in combination therapy, (*i.e.*, simultaneously or sequentially) with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. Different immune diseases can require use of specific auxiliary compounds useful for treating immune diseases, which can be determined on a patient-to-patient basis. For example, the pharmaceutical composition may be administered in combination with one or more suitable adjuvants, *e.g.*, cytokines (IL-10 and IL-13, for example) or other immune stimulators, e.g., chemokines, tumor-associated antigens, and peptides. Suitable adjuvants are known in the art.

For example, the disclosed pharmaceutical composition may be co-administered, concomitantly or sequentially, with a cytotoxic T-lymphocyte antigen 4 (CTLA4) mutant molecule, such as L104EA29Y-Ig (belatacept). CTLA4 binds to CD80 (B7-1) and CD86 (B7-2) with higher avidity than CD28, and it is transiently expressed on T cells following their activation, where it interrupts the interaction between CD28 and CD80/86. Oosterwegel et al., *Curr. Opin. Immunol.* 11: 294-300 (1999). This creates a negative feedback signal for T cell activation.

CTLA4 mutant molecules, including L104EA29Y-Ig, have increased binding avidity to CD80/86 compared to wild-type CTLA4. Intervention of the CD28-CD80/86 pathway by L104EA29Y-Ig has been successfully pursued, for example, to treat graft-related diseases in non-human primate transplant models, alone or in combination with other immunosuppressive agents. Larsen et al., *Amer. J. Transplant.* 5: 443 (2005). U.S. Patent Application number 2010/0166774 describes the structure of L104EA29Y-Ig, methods of producing it, and a formulation comprising a CTLA4 molecule; and the application is herein incorporated by reference. U.S. Patent Nos 7,094,874 and 7,482,327 further disclose administration (including co-administration with one or more other drugs) and dosage schedule of L104EA29Y-Ig, and the disclosures of these patents are herein incorporated by reference.

Any suitable method or route can be used to administer the antibody polypeptide or the pharmaceutical composition. Routes of administration include, for example, oral, intravenous, intraperitoneal, subcutaneous, or intramuscular administration. A therapeutically effective dose of administered antibody polypeptide(s) depends on numerous factors, including, for example, the type and severity of the immune disease being treated, the use of combination therapy, the route of administration of the antibody polypeptide(s) or pharmaceutical composition, and the weight of the patient. A non-limiting range for a therapeutically effective amount of a domain antibody is 0.1-20 mg/kg, and in an aspect, 1-10 mg/kg, relative to the body weight of the patient. The dose of antibody polypeptide(s) can be further guided by the amount of antibody polypeptide(s) required for CD40 antagonism in *in vitro* and/or *in vivo* models of disease states. Representative models are described below and in the examples.

4. *In Vitro* and *In Vivo* Models

The ability of antibody polypeptides of the disclosure to antagonize CD40L can be tested in one of several available *in vitro* or *in vivo* model systems. Appropriate human, animal, and cell model systems are described below. Further cell assay systems are described in the examples.

4.1. Immune Thrombocytopenic Purpura (ITP) *In Vivo* Model:

The potential role of CD40-CD40L in the pathogenesis of ITP is reported by Patel et al., *British J. Haematology* 141: 545-548 (2008). Antiplatelet autoantibodies in patients with ITP bind to circulating platelets and accelerate their destruction. The primary mechanism by which anti-CD40L antibodies are thought to increase the platelet count in ITP is by blocking T-cell based activation of autoreactive B cells that produce anti-platelet antibodies. Anti-CD40L antibodies may also block expression of CD40L on platelets, thus preventing autopresentation of platelet glycoprotein antigens to macrophages. Furthermore, anti-CD40L mAbs inhibit direct interactions between platelet CD40L and other cells, such as plasmacytoid dendritic cells (DCs), which have recently been implicated in driving the type 1 interferon (IFN) response in human lupus patients. Duffau et al., *Sci. Transl. Med.* 2: 47 (2010).

Patel *et al*. demonstrated efficacy of two humanized anti-CD40L monoclonal antibodies, hu5c8 and IDEC-131, in 46 human patients with chronic ITP refractory to conventional therapies. The patients had an overall 24% response rate, characterized by increased platelet counts. This demonstrated the potential role of CD40-CD40L in the pathogenesis of ITP.

4.2. Lupus *In Vivo* and *In Vitro* Models:

Glomerular and tubular CD40 expression is markedly upregulated in proliferative nephritis. Several studies have reported hyperexpression of CD40L by T cells and elevated soluble sCD40L concentrations in human lupus. Kimura et al., *Therapeutic Apheriss and Dialysis* 9: 64-68 (2005); Vakkalanka et al., *Arthritis & Rheumatism* 42: 871-881 (1999).

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease characterized by the production of multiple autoantibodies and by B cell hyperactivity. Grammer et al., *J. Clin. Invest.* 112: 1506-1520 (2003) reports the results of treatment of patients with SLE with humanized anti-CD40L mAb 5c8 (BG9588). *See also* Huang et al., *Arthritis & Reumatism* 46: 1554-1562 (2002). Grammer et al. report that CD19+ peripheral B cells were examined before and after treatment with the anti-CD40L mAb. Before treatment, SLE patients manifested activated B cells that expressed CD40L, CD69, CD38, CD5, and CD27. The activated B cells disappeared from the periphery during and post-treatment. Before treatment, active SLE patients had circulating CD38^{bright} Ig-secreting cells that were not found in normal individuals. Disappearance of these plasma cells during treatment was associated with decreases in anti-double stranded DNA (anti-dsDNA) Ab levels, proteinuria, and SLE disease activity index. Consistent with this finding, peripheral B cells cultured *in vitro* spontaneously proliferated and secreted Ig in a manner that was inhibited by anti-CD40L mAb. The CD38+/++IgD+, CD38+++, and CD38+IgD- B cell subsets present in the peripheral blood of SLE patients also disappeared following treatment with the anti-CD40L mAb. Together, these results suggest that spontaneous CD40L-CD40 interactions in active SLE patients drive B cell activation, proliferation, and differentiation to autoantibody-secreting plasma cells that mediate proteinuria and disease activity.

Proliferative lupus glomerulonephritis is a protracted autoimmune disease with a waxing and waning course, characterized by increased level of anti-dsDNA antibodies, decreased serum C3 concentrations, and hematuria. Boumpas et al, *Arthritis & Rheumatism* 48: 719-727 (2003) report results of a phase II, multicenter, open-label study evaluating the toxicity and efficacy of BG9688, a humanized anti-CD40L monoclonal antibody, in patients with proliferative lupus glomerulonephritis. Although the study had to be terminated prematurely because of thromboembolic events occurring in patients in several BG9588 protocols, a short course of the anti-CD40L antibody treatment in patients with proliferative lupus nephritis reduced anti-dsDNA antibodies, increased C3 concentrations, and decreased hematuria, suggesting that the drug has immunomodulatory function.

4.3. Inflammatory Bowel Disease (IBD) *In Vivo* Models:

Crohn's disease (CD) and ulcerative colitis (UC) are IBDs that are characterized by leukocytic infiltrates in inflamed intestinal mucosa, which consists primarily of activated CD25+ cells, B cells, and macrophages. Ludwiczek et al., *Int. J. Colorectal Dis*. 18: 142-147 (2003) report that in CD patients, plasma levels of sCD40L were significantly higher than in healthy individuals. Moreover, CD patients with fistulas and/or abscesses had significantly higher levels of sCD40L than patients with uncomplicated CD. It has also been reported that the CD40-CD40L pathway contributes to the proinflammatory function of intestinal epithelial cells in IBD. Borcherding et al., *Am. J. Pathol*. 176: 1816-1827 (2010). Patients with CD also have an increased risk of systemic thromboembolism, and the hyperactive state of platelets from such patients likely results from the enhanced release of sCD40L as a consequence of their higher endogenous content of CD40L. Menchen et al., *Gut* 58: 920-928 (2009); *see also* Danese et al., *Gut* 52: 1435-1441 (2003).

Kasran et al., *Aliment. Pharmacol. Ther*. 22: 111-122 (2005) investigated the use of a chimeric anti-human CD40 mAb ch5D12 to treat Crohn's disease. The mAb was administered to 18 patients with moderate to severe CD in a single dose, open-label dose escalation phase I/Iia study. Of the 18 patients, 13 (or 72%) experienced a favorable response to the antibody infusion, and 4 patients (or 22%) experienced a remission. Treatment with the anti-CD40 mAb reduced microscopic disease activity and intensity of the lamina propria cell infiltrate, and the mAb was well tolerated.

4.4. Rheumatoid Arthritis (RA),Juvenile Idiopathic Arthritis (JIA), and Psoriatic Arthritis (PsA) *In Vivo* Models:

Rheumatoid arthritis is a systemic autoimmune disease with intra-articular inflammation as a dominant feature that affects up to 1% of the population. The disease can be subdivided clinically by the presence or absence of autoantibodies (antibodies to cyclic citrullinated peptide (CCP) or rheumatoid factor (RF), both of which are highly correlated to each other. Raychaudhuri et al., *Nature Genetics* 40: 1216-1223 (2008) reported that they conducted a meta-analysis of two published genome-wide association (GWA) studies totaling 3,393 cases and 12,462 controls, in order to identify RA risk loci in European populations. They genotyped 31 top-ranked short nucleotide polymorphisms (SNPs) not previously associated with RA in an independent replication of 3,929 autoantibody-positive RA cases and 5,807 matched controls from eight separate collections. They identified a common variant at the CD40 gene locus, which implied a central role for the CD40 signaling pathway in RA pathogenesis. The strong association of the CD40 gene with susceptibility to RA was robustly replicated in another study in a large UK cohort of 3,962 patients with RA. Orozso et al., *Ann. Rheum. Dis*. 69: 813-816 (2010).

A major role of CD40L has also been found in the pathogenesis of juvenile idiopathic arthritis (JIA). Prahalad et al., *Pediatric Rheumatology* 6: 1-8 (2008). JIA is a heterogeneous group of arthropathies of unknown etiology. It was found that sCD40L was significantly elevated in the serum of children with JIA, along with some cytokines. Logistic regression analysis suggested that sCD40L, as well as IL-6 and TNFα, were positively associated with JIA. sCD40L was elevated in all JIA subtypes, with highest levels among more severe subtypes. These results implicated sCD40L as a potential biomarker for treatment and monitoring of patients with JIA.

It has also been demonstrated that activated T cells from patients with psoriatic arthritis (PsA), and particularly those with active disease, have a significantly increased expression of CD40L. Daoussis et al., *Rheumatology* 46: 227-231 (2007). These results indicate a role of the CD40-CD40L pathway in the pathogenesis of PsA and that a therapy selectively targeting CD40L could benefit PsA patients.

4.5. Systemic Sclerosis *In Vivo* Models:

Systemic sclerosis (SSc) is an autoimmune connective tissue disorder characterized by fibrous and vascular changes in the skin and internal visceral organs. In a study involving 52 Japanese patients with SSc, serum sCD40L levels were elevated when compared with healthy controls. Komura et al., *J. Reumatol*. 31: 514-519 (2004). Moreover, levels of sCD40L in patients with SSc were higher than in patients with systemic lupus erythematosus (SLE) who had elevated sCD40L levels compared to controls, and sCD40L levels correlated positively with C reactive peptide levels in SSc patients. It has also been reported that blockade of CD40L with anti-CD40L antibody in cultured T and B cells from SSc patients inhibited anti-topoisomerase I antibody production. Kuwana et al., *J. Immunol*. 155: 2703-2714 (1995). These results suggest that inhibition of CD40-CD40L interactions may be potential therapeutic targets in therapy of SSc as well as SLE.

4.6. Atherosclerosis *In Vivo* Models:

Several studies have suggested a role of CD40-CD40L signaling pathway during atherogenesis. Mach et al. demonstrated that in mice, treatment with monoclonal anti-CD40L antibody limited atherosclerosis in mice lacking receptor for low-density lipoprotein that had been fed a high-cholesterol diet for 12 weeks. Nature 394: 200-203 (1998). The antibody reduced the size of aortic atherosclerotic lesions by 59% and their lipid content by 79%. Additionally, atheroma of mice treated with anti-CD40L antibody contained significantly fewer macrophages and T lymphocytes, and exhibited decreased expression of vascular cell adhesion molecule-1.

Anti-CD40L antibody treatment of low-density lipoprotein receptor-deficient mice during the second half of a 26-week regimen of a high-cholesterol diet did not regress, but did significantly reduce further progression of established atherosclerotic lesions within the aortic arch and particularly the thoracic and abdominal aorta, as compared to control treatment. Schonbeck et al., *Proc. Natl. Acad. Sci.* 97: 7458-7463 (2000). Furthermore, anti-CD40L treatment changed the composition of atheroma in manners thought to favor plaque stability, e.g., reduced relative content of macrophages and lipid, as well as increased relative content of smooth muscle cells and collagen. These studies lend support to the importance of the CD40-CD40L signaling pathway in atherosclerosis and its complications, such as coronary artery disease.

4.7. Allograft Rejection *In Vivo* Models:

Targeting the CD40-CD40L pathway has long been of much interest for prevention of rejection of solid organ transplants (SOT), particularly in light of the promising data from numerous published transplant studies in non-human primates. It has been demonstrated that reduced CD40L expression on *ex vivo* activated CD4+ T lymphocytes correlates with excellent renal allograft function. Lederer et al., *Int. Arch. Allergy Immunol*. 133: 276-284

(2004). Furthermore, several studies have demonstrated that anti-CD40L mAbs can both prevent and reverse acute allograft rejection in primates. For example, Kirk et al., *Proc. Natl. Acad. Sci. USA* 94: 8789-8794 (1997) reported that, in rhesus monkeys transplanted with renal allografts, anti-CD40L mAb 5C8 alone or in combination with CTLA4-Ig significantly prolonged rejection-free survival. The CD40L-specific mAb hu5c8 alone also allowed for allogeneic islet engraftment and long-term insulin independence in rhesus monkeys that were transplanted an adequate number of viable pancreatic islets. Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137 (1999). Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005) performed renal transplants in MHC-mismatched rhesus monkeys and treated the recipients with combinations of CD40L-specific mAb IDEC-131, and/or sirolimus, and/or pre-transplant donor-specific transfusion. IDEC-131 was highly effective in preventing renal allograft rejection in primates. In cynomolgus monkeys that underwent renal allotransplantation, treatment with anti-CD40L mAb ABI793 effectively prevented graft rejection. Schuler et al., *Transplantation* 77: 717-726 (2004). In addition to preventing allograft rejection, CD40L-specific mAbs induced donor specific tolerance in primate transplant models. Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005); Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137 (1999).

In pediatric human patients that were undergoing acute graft rejection after liver or small-bowel transplantation, a correlation was observed between the expression of CD40L on CD8+ T cells and the risk of transplant rejection. Ashokkumar et al., *Amer. J. Transplantation* 9: 179-191 (2009) and Ashokkumar et al., *Surgery* 146: 166-173 (2009). Similarly, in adult patients that were undergoing allograft rejection following liver or renal transplantation, histological analysis demonstrated an association between CD40L expression and acute or chronic rejection. Bartlett et al., *Amer. J. Transplantation* 3: 1363-1368 (2003) and Biancone et al., *Nephrol. Diall. Translpant*. 13: 716-722 (1998).

Several studies support targeting CD40L over CD40 to achieve better efficacy in transplantation. For example, graft survival is longer and more durable when CD40L is selectively blocked, compared to CD40. Gilson et al., *J. Immunol.* 183: 1625-35 (2009). Furthermore, recent data suggest that CD40L blockade may enhance induction of Tregs and/or suppressor cells to promote graft survival. Garcia et al., *J. Clin. Inv*. 120: 2486-96 (2010). Also, blockade of CD40L, but not CD40, has demonstrated induction of long-lived immunological tolerance resulting in indefinite graft survival, particularly when combined with blockade of the B7 pathway. Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137

(1999); Kawai et al., *Amer. J. Transplantation* 4: 1391-1398 (2004); Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005); Adams et al., *J. Immunol*. 174: 542-50 (2005). The synergy of blocking CD40-40L and B7-CD28 pathways in enhancing graft survival is especially important, because it presents the presently disclosed domain antibodies as a natural choice for combination with belatacept (CTLA4-Ig) for SOT.

4.8. Graft-versus-Host Disease *In Vivo* Model:

Chronic and acute graft-versus-host disease (cGVHD and aGVHD) are complications that can occur after a stem cell or bone marrow transplant in which the transplanted donor cells attack the transplant recipient's body. Acute GVHD in humans takes place withing about 60 days post-transplantation and results in damage to the skin, liver, and gut by the action of cytolytic lymphocytes. Chronic GVHD occurs later and is a systemic autoimmune disease that affects primarily the skin, resulting in the polyclonal activation of B cells and the hyperproduction of Ig and autoantibodies.

CD40L-CD40 interactions appear to be critical in the development of both cGVHD and aGVHD. Durie et al., *J. Clin. Invest*. 94: 1333-1338 (1994). In a mouse *in vivo* model, anti-CD40L antibodies blocked the following cGVHD-associated phenomena: splenomegaly, in vitro polyclonal Ig production, elevated levels of serum IgE and serum anti-DNA autoantibodies, and the generation of anti-host cytotoxic T cells. Antibody production remained inhibited for extended periods of time after the end of anti-CD40L antibody administration. In mice with aGVHD, which is associated with the induction of a profound antiallogenic cytotoxic T cell (CTL) response, treatment with anti-CD40L prevented the generation of H-2b-derived CTL. The results of the study suggest that CD40L-CD40 interactions are critical in GVHD and that CD40L may be a valuable ligand for targeting immunotherapeutic agents to control GVHD.

4.9. Myasthenia Gravis *In Vivo* Model:

Myasthenia gravis (MG) and its animal model, experimental autoimmune MG (EAMG), are T-cell dependent autoimmune disorders caused by autoantibodies against the nicotinic acetylcholine receptors (AChR) at the neuromuscular junction of skeletal muscle. The role of CD40-CD40L in EAMG was shown in CD40L (CD40L-/-) knockout mice. Shi et al, *Eur. J. Immunol*. 28: 3587-3593 (1998). The CD40L knockout mice were completely resistant to EAMG induction and had diminished Th1 and Th2 responses as well as severely impaired T-cell dependent AChR-reactive B cell responses.

It has also been demonstrated that blockade of CD40L-CD40 signaling by anti-CD40L antibodies is capable of suppressing EAMG. Im et al., *J. Immunol.* 166: 6893-6898 (2001). Antibodies given to rats at the chronic stage of EAMG suppress the clinical progression of the autoimmune response and lead to a decrease in the AChR-specific humoral response and delayed-type hypersensitivity. The effect of anti-CD40L treatment during the chronic phase of EAMG is of particular relevance to human MG, which is a chronic disease. It suggests that antagonizing CD40L can be used for immunotherapy of MG and other antibody-mediated autoimmune diseases.

5. Thromboembolism

CD40-CD40L interactions on T and antigen presenting cells are important for adaptive immune responses, such as B-cell proliferation, immunoglobulin (Ig) production, upregulation of co-stimulatory activity (CD80, CD86), cytokine production, and Ig class-switching. The receptor and ligand are also expressed on platelets (off-target cell population), where CD40 is constitutively found on platelets, while CD40L is expressed on activated platelets and cleaved to sCD40L (>90% of circulating sCD40L is derived from platelets). Feroni et al., *Curr. Med. Chem.* 14: 2170-2180 (2007). At least three anti-CD40L monoclonal antibodies (mAb) caused TE in the clinic and/or nonclinical studies conducted in non-human primates (NHP). hu5c8 (BG9588) caused TE in multiple clinical trials (lupus and renal transplantation). Boumpas et al., *Arthritis & Rheumatism* 48: 719-727 (2003). IDEC131 caused TE in one patient in a Crohn's disease trial, leading to termination of ongoing trials at the time. Sidiropoulus & Boumpas, Lupus 13: 391-397 (2004). Both hu5c8 and ABI1793 (which binds CD40 at a different epitope from 5c8) caused TE/thrombosis in renal transplantation studies in cynomolgus or rhesus monkeys. Schuler et al., *Transplantation* 77: 717-726 (2004); Kanmaz et al., *Transplantation* 77: 914-920 (2004); Koyama et al., Transplantation 77: 460-461 (2004). In a non-published disclosure, Biogen reported a thrombosis incidence of 1/4 and 6/12 in rhesus monkeys given 5 and 20 mg/kg weekly, respectively, for 6-months, but not in cynomolgus monkeys given 50 mg/kg at the same frequency and duration. The basis for the species difference is not clear.

One of the hypotheses is that the TE associated with administration of these antibodies is mediated by anti-CD40Lmab-CD40L immune complex (IC)-mediated cross linking of platelets, facilitated by IC binding to FcgRIIa, an IgG Fc receptor, causing activation and aggregation (FIG. 10). Blocking the interaction of Fc moiety of IgG with

FcgRIIa is, therefore, expected to mitigate platelet cross linking and thrombosis. Approaches and methods developed to evaluate the risk for TE/thrombosis are described in Examples below.

EXAMPLES

TABLE 1 lists representative anti-human CD40L VH domain amino acid sequences useful for the disclosed antibody polypeptides. TABLE 2 discloses representative nucleic acids that encode the VH domain sequences listed in TABLE 1. TABLE 3 lists representative anti-human CD40L VK domain amino acid sequences useful for the antibody polypeptides of the present disclosure. TABLE 4 in turn discloses representative nucleic acids that encode the VK domain sequences listed in TABLE 3. As well known in the art, multiple codons can encode the same amino acid. Nucleic acids encoding a protein sequence thus include nucleic acids having codon degeneracy. The antibody polypeptides disclosed in TABLE 1 and TABLE 3 specifically bind CD40L. They were made using the reiterative initial/primary screening and affinity methodologies described in the examples that follow.

TABLE 1

Anti-human CD40L VH Domain Amino Acid Sequences

BMS2h-10 (SEQ ID NO: 15)
EVQLLESGGG LVQPGGSLRL SCAASGFTFI AYDMSWVRQA PGKGLEWVSW IDEWGLQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKT PEE------- FDYWGQGTLV TVSS

BMS2h-11 (SEQ ID NO: 16)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYEMSWVRQA PGKGLEWVSG IDGEGSDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RS-------- FDYWGQGTLV TVSS

BMS2h-111 (SEQ ID NO: 17)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYPMTWVRQA PGKGLEWVST IHGSGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP YTSRHNSLGH FDYWGQGTLV TVSS

BMS2h-112 (SEQ ID NO: 18)
EVQLLESGGG LVQPGGSLRL SCAASGFTFM DYPMGWVRQA PGKGLEWVSS IGPVGMSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG GTSGRHNTK- FDYWGQGTLV TVSS

BMS2h-113 (SEQ ID NO: 19)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT EYPMSWVRQA PGKGLEWVSV ISPLGFTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT GGSGILNSS- FDYWGQGTLV TVSS

BMS2h-114 (SEQ ID NO: 20)
EVQLLESGGG LVQPGGSLRL SCAASGFRVS NYDLTWVRQA PGKGLEWVST ISATNGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAAVT WWLLRHNDN- LGFWGQGTLV TVSS

BMS2h-115 (SEQ ID NO: 21)

EVQLLESGGG LVQPGGSLRL SCAASGFSIS YKNMAWVRQA PGKGLEWVSA IKAANGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCATGS QKKRTYT--- FDFWGQGTLV TVSS

BMS2h-12 (SEQ ID NO: 22)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR LYEMAWVRQA PGKGLEWVSG IDILGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDL SWQG------ FDYWGQGTLV TVSS

BMS2h-120 (SEQ ID NO: 23)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR SYTMGWVRQA PGKGLEWVSS INPMGYQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHG VGKGTKPHN FDYWGQGTLV TVSS

BMS2h-121 (SEQ ID NO: 24)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE LYRMSWVRQA PGKGLEWVSE ISGSGFPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSL HDKTQHHQE FDYWGQGTLV TVSS

BMS2h-123 (SEQ ID NO: 25)
EVQLLESGGG LVQPGGSLRL SCAASGFTFI EYPMRWVRQA PGKGLEWVSL ISPSGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD ESST FDYWGQGTLV TVSS

BMS2h-124 (SEQ ID NO: 26)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYDMDWVRQA PGKGLEWVST IGSSGYPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAERM PGYFPGFARQ FDYWGQGTLV
TVSS

BMS2h-125 (SEQ ID NO: 27)
EVQLLESGGG LVQPGGSLRL SCAASGFTFW RYAMGWVRQA PGKGLEWVST INDEGRETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKR VSSSVNAPYE FDYWGQGTLV TVSS

BMS2h-126 (SEQ ID NO: 28)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA NYSMSWVRQA PGKGLEWVSS IDRLGTHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVL ADLIAGHAE FDYWGQGTLV TVSS

BMS2h-127 (SEQ ID NO: 29)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP SYDMAWVRQA PGKGLEWVSG ISRSGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGV DAHVYYMEPF FDYWGQGTLV TVSS

BMS2h-128 (SEQ ID NO: 30)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYQMAWVRQA PGKGLEWVST ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG TV FDYWGQGTLV TVSS

BMS2h-129 (SEQ ID NO: 31)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP KYEMAWVRQA PGKGLEWVSS IDGDGKSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD QF FDYWGQGTLV TVSS

BMS2h-13 (SEQ ID NO: 32)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS YYSMYWVRQA PGKGLEWVSS ISPFGWGTYY
ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCAKYG ETSGPISEN FDYWGQGTLV TVSS

BMS2h-130 (SEQ ID NO: 33)
EVQLLESGGG LVQPGGSLRL SCTASGFTFA GYQMSWVRQA PGKGLEWVSS ITNEGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KY FDYWGQGTLV TVSS

BMS2h-131 (SEQ ID NO: 34)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EYEMVWVRQA PGKGLEWVSS ITSDGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG IRFDYWGQGTLV TVSS

BMS2h-132 (SEQ ID NO: 35)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYDMAWVRQA PGKGLEWVSG IVDDGLMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD VAFDYWGQGTLVTVSN

BMS2h-133 (SEQ ID NO: 36)
EVQLLESGGG LVQPGGSLRL SCAASGFTFI GYAMAWVRQA PGKGLEWVSS IGPLGATTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP AGTSSHSVDFDYWGQGTLV TVSS

BMS2h-134 (SEQ ID NO: 37)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYEMTWVRQA PGKGLEWVSS ITSDGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS VQ FDYWGQGTLV TVSS

BMS2h-135 (SEQ ID NO: 38)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR RYVMGWVRQA PGKGLEWVSW IEADGRTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL TDQHVIE FDYWGQGTLV TVSS

BMS2h-136 (SEQ ID NO: 39)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD GYRMGWVRQA PGKGLEWVSS IAPDGNYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFW GMQFDYWGQGTLV TVSS

BMS2h-137 (SEQ ID NO: 40)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYPMGWVRQA PGKGLEWVSS IGPIGFTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEMK SPYKPQ---- FDYWGQGTLV TVSS

BMS2h-138 (SEQ ID NO: 41)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL AYWMVWVRQA PGKGLEWVSS ISPSGTHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRVED TAVYYCAKYT EPGLGS---- FDYWGQGTLV TVSS

BMS2h-139 (SEQ ID NO: 42)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYEMGWVRQA PGKGLEWVSV ISEVGSLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPH DSSIG----- FDYWGQGTLV TVSS

BMS2h-14 (SEQ ID NO: 43)
EVQLLESGGG LVQPGGSLRL SCAASGFTFW SYDMTWVRQA PGKGLEWVSS IMASGDDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWD RD-------- FDYWGQGTLV TVSS

BMS2h-15 (SEQ ID NO: 44)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYVMSWVRQA PGKGLEWVST ISPIGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEFP LIILPD---- FDYWGQGTLV TVSS

BMS2h-16 (SEQ ID NO: 45)
EVQLLESGGG LVQPGGSLRL SCAASGFTFM EYAMIWVRQA PGKGLEWVSI ISPLGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYQ DSSDSQYTN- FDYWGQGTLV TVSS

BMS2h-17 (SEQ ID NO: 46)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE DYGMGWARQA PGKGLEWVSS IGPLGLWTYY
ADSAKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSP LEGLITN--- FDYWGQGTLV TVSS

BMS2h-176 (SEQ ID NO: 47)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD AYEMGWVRQA PGKGLEWVSI IDWDGNSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG DNVGI----- FDYWGQGTLV TVSS

BMS2h-177 (SEQ ID NO: 48)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYYMVWVRQA PGKGLEWVSA IDEWGFATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHW EFTSDTSR—FDYWGQGTLV TVSS

BMS2h-178 (SEQ ID NO: 49)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE DFDMAWVRQA PGKGLEWVSS INDQGSLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD QF-------- FDYWGQGTLV TVSS

BMS2h-179 (SEQ ID NO: 50)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYDMMWVRQA PGKGLEWVSR ISPQGQRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR GQSRIPMR—FDYWGQGTLV TVSS

BMS2h-18 (SEQ ID NO: 51)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP EYDMTWVRQA PGKGLEWVSY ISSDGYSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPH GSPRE----- FDYWGQGTLV TVSS

BMS2h-180 (SEQ ID NO: 52)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DYEMGWVRQA PGKGLEWVST ITSLGESTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RI-------- FDYWGQGTLV TVSS

BMS2h-181 (SEQ ID NO: 53)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA FYPMMWVRQA PGKGLEWVSW IDATGTRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGN YGSSYTMGV- FDYWGQGTLV TVSS

BMS2h-182 (SEQ ID NO: 54)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD EYPMYWVRQA PGKGLEWVSS IGPSGPNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSP YFDVIPSY—FDYWGQGTLV TVSS

BMS2h-183 (SEQ ID NO: 55)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYGMGWVRQA PGKGLEWVSS IQSSGLRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRA NSRRG----- FDYWGQGTLV TVSS

BMS2h-184 (SEQ ID NO: 56)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYEMMWVRQA PGKGLEWVSS ITSHGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KD-------- FDYWGQGTLV TVSS

BMS2h-185 (SEQ ID NO: 57)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA HYPMSWVRQA PGKGLEWVSS IGRLGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRA TPVPIKGL—FDYWGQGTLV TVSS

BMS2h-186 (SEQ ID NO: 58)
EVQLLESGGG LVQPGGSLRL SCAASGLTFG RYEMAWVRQA PGKGLEWVSS IDSDGWVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQPD SL-------- FDYWGQGTLV TVSS

BMS2h-187 (SEQ ID NO: 59)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYSMVWVRQA PGKGLEWVSG INRGGTRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGW RRG------- FDYWGQGTLV TVSS

BMS2h-188 (SEQ ID NO: 60)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT RYRMSWVRQA PGKGLEWVSG ISRDGYRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGM TAS------- FDYWGQGTLV TVSS

BMS2h-189 (SEQ ID NO: 61)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ MYPMGWVRQA PGKGLEWVSM IEPAGDLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYQ EQPW------ FDYWGQGTLV TVSS

BMS2h-19 (SEQ ID NO: 62)
EVQLLESGGG LVQPGGSLRL SCAASGFPFP QYQMAWVRQA PGKGLEWVSM ITSDGLDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPE PL-------- FDYWGQGTLV TVSS

BMS2h-190 (SEQ ID NO: 63)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS MYDMHWVRQA PGKGLEWVST ILSDGTDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG AM-------- FDYWGQGTLV TVSS

BMS2h-191 (SEQ ID NO: 64)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK LYPMTWVRQA PGKGLEWVSS IDAGGHETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDW WDYL------ FDYWGQGTLV TVSS

BMS2h-192 (SEQ ID NO: 65)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYPMSWVRQA PGKGLEWVSS INRSGMRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGH QAP------- FDYWGQGTLV TVSS

BMS2h-193 (SEQ ID NO: 66)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT GYAMSWVRQA PGKGLEWVST INANGIRTYY
ADSVKGRFTI SRDNSKNTLY LQMNGLRAED TAVYYCAKGG VWRWGTGHK- FDYWGQGTLV
TVSS

BMS2h-194 (SEQ ID NO: 67)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK QYDMRWVRQA PGKGLEWVST ISQNGTKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSR TGRY------ FDYWGQGTLV TVSS

BMS2h-195 (SEQ ID NO: 68)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG TYDMGWVRQA PGKGLEWVSR INWQGDRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG FGHYVDGLG- FDYWGQGTLV TVSS

BMS2h-196 (SEQ ID NO: 69)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS GYEMAWVRQA PGKGLEWVSS ITDMGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG TA-------- FDYWGPGTLV TVSS

BMS2h-197 (SEQ ID NO: 70)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA KYKMWWVRQA PGKGLEWVSS ITPKGHSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRP MTP------- FDYWGQGTLV TVSS

BMS2h-198 (SEQ ID NO: 71)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYNMSWVRQA PGKGLEWVSS IRPRGGKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWR REGYTGSK—FDYWGQGTLV TVSS

BMS2h-199 (SEQ ID NO: 72)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYGMTWVRQA PGKGLEWVSS IWPRGQKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGN SRYV------ FDYWGQGTLV TVSS

BMS2h-2 (SEQ ID NO: 73)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYEMMWVRQA PGKGLEWVST ITSDGISTYY
ADSVKGRFTI FRDNSKNTLY LQMNSLRAED TAVYYCAKSG RF-------- FDYWGQGTLV TVSS

BMS2h-20 (SEQ ID NO: 74)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS GYQMAWVRQA PGKGLEWVSG ISSEGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG RR-------- FDYWGQGTLV TVSS

BMS2h-200 (SEQ ID NO: 75)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT NYSMGWVRQA PGKGLEWVST IRPNGTKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRS SAHLQR---- FDYWGQGTLV TVSS

BMS2h-201 (SEQ ID NO: 76)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NYSMGWVRQA PGKGLEWVSS IGRHGGRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKG STYPR----- FDYWGQGTLV TVSS

BMS2h-202 (SEQ ID NO: 77)
EVQLLESGGG LVQPGGSLRL SCTASGFTFS HYEMGWVRQA PGKGLEWVSS IEPFGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVY PQGS------ FDYWGQGTLV TVSS

BMS2h-203 (SEQ ID NO: 78)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYTMGWVRQA PGKGLEWVSS IRPDGKITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEVY SSCAMCTPLL FDYWGQGTLV TVSS

BMS2h-204 (SEQ ID NO: 79)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYSMAWVRQA PGKGLEWVSD IGPRGFSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG RGQRDTSQP- FDYWGQGTLV TVSS

BMS2h-205 (SEQ ID NO: 80)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYQMAWVRQA PGKGLEWVSG ITSGGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RG-------- FDYWGQGTLV TVSS

BMS2h-206 (SEQ ID NO: 81)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYEMTWVRQA PGKGLEWVSG ISSDGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VL-------- FDYWGQGTLV TVSS

BMS2h-207 (SEQ ID NO: 82)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD KYLMSWVRQA PGKGLEWVSG IEPLGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEA SGD------- FDYWGQGTLV TVSS

BMS2h-208 (SEQ ID NO: 83)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT EYEMSWVRQA PGKGLEWVSS IDNVGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KL-------- FDYWGQGTLV TVSS

BMS2h-209 (SEQ ID NO: 84)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYEMWWVRQA PGKGLEWVSA ISRQGFATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDL ERDD------ FDYWGQGTLV TVSS

BMS2h-21 (SEQ ID NO: 85)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA NYEMGWARQA PGKGLEWVSV ISEWGYSTYY
ADSAKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLV GGTQYE---- FDYWGQGTLV TVSS

BMS2h-22 (SEQ ID NO: 86)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH NYEMSWVRQA PGKGLEWVSS ISSGGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VK-------- FDYWGQGTLV TVSS

BMS2h-23 (SEQ ID NO: 87)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG LYEMTWVRQA PGKGLEWVSS ITGDGISTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKAG RK-------- FDYWGQGTLV TVSS

BMS2h-24 (SEQ ID NO: 88)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYQMAWVRQA PGKGLEWVSS ITSEGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KN-------- FDYWGQGTLV TVSS

BMS2h-24-1 (SEQ ID NO: 89)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYQMAWVRQA PGKGLEWVSS ITSEGGSTYY
ADSVKGRFTI SRDNSKNTVY LQMNSLRAED TAVYYCAKPG KN-------- FDYWGQGTLV TVSS

BMS2h-25 (SEQ ID NO: 90)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NYEMTWVRQA PGKGLEWVST ITSQGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RS-------- FDYWGQGTLV TVSS

BMS2h-26 (SEQ ID NO: 91)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR SYEMTWVRQA PGKGLEWVSS ITSDGGTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KT-------- FDYWGQGTLV TVSS

BMS2h-27 (SEQ ID NO: 92)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN LYEMTWVRQA PGKGLEWVSS ITSDGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD SP-------- FDYWGQGTLV TVSS

BMS2h-28 (SEQ ID NO: 93)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HYDMAWVRQA PGKGLEWVST ISDNGNGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RD-------- FDYWGQGTLV TVSS

BMS2h-29 (SEQ ID NO: 94)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG RYQMAWVRQA PGKGLEWVSS ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RA-------- FDYWGQGTLV TVSS

BMS2h-30 (SEQ ID NO: 95)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA RYQMAWVRQA PGKGLEWVST ISDDGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLD KL-------- FDYWGQGTLV TVSS

BMS2h-300 (SEQ ID NO: 96)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NDEMTWVRQA PGKGLEWVSA IDTTGGQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KE-------- FDYWGQGTLV TVSS

BMS2h-301 (SEQ ID NO: 97)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG ESEMSWVRQA PGKGLEWVSS ILDEGSGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KD-------- FDYWGQGTLV TVSS

BMS2h-302 (SEQ ID NO: 98)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSA ITDDGDDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN AGA------- FDYWGQGTLV TVSS

BMS2h-303 (SEQ ID NO: 99)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE VYDMAWVRQA PGKGLEWVSG IVNDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KD-------- FDYWGQGTLV TVSS

BMS2h-304 (SEQ ID NO: 100)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NTEMTWVRQA PGKGLEWVSS IADDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG QA-------- FDYWGQGTLV TVSS

BMS2h-31 (SEQ ID NO: 101)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYQMAWVRQA PGKGLEWVST ISDDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD LY-------- FDYWGQGTLV TVSS

BMS2h-32 (SEQ ID NO: 102)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE VYQMGWVRQA PGKGLEWVSF IVPGGDLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETW PE-------- FDYWGQGTLV TVSS

BMS2h-4 (SEQ ID NO: 103)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NYEMTWVRQA PGKGLEWVSS ITSDGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN PP-------- FDYWGQGTLV TVSS

BMS2h-40 (SEQ ID NO: 104)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK AYDMGWVRQA PGKGLEWVSQ IGRDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPR RYAIF----- TFDRGQGTLV TVSS

BMS2h-400 (SEQ ID NO: 105)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK QYPMVWVRQA PGKGLEWVST ISTNGVRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT DIISSSE--- FDYWGQGTLV TVSS

BMS2h-401 (SEQ ID NO: 106)
EVQLLESGGG LVQPGGSLRL SCAASGFTFF NYDMSWVRQA PGKGLEWVSA ISGSGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVF VWSADIDFD- FDYWGQGTLV TVSS

BMS2h-402 (SEQ ID NO: 107)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS WYDMSWVRQA PGKGLEWVSH IASWGGKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVT VKDGGYLMD- FDYWGQGTLV TVSS

BMS2h-403 (SEQ ID NO: 108)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA EYAMAWVRQA PGKGLEWVSS IGRDGAVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWK AAKERGSW—FDYWGQGTLV TVSS

BMS2h-404 (SEQ ID NO: 109)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ AYQMQWVRQA PGKGLEWVST ISPNGLFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWL SS-------- FDYWGQGTLV TVSS

BMS2h-407 (SEQ ID NO: 110)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA MYSMAWVRQA PGKGLEWVSG ISPRGVETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTN WNGVDL---- FDYWGQGTLV TVSS

BMS2h-408 (SEQ ID NO: 111)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP TYMMSWVRQA PGKGLEWVST INTNGRDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD SNMSF----- FDYWGQGTLV TVSS

BMS2h-409 (SEQ ID NO: 112)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GYSMTWVRQA PGKGLEWVSS INASGTLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDG NRSEVF---- FDYWGQGTLV TVSS

BMS2h-41 (SEQ ID NO: 113)
EVQLLESGGG LVQPGGSLRL SCAASGFTFF EYEMTWVRQA PGKGLEWVSS IANDGSTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RQ-------- FDYWGQGTLV TVSS

BMS2h-410 (SEQ ID NO: 114)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ DYLMAWVRQA PGKGLEWVSE INQDGTVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAESS PY-------- FDYWGQGTLV TVSS

BMS2h-411 (SEQ ID NO: 115)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NYAMSWVRQA PGKGLEWVSS ISRDGHVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS SKGGTFASS- FDYWGQGTLV TVSS

BMS2h-412 (SEQ ID NO: 116)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AVPMTWVRQA PGKGLEWVSA ITDDGLRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGH IYGDY----- FDYWGQGTLV TVSS

BMS2h-413 (SEQ ID NO: 117)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE LYRMMWVRQA PGKGLEWVSA ISSDGDTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEHW LGTTLSLRD- FDYWGQGTLV TVSS

BMS2h-414 (SEQ ID NO: 118)
EVQLLESGGG LVQPGGSLRL SCAASGFTFY RYTMAWVRQA PGKGLEWVSQ ISPRGNITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSG VAGAESPEY- FDYWGQGTLV TVSS

BMS2h-415 (SEQ ID NO: 119)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL GYYMSWIRQA PGKGLEWVST IGPIGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSQ NIYGP----- FDYWGQGTLV TVSS

BMS2h-416 (SEQ ID NO: 120)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE QYDMAWVRQA PGKGLEWVSE ISRDGGRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEEY PY-------- FDYWGQGTLV TVSS

BMS2h-417 (SEQ ID NO: 121)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP QYSMVWVRQA PGKGLEWVST ISPLGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKMS KLLLSRE--- FDYWGQGTLV TVSS

BMS2h-418 (SEQ ID NO: 122)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA MYSMAWVRQA PGKGLEWVSG ISPRGVETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTN WNGVDL---- FDYWGQGTLV TVSS

BMS2h-419 (SEQ ID NO: 123)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT RHGMAWVRQA PGKGLEWVST ITPTGNTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDA HDEGY----- FDYWGQGTLV TVSS

BMS2h-42 (SEQ ID NO: 124)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG PYEMTWVRQA PGKGLEWVSS IVGDGLDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RV-------- FDYWGQGTLV TVSS

BMS2h-420 (SEQ ID NO: 125)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG STPMMWVRQA PGKGLEWVSE IRDTGLATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASVS ---------- FDYWGQGTLV TVSS

BMS2h-421 (SEQ ID NO: 126)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH LGDMHWVRQA PGKGLEWVSS ISGTGHTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPM NDQG------ FDYWGQGTLV TVSS

BMS2h-422 (SEQ ID NO: 127)
EVQLLESGGG LVQPGGSLRL SCAASGFTFM DEDMLWVRQA PGKGLEWVSR INSLGTHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSF MM-------- FDYWGQGTLV TVSS

BMS2h-423 (SEQ ID NO: 128)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR NYQMHWVRQA PGKGLEWVSG IDATGRATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARST RS-------- FDYWGQGTLV TVSS

BMS2h-424 (SEQ ID NO: 129)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT NADMVWVRQA PGKGLEWVSS ISGSGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY LTSH------ FDYWGQGTLV TVSS

BMS2h-425 (SEQ ID NO: 130)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYSMAWVRQA PGKGLEWVST ITPSGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS QAVTRS---- FDYWGQGTLV TVSS

BMS2h-426 (SEQ ID NO: 131)
EVQLLESGGD LVQPGGSLRL SCAASGFTFS DEGMMWVRQA PGKGLEWVSE INQQGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTI GM-------- FDYWGQGTLV TVSS

BMS2h-427 (SEQ ID NO: 132)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DQPMVWVRQA PGKGLEWVSS IGARGGPTYY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAKWF DIIAWDPFS- FDYWGQGTLV TVSS

BMS2h-428 (SEQ ID NO: 133)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN QYPMMWVRQA PGKGLEWVSS ITPSGFLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWN PFITT----- FDYWGQGTLV TVSS

BMS2h-429 (SEQ ID NO: 134)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFD YSLR------ FDYWGQGTLV TVSS

BMS2h-43 (SEQ ID NO: 135)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYEMAWVRQA PGKGLEWVSS IGSDGGPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKPD RA-------- FDYWGQGTLV TVSS

BMS2h-430 (SEQ ID NO: 136)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AEQMTWARQA PGKGLEWVST ITPHGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWR TLVDWPTSES FDYWGQGTLV
TVSS

BMS2h-44 (SEQ ID NO: 137)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT SYEMGWVRQA PGKGLEWVSS IEPTGITTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPH FTELG----- FDYWGQGTLV TVSS

BMS2h-449 (SEQ ID NO: 138)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GEQMAWVRQA PGKGLEWVST ITLPGPYTFY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGN GTF------- FDYWGQGTLV TVSS

BMS2h-45 (SEQ ID NO: 139)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NYAMAWVRQA PGKGLEWVSK IGAQGLHTYY
AGSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQT TMDYER---- FDYWGQGTLV TVSS

BMS2h-450 (SEQ ID NO: 140)

EVQLLESGGG LVQPGGSLRL SCAASGFTFD EVDMSWVRQA PGKGLEWVSA IGNNGLKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA LSYRPPV--- FDYWGQGTLV TVSS

BMS2h-451 (SEQ ID NO: 141)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ DDTMSWVRQA PGKGLEWVST ITLKGPSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSR DGLY------ FDYWGQGTLV TVSS

BMS2h-452 (SEQ ID NO: 142)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SSPMAWVRQA PGKGLEWVSS IGRDGSTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS PYRR------ FDYWGQGTLV TVSS

BMS2h-453 (SEQ ID NO: 143)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DYSMVWVRQA PGKGLEWVST IVSHGGTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGK GYNAQY---- FDYWGQGTLV TVSS

BMS2h-454 (SEQ ID NO: 144)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFD YSLR------ FDYWGQGTLV TVSS

BMS2h-455 (SEQ ID NO: 145)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN DYDMIWVRQA PGKGLEWVST ISSHGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD VF-------- FDYWGQGTLV TVSS

BMS2h-456 (SEQ ID NO: 146)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS DS-------- FDYRGQGTLV TVSS

BMS2h-457 (SEQ ID NO: 147)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYEMAWVRQA PGKGLEWVSG IQSNGNITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAN SQVEY----- FDYWGQGTLV TVSS

BMS2h-458 (SEQ ID NO: 148)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG VEPMSWVRQA PGKGLEWVSN IGRDGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG KHGT------ FDYWGQGTLV TVSS

BMS2h-459 (SEQ ID NO: 149)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP EYRMMWVRQA PGKGLEWVSW IDERGSLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRR KGTKQ----- FDYWGQGTLV TVSS

BMS2h-46 (SEQ ID NO: 150)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE LYAMAWVRQA PGKGLEWVSG IGAVGETTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEA NNLSDNLV—FDYWGQGTLV TVSS

BMS2h-460 (SEQ ID NO: 151)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWS VEW------- FDYWGQGTLV TVSS

BMS2h-461 (SEQ ID NO: 152)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN SYTMNWVRQA PGKGLEWVSS INPWGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL VL-------- FDYWGQGTLV TVSS

BMS2h-462 (SEQ ID NO: 153)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD GDMMSWVRQA PGKGLEWVSS ITQLGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQN WRTLT----- FDYWGQGTLV TVSS

BMS2h-463 (SEQ ID NO: 154)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN AYGMMWVRQA PGKGLEWVSS ILSDGVITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA RGANF----- FDYWGQGTLV TVSS

BMS2h-464 (SEQ ID NO: 155)

EVQLLESGGG LVQPGGSLRL SCAASGFTFG HYMMVWVRQA PGKGLEWVSS ITPHGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEFN AIFSEA---- FDYWGQGTLV TVSS

BMS2h-465 (SEQ ID NO: 156)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYSMAWVRQA PGKGLEWVST ITPSGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS QAVTRS---- FDYWGQGTLV TVSS

BMS2h-466 (SEQ ID NO: 157)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD LYAMAWVRQA PGKGLEWVSM IGRDGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLA GSLRGR---- FDYWGQGTLV TVSS

BMS2h-467 (SEQ ID NO: 158)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN KASMGWVRQA PGKGLEWVST ITPHGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQR WGVE------ FDYWGQGTLV TVSS

BMS2h-468 (SEQ ID NO: 159)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ GYSMGWVRQA PGKGLEWVSS IAGRGGVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL YIYHSL---- FDYWGQGTLV TVSS

BMS2h-469 (SEQ ID NO: 160)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP GMEMSWVRQA PGKGLEWVSA ITGTGSTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY HP-------- FDYWGQGTLV TVSS

BMS2h-470 (SEQ ID NO: 161)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP MVAMSWVRQA PGKGLEWVSS IARDGNVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAKVS PTG------- FDYWGQGTLV TVSS

BMS2h-471 (SEQ ID NO: 162)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HQDMSWVRQA PGKGLEWVSG ITDDGESTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD YD-------- FDYWGQGTLV
TVSS

BMS2h-472 (SEQ ID NO: 163)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EYNMMWVRQA PGKGLEWVSQ ITRDGSRTYY
ADSVRGRFTI SRDNSRNTLY LQMNSLRAED SAVYYCAKLS NIG------- FDYWGQGTLV TVSS

BMS2h-473 (SEQ ID NO: 164)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYSMIWARQA PGKGLEWVSS ITPYGSYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTD YL-------- FDYWGQGTLV TVSS

BMS2h-474 (SEQ ID NO: 165)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD TYSMMWVRQA PGKGLEWVST ITPYGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWG LV-------- FDYWGQGTLV TVSS

BMS2h-475 (SEQ ID NO: 166)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT TGPMMWVRQA PGKGLEWVSA IGIGGDTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLT PSNQ------ FDYWGQGTLV TVSS

BMS2h-476 (SEQ ID NO: 167)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK QYQMMWVRQA PGKGLEWVSS ITPSGFLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWN PFIST----- FDYWGQGTLV TVSS

BMS2h-477 (SEQ ID NO: 168)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP NYDMVWVRQA PGKGLEWVSS ISALGNVTYY
ADSVKGRFTI SRDNSKNTLY LQTNSLRAED TAVYYCAKWR SAITGN----
FDYWGQGTLV TVSS

BMS2h-478 (SEQ ID NO: 169)

EVQLLESGGG LVQPGGSLRL SCAASGFTFK EYQMSWVRQA PGKGLEWVST ISPSGMNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWR SVVRPWPGV- FDYWGQGTLV
TVSS

BMS2h-479 (SEQ ID NO: 170)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DESMAWVRQA PGKGLEWVSS ITPHGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLH LKLYESH--- FDYWGQGTLV TVSS

BMS2h-480 (SEQ ID NO: 171)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GGEMGWVRQA PGKGLEWVSM IPMDGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG ST-------- FDYWGQGTLV TVSS

BMS2h-481 (SEQ ID NO: 172)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD FMPMAWVRQA PGKGLEWVSS IGRDGAYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLA SPAQ------ FDYWGQGTLV TVSS

BMS2h-482 (SEQ ID NO: 173)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DEPMLWVRQA PGKGLEWVSS IGGTGTTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGN QGDFINR--- FHYWGQGTLV TVSS

BMS2h-483 (SEQ ID NO: 174)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH AYNMAWVRQA PGKGLEWVST ISPRGSYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWP PPSSH----- FDYWGQGTLV TVSS

BMS2h-5 (SEQ ID NO: 175)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD GYEMAWVRQA PGKGLEWVSS ITSDGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG LR-------- FDYWGQGTLV TVSS

BMS2h-505 (SEQ ID NO: 176)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GYMMYWVHQA PGKGLEWVSS ISPQGHFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAELR ELPRL----- FDYWGQGTLV TVSS

BMS2h-506 (SEQ ID NO: 177)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMGWVRQA PGKGLEWVSS IDASGGPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAN GKKFPFTKY- FDYWGQGTLV TVSS

BMS2h-507 (SEQ ID NO: 178)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP SVHMAWVRQA PGKGLEWVSG INLTGVDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA TTRQAHPLY- FDYWGQGTLV TVSS

BMS2h-515 (SEQ ID NO: 179)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK EGEMYWVRQA PGKGLEWVST ISTNGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKST RDLG------ FAYWGQGTLV TVSS

BMS2h-516 (SEQ ID NO: 180)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYEMAWARQA PGKGLEWVSF ISPRGHFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPA KT-------- FDYWGQGTLV TVSS

BMS2h-517 (SEQ ID NO: 181)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD TYEMLWVRQA PGKGLEWVSR ISVDGSITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTR MR-------- FDYWGQGTLV TVSS

BMS2h-518 (SEQ ID NO: 182)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSN ISRDGSKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAQ SGGLRSGLTT FDYWGQGTLV TVSS

BMS2h-519 (SEQ ID NO: 183)
EVQLLESGGG LVQPGGSLRL SCADSGFTFS SYAMSWVRQA PGKGLEWVSS IGRDGAYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG PKGIA----- FDYWGQGTLV TVSS

BMS2h-520 (SEQ ID NO: 184)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS PHAMAWVRQA PGKGLEWVSG IDGGGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSD PP-------- FDYWGQGTLV TVSS

BMS2h-521 (SEQ ID NO: 185)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH AGEMHWVRQA PGKGLEWVSS ITLPGDMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN TGYT------ FDYWGQGTLV TVSS

BMS2h-522 (SEQ ID NO: 186)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NYGMSWVRQA PGKGLEWVSS ISWDGSLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQNT RL-------- FDYWGQGTLV TVSS

BMS2h-523 (SEQ ID NO: 187)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH DADMLWVRQA PGKGLEWVSG ILSPGEDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFG LP-------- FDYWGQGTLV TVSS

BMS2h-524 (SEQ ID NO: 188)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR TDQMNWVRQA PGKGLEWVSS ISPSGAYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL GA-------- FDYWGQGTLV TVSS

BMS2h-525 (SEQ ID NO: 189)
EVQLLESGGG LVQPGGSLRL SCAASGFIFE QYQMVWVRQA PGKGLEWVSW ISPDGTHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFS LRKMEK---- FDYWGQGTLV TVSS

BMS2h-526 (SEQ ID NO: 190)
EVQLLESGGG LVQPGGSLRL SCAASGFTFQ DEQMAWVRQA PGKGLEWVSS IASDGMSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQPG KN-------- FDHWGQGTLV TVSS

BMS2h-527 (SEQ ID NO: 191)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYAMSWVRQA PGKGLEWVSS ITTGGERTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRW NLYTES---- FDYWGQGTLV TVSS

BMS2h-528 (SEQ ID NO: 192)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG GQPMDWVRQA PGKGLEWVSS IAPDGIHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNL GQG------- FDYWGQGTLV TVSS

BMS2h-529 (SEQ ID NO: 193)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYQMTWVRQA PGKGLEWVSS ISPSGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWK AL-------- FDYWGQGTLV TVSS

BMS2h-530 (SEQ ID NO: 194)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP HSTMYWVRQA PGKGLEWVSL ILPSGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFS DER------- FDYWGQGTLV TVSS

BMS2h-531 (SEQ ID NO: 195)
EVQLSESGGG LVQPGGSLRL SCAASGFTFG DGNMDWVRQA PGKGLEWVSG ISSDGVTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR GQG------- FDYWGQGTLV TVSS

BMS2h-532 (SEQ ID NO: 196)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DYMMWWVRQA PGKGLEWVSS ISPHGVYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWL HT-------- FDYWGQGTLV TVSS

BMS2h-533 (SEQ ID NO: 197)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYTMAWGRQA PGKGLEWVSF IAGPGNYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG STATYNNGQ- FDYWGQGTLV TVSS

BMS2h-534 (SEQ ID NO: 198)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT EYSMVWVRQA PGKGLEWVSS ISGSGRVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWL KLVRAPNP—FDYWGQGTLV TVSS

BMS2h-535 (SEQ ID NO: 199)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYQMAWVRQA PGKGLEWVSG ISKTGHSTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKAS HSLGPL---- FDYWGQGTLV TVSS

BMS2h-54 (SEQ ID NO: 200)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT AYRMAWVRQA PGKGLEWVSW ISPSGSGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTL TDSPSGHYE- FDYWGQGTLV TVSS

BMS2h-55 (SEQ ID NO: 201)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA RYEMGWVRQA PGKGLEWVSR ITAQGLGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYL TDFSSGHQE- FDYWGQGTLV TVSS

BMS2h-553 (SEQ ID NO: 202)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DYGMSWVRQV PGKGLEWVSG ISHNGMLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYW PSTSWETD—FDYWGQGTLV TVSS

BMS2h-554 (SEQ ID NO: 203)
EVQLLESGGG SVQPGGSLRL SCAASGFTFG NEPMAWVRQA PGKGLEWVSS IEMQGKNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR GQG------- FDYWGQGTLV TVSS

BMS2h-555 (SEQ ID NO: 204)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSC IDNLGSPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAKTI SHQYDR---- FDYWGQGTLV TVSS

BMS2h-556 (SEQ ID NO: 205)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSS IDEGGRWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT PHKQLS---- FDYWGQGTLV TVSS

BMS2h-557 (SEQ ID NO: 206)
EVQLLESGGG LVQPGGSLRL SCAASGFSFA DEYMVWARQA PGKGLEWVSE IDPLGTGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG TA-------- FDYWGQGTLV TVSS

BMS2h-558 (SEQ ID NO: 207)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS THDMMWVRQA PGKGLEWVSS ISDDGISTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD MSLIE----- FDYWGQGTLV TVSS

BMS2h-559 (SEQ ID NO: 208)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD GTPMVWVRQA PGKGLEWVSG ISGDGRNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPY ALTSSKP--- FDYWGQGTLV TVSS

BMS2h-56 (SEQ ID NO: 209)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN DYTMGWVRQA PGKGLEWVSW IHGTGGQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAL ADRSGGVVE- FDYWGQGTLV TVSS

BMS2h-560 (SEQ ID NO: 210)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE AETMAWVRQA PGKGLEWVSC ISNDGNTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKES LISPGL---- FDYWGQGTLV TVSS

BMS2h-561 (SEQ ID NO: 211)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT GEYMNWVRQA PGKGLEWVST INETGYMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS TRGVP----- FDYWGQGTLV TVSS

BMS2h-562 (SEQ ID NO: 212)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR SYDMGWVRQA PGKGLEWVST ISPMGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSN QHAHDP---- FDYWGQGTLV TVSS

BMS2h-563 (SEQ ID NO: 213)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYDMGWVRQA PGKGLEWVSS ISPMGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAA LTEPM----- FDYWGQGTLV TVSS

BMS2h-564 (SEQ ID NO: 214)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYDMGWVRQA PGKGLEWVST ISPLGHFTYY
ADSVKGRSTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAE EA-------- FDYWGQGTLV TVSS

BMS2h-565 (SEQ ID NO: 215)
EVQLLESGGG LVQPGGSLRL SCAASGFAFP RYGMTWVRQA PGKGLEWVSN IDQFGMKTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEEY AS-------- FDYWGQGTLV TVSS

BMS2h-566 (SEQ ID NO: 216)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD KYDMGWVRQA PGKGLEWVST ISPMGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGR GNTSD----- FDYWGQGTLV TVSS

BMS2h-567 (SEQ ID NO: 217)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYDMAWVRQA PGKGLEWVST ISGAGHFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSF PRDE------ FDYWGQGTLV TVSS

BMS2h-568 (SEQ ID NO: 218)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP KYEMRWVRQA PGKGLEWVSE IGLDGSPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG DPNG------ FDYWGQGTLV TVSS

BMS2h-569 (SEQ ID NO: 219)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP TSEMDWVRQA PGKGLEWVSG IGPDGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHA DW-------- FDYWGQGTLV TVSS

BMS2h-57 (SEQ ID NO: 220)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS EYDMYWVRQA PGKGLEWVSW IDTDGGDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG LK-------- FDYWGQGTLV TVSS

BMS2h-570 (SEQ ID NO: 221)
EVQLLESGGG LVQPGGSLRL SCTASGFTFE NASMQWVRQA PGKGLEWVSS IEGQGNATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSS SWS------- FDYWGQGTLV TVSS

BMS2h-571 (SEQ ID NO: 222)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT RNEMGWVRQA PGKGLEWVST ITPTGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTD PGNRY----- FDYWGQGTLV TVSS

BMS2h-572 (SEQ ID NO: 223)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-1 (SEQ ID NO: 224)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWFRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-10 (SEQ ID NO: 225)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-11 (SEQ ID NO: 226)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTQV TVSS

BMS2h-572-12 (SEQ ID NO: 227)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-13 (SEQ ID NO: 228)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKDRFTI SRDNSKNTLY LLMNSLRAED TAVYYCAKVG KESN------ FDYWGQGTLV TVSS

BMS2h-572-14 (SEQ ID NO: 229)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-15 (SEQ ID NO: 230)
EVRLLESGGG LVQPGGSLRL SCAASGFNFN WQLMGWIRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-16 (SEQ ID NO: 231)
EVQLLESGGG LVRPGGSLRL SCVASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-17 (SEQ ID NO: 232)
EVQLLESGGG LVQTGGSLRL SCAASGFTYN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRADD TAVYYCVKVG KESN------ FDYRGHGTLV TVSS

BMS2h-572-18 (SEQ ID NO: 233)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRKA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-19 (SEQ ID NO: 234)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-2 (SEQ ID NO: 235)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESK------ FDYLGQGTLV TVSS

BMS2h-572-21 (SEQ ID NO: 236)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
AESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ LDYRGQGTLV TVSS

BMS2h-572-22 (SEQ ID NO: 237)
EVQLFESGGG SVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-23 (SEQ ID NO: 238)
EVQLLESGGG LVQPGGSLRL TCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFII SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-24 (SEQ ID NO: 239)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSTNTLY LQMNSLRAED TAVYYCAKVG KESE------ FDYRGQGTLV TVSS

BMS2h-572-3 (SEQ ID NO: 240)
EVRLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI TRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ LDYRGQGTLV TVSS

BMS2h-572-4 (SEQ ID NO: 241)
EVQLLVSGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-5 (SEQ ID NO: 242)
EVQLLVSGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNMLY LQMNGLRAED TAVYYCAKVG KESN------ FDYRGQGTLV TVSS

BMS2h-572-6 (SEQ ID NO: 243)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-601 (SEQ ID NO: 244)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-602 (SEQ ID NO: 245)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WHLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESS------ SDYRGQGTLV TVSS

BMS2h-572-603 (SEQ ID NO: 246)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WHLMAWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-604 (SEQ ID NO: 247)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-605 (SEQ ID NO: 248)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMAWARQA PGKGLEWVSG IEGPGDITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-606 (SEQ ID NO: 249)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WHLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-607 (SEQ ID NO: 250)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-608 (SEQ ID NO: 251)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-609 (SEQ ID NO: 252)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-610 (SEQ ID NO: 253)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK------ SDYRGQGTLV TVSS

BMS2h-572-611 (SEQ ID NO: 254)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRRA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK------ SDYRGQGTLV TVSS

BMS2h-572-612 (SEQ ID NO: 255)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSN------ SDYRGQGTLV TVSS

BMS2h-572-613 (SEQ ID NO: 256)
EVQLLESGGG LAQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK------ SDYRGQGTLV TVSS

BMS2h-572-614 (SEQ ID NO: 257)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK------ SDYRGQGTLV TVSS

BMS2h-572-615 (SEQ ID NO: 258)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDKN------ SDYRGQGTLV TVSS

BMS2h-572-616 (SEQ ID NO: 259)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESK------ SDYRGQGTLV TVSS

BMS2h-572-617 (SEQ ID NO: 260)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG RDSK------ SDYRGQGTLV TVSS

BMS2h-572-618 (SEQ ID NO: 261)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KYSN------ SDYRGQGTLV TVSS

BMS2h-572-619 (SEQ ID NO: 262)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR------ SDYRGQGTLV TVSS

BMS2h-572-620 (SEQ ID NO: 263)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDDS------ SDYRGQGTLV TVSS

BMS2h-572-621 (SEQ ID NO: 264)
EVQLLEFGGG LVQPGGSLRF SCAASGFTFN WQLMGWFRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG RDSN------ SDYRGQGTLV TVSS

BMS2h-572-622 (SEQ ID NO: 265)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDST------ SDYRGQGTLV TVSS

BMS2h-572-623 (SEQ ID NO: 266)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESS------ SDYRGQGTLV TVSS

BMS2h-572-624 (SEQ ID NO: 267)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI FRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSA------ SDYRGQGTLV TVSS

BMS2h-572-625 (SEQ ID NO: 268)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG NDSY------ SDYRGQGTLV TVSS

BMS2h-572-626 (SEQ ID NO: 269)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNGLRAED TAVYYCVKVG KDSS------ SDYRGQGTLV TVSS

BMS2h-572-627 (SEQ ID NO: 270)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCVKVG KDSA------ SDYRGQGTLV TVSS

BMS2h-572-630 (SEQ ID NO: 271)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK------ SDYRGQGTLV TVSS

BMS2h-572-631 (SEQ ID NO: 272)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR------ SDYRGQGTLV TVSS

BMS2h-572-632 (SEQ ID NO: 273)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK------ SDYRGQGTLV TVSS

BMS2h-572-633 (SEQ ID NO: 274)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK------ SDYRGQGTLV TVSS

BMS2h-572-634 (SEQ ID NO: 275)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR------ SDYRGQGTLV TVSS

BMS2h-572-635 (SEQ ID NO: 276)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK------ SDYRGQGTLV TVSS

BMS2h-572-7 (SEQ ID NO: 277)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKVG KESN------ FDYLGQGTLV TVSS

BMS2h-572-8 (SEQ ID NO: 278)
EVQLLESGGG LVQPGGSLRL SCVASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-572-9 (SEQ ID NO: 279)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN------ SDYRGQGTLV TVSS

BMS2h-573 (SEQ ID NO: 280)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS GWEMGWVRQA PGKGLEWVSS IDESGLNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGA PQYQIT---- FDYWGQGTLV TVSS

BMS2h-574 (SEQ ID NO: 281)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP NYGMYWVRQA PGKGLEWVSY ISRRGLLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTS HYMNNG---- FDYWGQGTLV TVSS

BMS2h-575 (SEQ ID NO: 282)
EVQLLESGGG LVQPGGSLRL SCAASGFTFV DYTMAWVRQA PGKGLEWVSS ISPIGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDP YGMEDGLTW- FDYWGQGTLV TVSS

BMS2h-576 (SEQ ID NO: 283)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD AYDMQWVRQA PGKGLEWVST ITSEGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS DL-------- FDYWGQGTLV TVSS

BMS2h-577 (SEQ ID NO: 284)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD GYDMGWVRQA PGKGLEWVST ISRGGWFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGT SQSSTGS--- FDYWGQGTLV TVSS

BMS2h-578 (SEQ ID NO: 285)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR RYDMLWARQA PGKGLEWVSE ISPTGALTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG ST-------- FDYWGQGTLV TVSS

BMS2h-579 (SEQ ID NO: 286)
EVQLLESGGG LVQPGGSLRL SCAASGFTFF PYYMSWVRQA PGKGLEWVSS ISGTGGLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTT QNATL----- FDYWGQGTLV TVSS

BMS2h-58 (SEQ ID NO: 287)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE VYTMAWVRQA PGKGLEWVST IDESGRDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VW-------- FDYWGQGTLV TVSS

BMS2h-580 (SEQ ID NO: 288)

EVQLLESGGG LVQPGGSLRL SCAASGFTFA FYKMGWVRQA PGKGLEWVST ITPKGHHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVF KGKGWTRPSG FDYWGQGTLV
TVSS

BMS2h-581 (SEQ ID NO: 289)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN EYSMMWVRQA PGKGLEWVSS IGRRGWLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAV LLDSTK---- FDYWGQGTLV TVSS

BMS2h-582 (SEQ ID NO: 290)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD EYPMTWVRQA PGKGLEWVST ISARGPFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGR HWLRNGR--- FDYWGQGTLV TVSS

BMS2h-583 (SEQ ID NO: 291)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG MQSMQWVRQA PGKGLEWVSS ITDDGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RV-------- FDYWGQGTLV TVSS

BMS2h-584 (SEQ ID NO: 292)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG AADMQWVRQA PGKGLEWVSL ITNDGISTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DR-------- FDYWGQGTLV TVSS

BMS2h-586 (SEQ ID NO: 293)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN KYRMQWVRQA PGKGLEWVSS IDSSGELTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEEV PMGNQTF--- FDYWGQGTLV TVSS

BMS2h-587 (SEQ ID NO: 294)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DYTMGWVRQA PGKGLEWVSS ITSQGAFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAT GTDSS----- FDYWGQGTLV TVSS

BMS2h-588 (SEQ ID NO: 295)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE DYEMSWVRQA PGKGLEWVSC IGPGGKPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVD GH-------- FDYWGQGTLV TVSS

BMS2h-589 (SEQ ID NO: 296)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS QYDMGWVRQA PGKGLEWVST ISSRGWLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP GGRRR----- FDYWGQGTLV TVSS

BMS2h-59 (SEQ ID NO: 297)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL DYAMGWVRQA PGKGLEWVST ISPMGMGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSS AISFTSDISN FDYWGQGTLV TVSS

BMS2h-590 (SEQ ID NO: 298)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYPMSWVRQA PGKGLEWVSS ISWSGFQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VARMPTGIA- FDYWGQGTLV TVSS

BMS2h-591 (SEQ ID NO: 299)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYEMQWVRQA PGKGLEWVSS IDSAGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF GM-------- FDYWGQGTLV TVSS

BMS2h-592 (SEQ ID NO: 300)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS EYPMKWVRQA PGKGLEWVST IDRQGDRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTV RRGLPRPSRY FDYWGQGTLV TVSS

BMS2h-593 (SEQ ID NO: 301)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYDMGWVRQA PGKGLEWVSS ISPMGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL SVYSGLD--- FDYWGQGTLV TVSS

BMS2h-594 (SEQ ID NO: 302)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYDMGWVRQA PGKGLEWVSD IDYIGKTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAS DEVGVNTSK- FDYWGQGTLV TVSS

BMS2h-595 (SEQ ID NO: 303)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA RYDMGWVRQA PGKGLEWVST ISPTGVLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGF ED-------- FDYWGQGTLV TVSS

BMS2h-596 (SEQ ID NO: 304)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE AYPMSWVRQA PGKGLEWVSL ISHTGHATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGH WP-------- FDYRGQGTLI TVSS

BMS2h-597 (SEQ ID NO: 305)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE DEWMSWVRQA PGKGLEWVSD ISPGGWTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY RPFDE----- FDYWGQGTLV TVSS

BMS2h-598 (SEQ ID NO: 306)
EVQLLESGGG LVQPGGSLRL SCAASGVTFD AIEMSWVRQA PGKGLEWVSS ISRHGEYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEDA WSRH------ FDYWGQGTLV TVSS

BMS2h-599 (SEQ ID NO: 307)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD STDMSWVRQA PGKGLEWVSG ILDNGSNTYY
ADSVKGRFTI SRDNSKNMLY LQMNSLRAED TAVYYCAKGA RD-------- FDYWGQGTLV TVSS

BMS2h-600 (SEQ ID NO: 308)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG RQSMQWVRQA PGKGLEWVSS IDDDGFSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD PWG------- FDYWGQGTLV TVSS

BMS2h-601 (SEQ ID NO: 309)
EVQLLESGGG LVQPGGSLRL SCTASGFTFS DTQMAWVRQA PGKGLEWVSG IDDGGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RH-------- FDYWGQGTLV TVSS

BMS2h-602 (SEQ ID NO: 310)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG STTMGWVRQA PGKGLEWVSV ISDDGGFTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKVD GYGV------ FDYWGQGTLV TVSS

BMS2h-603 (SEQ ID NO: 311)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR SGDMNWVRQA PGKGLEWVST ITNDGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSD SD-------- FDYWGQGTLV TVSS

BMS2h-61 (SEQ ID NO: 312)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA AYAMTWVRQA PGKGLEWVSY ISPNGTATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEYV GMRWNS---- FDYWGQGTLV TVSS

BMS2h-62 (SEQ ID NO: 313)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYEMAWVRQA PGKGLEWVSS ITSLGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RK-------- FDYWGQGTLV TVSS

BMS2h-65 (SEQ ID NO: 314)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN EYEMTWVRQA PGKGLEWVST ITSEGSGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN GK-------- FDYWGQGTLV TVSS

BMS2h-66 (SEQ ID NO: 315)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYEMLWVRQA PGKGLEWVST ITSEGHSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG TS-------- FDYWGQGTLV TVSS

BMS2h-67 (SEQ ID NO: 316)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYEMSWVRQA PGKGLEWVST IDSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VK-------- FDYWGQGTLV TVSS

BMS2h-68 (SEQ ID NO: 317)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYEMTWVRQA PGKGLEWVSS ISSTGQSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG NK-------- FDYWGQGTLV TVSS

BMS2h-69 (SEQ ID NO: 318)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL DYGMAWVRQA PGKGLEWVSA ISPLGLSTYY
ADSVKSRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEV RVGRGVHPPK FDYWGQGTLV TVSS

BMS2h-7 (SEQ ID NO: 319)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN LYEMTWVRQA PGKGLEWVSS ITSDGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG VI-------- FDYWGQGTLV TVSS

BMS2h-70 (SEQ ID NO: 320)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE NYAMSWVRQA PGKGLEWVST IAPLGVPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKK VGAWLQSRS- FDYWGQGTLV TVSS

BMS2h-701 (SEQ ID NO: 321)
EVQLLESGGG LVQPGGSLRL SCAASGFTFM DYEMHWVRQA PGKGLEWVST IGASGHYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYL DMLLFG---- FDYWGQGTLV TVSS

BMS2h-702 (SEQ ID NO: 322)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA EYEMMWARQA PGKGLEWVSR IAGNGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIML SH-------- FDYWGQGTLV TVSS

BMS2h-703 (SEQ ID NO: 323)
EVQLLESGGG LVQPGGSLRL SCAASGFTFY NYDMSWVRQA PGKGLEWVSG IDSMGLVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGS NASDWVV--- FDYWGQGTLV TVSS

BMS2h-704 (SEQ ID NO: 324)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYHMTWVRQA PGKGLEWVSS IADTGDRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLR GMARVWG--- FDYWGQGTLV TVSS

BMS2h-705 (SEQ ID NO: 325)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS YYDMMWVRQA PGKGLEWISS ISDRGLQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFT EIPLDWLEV- FDYWGQGTLV TVSS

BMS2h-706 (SEQ ID NO: 326)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG SYKMLWVRQA PGKGLEWVSS ITNSGTETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSM YPDLEIVH—FDYWGQGTLV TVSS

BMS2h-707 (SEQ ID NO: 327)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE TYRMSWVRQA PGKGLEWVSA IDQEGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNS GTRPGLR--- FDYWGQGTLV TVSS

BMS2h-708 (SEQ ID NO: 328)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYDMLWVRQA PGKGLEWVSR IDASGYFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQLL KLSLNPN--- FDYWGQGTLV TVSS

BMS2h-709 (SEQ ID NO: 329)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSS IHNTGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGT QHRFVV---- FDYWGQGTLV TVSS

BMS2h-71 (SEQ ID NO: 330)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GYPMSWVRQA PGKGLEWVST ISPLGPDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLL MGEYLNSRT- FDYWGQGTLV TVSS

BMS2h-710 (SEQ ID NO: 331)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN TYSMSWVRQA PGKGLEWVSW IDADGWVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQTG HT-------- FDYWGQGTLV TVSS

BMS2h-711 (SEQ ID NO: 332)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DGEMGWARQA PGKGLEWVSR IVDPGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DQ-------- FDYWGQGTLV TVSS

BMS2h-712 (SEQ ID NO: 333)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP EYEMKWVRQA PGKGLEWVST ITPSGGHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAIPL SS-------- FDYWGRGTLV TVSS

BMS2h-713 (SEQ ID NO: 334)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYVMIWVRQA PGKGLEWVSL INGAGDMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGG ARSFGVPPN- FDYWGQGTLV TVSS

BMS2h-714 (SEQ ID NO: 335)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DGEMGWARQA PGKGLEWVSR IVDPGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DQ-------- FDYWGQGTLV TVSS

BMS2h-715 (SEQ ID NO: 336)
EVQLLESGGG LVQPGGSLRL SCVASGFTFT LYNMSWVRQA PGKGLEWVSV ISSKGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQTS SV-------- FDYWGQGTLV TVSS

BMS2h-716 (SEQ ID NO: 337)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE AYYMSWVRQA PGKGLEWVSG IVNNGLLTYY
ADSVKGRFTI SRDNSKNMLY LQMNSLRAED TAVYYCAKSA VHPSYRAEL- FDYWGQGTLV TVSS

BMS2h-717 (SEQ ID NO: 338)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYEMAWVRQA PGKGLEWVSR IEPDGSNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP DNFTM----- FDYWGQGTLV TVSS

BMS2h-718 (SEQ ID NO: 339)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN KYMMGWVRQA PGKGLEWVSS IDSLGHYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAE FP-------- FDYWGQGTLV TVSS

BMS2h-719 (SEQ ID NO: 340)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-1 (SEQ ID NO: 341)
EVQLLESGGG MVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGQGTQV TVSS

BMS2h-719-10 (SEQ ID NO: 342)
EVQLLESGGG MVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-11 (SEQ ID NO: 343)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRKA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSENTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-12 (SEQ ID NO: 344)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-13 (SEQ ID NO: 345)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCADPF TE-------- LDYWGHGTLV TVSS

BMS2h-719-14 (SEQ ID NO: 346)
EVQLLESGGG LVRPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-15 (SEQ ID NO: 347)
EVQLLESGGG LVQPGGSLRL SCAASGFAFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LHMNSLRAED TAVYYCADPF TE-------- IDYWGQGTLV TVSS

BMS2h-719-16 (SEQ ID NO: 348)
EVQLLESGGG LVQPGGSLRL SCAASGFPFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYRAQGTLV TVSS

BMS2h-719-17 (SEQ ID NO: 349)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMSWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- IDYWGQGTQV TVSS

BMS2h-719-18 (SEQ ID NO: 350)
EVQLLESGGG LVHPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRDED TAVYYCAEPF TE-------- FDYGGQGTLV TVSS

BMS2h-719-19 (SEQ ID NO: 351)
EVQLLESGGG WVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-2 (SEQ ID NO: 352)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-20 (SEQ ID NO: 353)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- IDYRGQGTLV TVSS

BMS2h-719-202 (SEQ ID NO: 354)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK KYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-203 (SEQ ID NO: 355)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN SYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-21 (SEQ ID NO: 356)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-213 (SEQ ID NO: 357)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- MDYWGHGTLV TVSS

BMS2h-719-214 (SEQ ID NO: 358)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-215 (SEQ ID NO: 359)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- LDYWGHGTLV TVSS

BMS2h-719-218 (SEQ ID NO: 360)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
AESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-225 (SEQ ID NO: 361)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN TYEMQWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-226 (SEQ ID NO: 362)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN KYEMMWARQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGHGTLV TVSS

BMS2h-719-3 (SEQ ID NO: 363)
EVQLSESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-4 (SEQ ID NO: 364)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQT PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-5 (SEQ ID NO: 365)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LEMNSMRAED TAVYYCAEPF TE-------- FDNWGQGTLV TVSS

BMS2h-719-6 (SEQ ID NO: 366)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGQGTQV TVSS

BMS2h-719-7 (SEQ ID NO: 367)
EVQLLESGGG LVQPGGSLRL SCAASGFNFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE-------- FDYWGQGTLV TVSS

BMS2h-719-8 (SEQ ID NO: 368)
EVQLLESGGD LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYRGQGTLV TVSS

BMS2h-719-9 (SEQ ID NO: 369)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMSWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE-------- FDYWGRGTLV TVSS

BMS2h-72 (SEQ ID NO: 370)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE AYPMSWVRQA PGKGLEWVSS ISPLGLWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS AGAETHVYRL FDYWGQGTLV TVSS

BMS2h-720 (SEQ ID NO: 371)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NYEMMWVRQA PGKGLEWVSS IGVLGHTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLM SLRTFENL—FDYWGQGTLV TVSS

BMS2h-722 (SEQ ID NO: 372)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT KYPMAWVRQA PGKGLEWVSG IDANGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGT WRRHFAI--- FDYWGQGTLV TVSS

BMS2h-723 (SEQ ID NO: 373)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD LYDMMWVRQA PGKGLEWVSS ISDLGTLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNG FRVTSNDRR- FDYWGQGTLV TVSS

BMS2h-724 (SEQ ID NO: 374)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT GGDMWWVRQA PGKGLEWVSM IEGGGVTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAELD LRTGQ----- FDYWGQGTLV TVSS

BMS2h-725 (SEQ ID NO: 375)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-1 (SEQ ID NO: 376)
EVQLLESGGG LVQPGGSLHL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCADPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-10 (SEQ ID NO: 377)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-11 (SEQ ID NO: 378)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMSSLRAED TAVYYCADPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-12 (SEQ ID NO: 379)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDDSKNTLY LQMNSLRVED TAVYYCAEPS DPTM------ FVYWGQGTLV TVSS

BMS2h-725-13 (SEQ ID NO: 380)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTM------ FVYWGQGTLV TVSS

BMS2h-725-14 (SEQ ID NO: 381)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTM------ FDYWGQGTLV TVSS

BMS2h-725-15 (SEQ ID NO: 382)
EVQLLESGGG MVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSMRAED TAVYYCADPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-16 (SEQ ID NO: 383)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVTL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTM------ FDYWGQGTLV TVSS

BMS2h-725-17 (SEQ ID NO: 384)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ LDYWGQGTLV TVSS

BMS2h-725-18 (SEQ ID NO: 385)
EVQLSESGGG LVQPGGSLRL TCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK------ FVYWGQGTLV TVSS

BMS2h-725-19 (SEQ ID NO: 386)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK------ FVYWGQGTLV TVSS

BMS2h-725-2 (SEQ ID NO: 387)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FVYWGQGTPV TVSS

BMS2h-725-3 (SEQ ID NO: 388)
VQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSRNMLY LQMKSLRAED TAVYYCADPS DPTK------ FVYWGQGTQV TVSS

BMS2h-725-4 (SEQ ID NO: 389)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI FRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK------ FVYWGQGTLV TVSS

BMS2h-725-5 (SEQ ID NO: 390)
EVQLLESGGG LLQPGGSLRL SCAASGFTFS DYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FDYWGRGTLV TVSS

BMS2h-725-6 (SEQ ID NO: 391)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FVYWGQGTLV TVSS

BMS2h-725-7 (SEQ ID NO: 392)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGTWTYY
ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-8 (SEQ ID NO: 393)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FDYWGQGTLV TVSS

BMS2h-725-9 (SEQ ID NO: 394)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMGWVRQA PGMGLEWVSL IGDRGSWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK------ FDYWGQGTLV TVSS

BMS2h-726 (SEQ ID NO: 395)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NYKMYWVRQA PGKGLEWVSS ISEIGNLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIAL TR-------- FDYWGQGTLV TVSS

BMS2h-727 (SEQ ID NO: 396)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA SYRMYWVRQA PGKGLEWVSY IDPPGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSL NLSFPYIN—FDYWGQGTLV TVSS

BMS2h-728 (SEQ ID NO: 397)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYEMLWVRQA PGKGLEWVSR ISHSGRTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQLD GP-------- FDYWGQGTLV TVSS

BMS2h-729 (SEQ ID NO: 398)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYYMDWVRQA PGKGLEWVSR INHNGSVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKMP QGTSDWYY—FDYWGQGTLV TVSS

BMS2h-73 (SEQ ID NO: 399)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS KYDMSWVRQA PGKGLEWVST ILEDGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RL-------- FDYWGQGTLV TVSS

BMS2h-74 (SEQ ID NO: 400)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYPMTWVRQA PGKGLEWVST ILSPGTETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAE KD-------- FDYWGQGTLV TVSS

BMS2h-741 (SEQ ID NO: 401)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE GGEMGWVRQA PGKGLEWVSM IPMDGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG EV-------- FDYWGQGTLV TVSS

BMS2h-742 (SEQ ID NO: 402)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR EYHMKWARQA PGKGLEWVSG ISRDGMNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIQL AL-------- FDYWGQGTLV TVSS

BMS2h-743 (SEQ ID NO: 403)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYEMLWARQA PGKGLEWVSG ILPSGGATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG SGNGPIL--- FDYWGQGTLV TVSS

BMS2h-744 (SEQ ID NO: 404)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK EHDMFWVRQA PGKGLEWVSG IGAEGVWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPT MSNGSQSR—FDYWGQGTLV TVSS

BMS2h-745 (SEQ ID NO: 405)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-1 (SEQ ID NO: 406)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-10 (SEQ ID NO: 407)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-11 (SEQ ID NO: 408)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNFKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-12 (SEQ ID NO: 409)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSMNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

BMS2h-745-13 (SEQ ID NO: 410)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-14 (SEQ ID NO: 411)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-15 (SEQ ID NO: 412)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNALY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGLGTLV TVSS

BMS2h-745-16 (SEQ ID NO: 413)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

BMS2h-745-17 (SEQ ID NO: 414)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-18 (SEQ ID NO: 415)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYHCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-19 (SEQ ID NO: 416)
EVQLLESGGG LVQPEGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-2 (SEQ ID NO: 417)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ISEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

BMS2h-745-3 (SEQ ID NO: 418)
EVQLLESGGG LVEPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMSSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-4 (SEQ ID NO: 419)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ISEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYHCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-5 (SEQ ID NO: 420)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFII SRDNSKNTLN LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-6 (SEQ ID NO: 421)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGRGLEWVSG VTEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-7 (SEQ ID NO: 422)
EVQLLESGGG LVQPGGSLRL SCEASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-8 (SEQ ID NO: 423)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGDRTYY
ADSVKGRFTI SRDNSKSSLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-745-9 (SEQ ID NO: 424)
EVQLLESGGG SVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

BMS2h-746 (SEQ ID NO: 425)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG SAEMGWVRQA PGKGLEWVSG ISRPGQVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-747 (SEQ ID NO: 426)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DGTMGWARQA PGKGLEWVSL ILPSGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHS LTNRP----- FDYWGQGTLV TVSS

BMS2h-748 (SEQ ID NO: 427)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS KYDMRWARQA PGKGLEWVSD IDAVGTRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIPG GT-------- FDYWGQGTLV TVSS

BMS2h-749 (SEQ ID NO: 428)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE MYGMMWARQA PGKGLEWVSS IEGAGHATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIVL GM-------- FDYWGQGTLV TVSS

BMS2h-75 (SEQ ID NO: 429)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL QYPMGWVRQA PGKGLEWVST ISPVGLTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLF EGSRIQRDVG FDYWGQGTLV TVSS

BMS2h-750 (SEQ ID NO: 430)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE KYQMGWARQA PGKGLEWVSS IRGSGLVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVH TTLHTEVIG- FDYWGQGTLV TVSS

BMS2h-751 (SEQ ID NO: 431)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS QYTMYWARQA PGKGLEWVSE ISHSGSNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAISG LH-------- FDYWGQGTLV TVSS

BMS2h-752 (SEQ ID NO: 432)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYAMAWVRQA PGKGLEWVSR IGVEGGDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLL RLYRLG---- FDYWGQGTLV TVSS

BMS2h-753 (SEQ ID NO: 433)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA KYDMTWVRQA PGKGLEWVSK INSDGGLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL HGRGFVI--- FDYWGQGTLV TVSS

BMS2h-754 (SEQ ID NO: 434)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYDMVWVRQA PGKGLEWVSR INSMGLATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDY SVAPHGYPLG FDYWGQGTLV TVSS

BMS2h-755 (SEQ ID NO: 435)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYSMMWVRQA PGKGLEWVST ITDNGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHM SLATYLQF—FDYWGQGTLV TVSS

BMS2h-756 (SEQ ID NO: 436)
EVQLLESGGG LVQPGGSLRL SCAASGFTFM EYDMLWVRQA PGKALEWVSR ISSDGLWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGV SALAPFDIG- FDYWGQGTLV TVSS

BMS2h-757 (SEQ ID NO: 437)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK EYNMAWVRQA PGKGLEWVSS INFAGRTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS LPLDIFS--- FDYWGQGTLV TVSS

BMS2h-758 (SEQ ID NO: 438)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY-------- FDYWGQGTLV TVSS

BMS2h-758-1 (SEQ ID NO: 439)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNMLY LRMNSLRAED TAVYYCAETS GY-------- YEYWGQGTLV TVSS

BMS2h-758-2 (SEQ ID NO: 440)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY-------- FEYWGQGTLV TVSS

BMS2h-758-3 (SEQ ID NO: 441)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS SY-------- FEYWGQGTLV TVSS

BMS2h-758-4 (SEQ ID NO: 442)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCAETS GY-------- YEYWGHGTLV TVSS

BMS2h-758-5 (SEQ ID NO: 443)
EVQLLESGGG LVQPGGSLRL SCAASGFAFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY-------- FEYWGQGTLV TVSS

BMS2h-758-6 (SEQ ID NO: 444)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFIYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY-------- FEYWGQGTLV TVSS

BMS2h-759 (SEQ ID NO: 445)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR EYVMGWVRQA PGKGLEWVST INGLGNVTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAEE TAVYYCAIQL PN-------- FDYWGQGTLV TVSS

BMS2h-760 (SEQ ID NO: 446)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NDGMWWVRQA PGKGLEWVSF INVDGRETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS PGRVQ----- FDYWGQGTLV TVSS

BMS2h-761 (SEQ ID NO: 447)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG GWDMAWVRQA PGKGLEWVSS IAHEGGETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYV PGSPL----- FDYWGQRTLV TVSS

BMS2h-762 (SEQ ID NO: 448)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD QGWMYWVRQA PGKGLEWVSG IGSNGPRTSY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSG EY-------- FDYWGQGTLV TVSS

BMS2h-763 (SEQ ID NO: 449)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR QSDMWWVRQA PGKGLEWVSV IGNNGEFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDN WLL------- FDYWGQGTLV TVSS

BMS2h-764 (SEQ ID NO: 450)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD LSTMYWVRQA PGKGLEWVST IGGDGSHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGT QY-------- FDYWGQGTLV TVSS

BMS2h-765 (SEQ ID NO: 451)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS AYTMEWVRQA PGKGLEWVSS IGVTGYDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGG QG-------- FDYWGQGTLV TVSS

BMS2h-766 (SEQ ID NO: 452)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYGMSWVRQA PGKGLEWVSY IDPLGRLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEDL SSLQYGVSPN FDYWGQGTLV TVSS

BMS2h-767 (SEQ ID NO: 453)
EVQLLESGGG LVQPGGSLRL SCAASGFTFF HYSMSWVRQA PGKGLEWVSS IGPVGRETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKMI QSPLFKD--- FDYWGQGTLV TVSS

BMS2h-768 (SEQ ID NO: 454)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE WYDMYWVRQA PGKGLEWVSR IDSGGNQTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAS LWKWRL---- FDYWGQGTLV TVSS

BMS2h-77 (SEQ ID NO: 455)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYGMAWVRQA PGKGLEWVST ISPLGISTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHA TSQESLRS—FDYWGQGTLV TVSS

BMS2h-770 (SEQ ID NO: 456)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS KYEMMWVRQA PGKGLEWVSA ISGSGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP LPDAFWTRG- FDYWGQGTLV TVSS

BMS2h-771 (SEQ ID NO: 457)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG TYSMAWVRQA PGKGLEWVST IDRHGLATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTP GSSWQTV--- FGYWGQGTLV TVSS

BMS2h-772 (SEQ ID NO: 458)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE SYPMGWVRQA PGKGLEWVSS IDHHGHSTYY
ADSAKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLL RVSMIFG--- FDYWGQGTLV TVSS

BMS2h-773 (SEQ ID NO: 459)
EVQLLESGGG LVQPGGSLRL SCAASGFTFV QYGMSWVRQA PGKGLEWVSW ISSSGTYTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS RM-------- FDYWGQGTLV TVSS

BMS2h-774 (SEQ ID NO: 460)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR EYDMGWVRQA PGKGLEWVSL ISPPGRTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVV ILGYTNR--- FDYWGQGTLV TVSS

BMS2h-775 (SEQ ID NO: 461)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP NYGMLWVRQA PGKGLEWVSS INSSGMETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFF RLNDHNSVFG FDYWGQGTLV TVSS

BMS2h-776 (SEQ ID NO: 462)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYKMMWIRQA PGKGLEWVSS IVGSGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP GY-------- FDYWGQGTLV TVSS

BMS2h-777 (SEQ ID NO: 463)
EVQLLESGGG LVQPGGSLRL SCAASGFTFH NYAMGWVRRA PGKGLEWVSS IDEHGTITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDS LDRVWI---- FDYWGQGTLV TVSS

BMS2h-778 (SEQ ID NO: 464)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA DYPMTWVRQA PGKGLEWVSS IYSAGSPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLY HREPILFG—FDYWGQGTLV TVSS

BMS2h-78 (SEQ ID NO: 465)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYQMAWVRQA PGKGLEWVST ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG HR-------- FDYWGQGTLV TVSS

BMS2h-780 (SEQ ID NO: 466)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG SYTMMWVRQA PGKGLEWVSE IDRTGERTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPG FASLP----- FDYWGQGTLV TVSS

BMS2h-781 (SEQ ID NO: 467)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DYTMYWVRQA PGKGLEWVSK ISPSGRSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDP FG-------- FDYWGQGTLV TVSS

BMS2h-782 (SEQ ID NO: 468)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DAEMFWVRQA PGKGLEWVSS IDARGLTTYY
ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAT SAMYP----- FDYWGQGTLV TVSS

BMS2h-783 (SEQ ID NO: 469)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYDMGWVRQA PGKGLEWVST ISPLGHFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSG FHEYTEG--- FDYWGQGTLV TVSS

BMS2h-784 (SEQ ID NO: 470)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD RAGMGWVRQA PGKGLEWVSL IGRGGDITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

BMS2h-80 (SEQ ID NO: 471)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG RYQMAWVRQA PGKGLEWVSS ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS RR-------- FDYWGQGTLV TVSS

BMS2h-81 (SEQ ID NO: 472)
EVQLLESGGG LVQPGGFLRL SCAASGFTFE LYPMAWVRQA PGKGLEWVSS ISPVGFLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGH EGSYTPRSA- FDYWGQGTLV TVSS

BMS2h-82 (SEQ ID NO: 473)
EVQLLESGGG LVQPGGSLRL SCAASGFTFV AYPMAWVRQA PGKGLEWVST IAPLGGNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRP EGLQIDSQN- FDYWGQGTLV TVSS

BMS2h-83 (SEQ ID NO: 474)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA LYQMAWVRQA PGKGLEWVSS IDSSGSDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPE RD-------- FDYWGQGTLV TVSS

BMS2h-84 (SEQ ID NO: 475)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR QYQMAWARQA PGKGLEWVST IASDGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG RD-------- FDYWGQGTLV TVSS

BMS2h-85 (SEQ ID NO: 476)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE QYDMRWVRQA PGKGLEWVSW IDEAGHETYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKGM DG-------- FDYWGQGTLV TVSS

BMS2h-92 (SEQ ID NO: 477)
EVQLLESGGG LVQPGGSLRL SCAASGFTFV DYPMGWVRQA PGKGLEWVST ISTGGFSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAR YYYLSQIKN- FDYWGQGTLV TVSS

BMS2h-93 (SEQ ID NO: 478)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD IYGMTWVRQA PGKGLEWVSS ISPLGLVTYY
ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLK EHGDVP---- FDYWGQGTLV TVSS

BMS2h-94 (SEQ ID NO: 479)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE LYPMSWVRQA PGKGLEWVST ISPTGLLTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFK RSGKTDDTN- FDYWGQGTLV TVSS

BMS2h-95 (SEQ ID NO: 480)
EVQLLESGGG LVQPGGSLRL SCAASGFTFR EYDMLWVRQA PGKGLEWVST IVGDGNGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQD RQ-------- FDYWGQGTLV TVSS

BMS2h-97 (SEQ ID NO: 481)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYGMSWVRQA PGKGLEWVST ISPIGVTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNA YDRKSN---- FDYWGQGTLV TVSS

BMS2h-98 (SEQ ID NO: 482)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD RYVMVWVRQA PGKDLEWVSG ITPSGRRTYY
ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCAKVL GRHFDPLLPS FDYWGQGTLV TVSS

BMS2h-99 (SEQ ID NO: 483)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE DYAMSWVRQA PGKGLEWVST ITPGGFWTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTS SGELQLVED-FDYWGQGTLV TVSS

TABLE 2

Human Anti-CD40L VH Domain Encoding Nucleotide Sequences

BMS2h-10 (SEQ ID NO: 484)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATTGCTTATGATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGAGTGGGGTCTGCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGACG
CCTGAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-11 (SEQ ID NO: 485)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGATGGTGAGGGTTCTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGGG
AGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-111 (SEQ ID NO: 486)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGTTATCCTATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTCATGGTTCTGGTAGTGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCCG
TATACTAGTCGGCATAATAGTCTTGGGCATTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-112 (SEQ ID NO: 487)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATGGATTATCCTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGCCTGTTGGTATGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATGGG
GGGACTAGTGGTAGGCATAATACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-113 (SEQ ID NO: 488)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGAGTATCCTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTTCTCCTCTTGGTTTTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGACT
GGTGGGAGTGGTATTTTGAATTCTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-114 (SEQ ID NO: 489)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTTAGGGTTAGCAATTACGATTTGACCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTATCAACCATTAGTGCCACAAACGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGCGCGGCAGTGACG
TGGTGGTTGTTGCGTCATAACGACAACTTGGGGTTTTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-115 (SEQ ID NO: 490)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTTAGCATTAGCTATAAGAATATGGCCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTATCAGCCATTAAGGCGGCAAACGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGCGCGACAGGGAGT
CAGAAGAAGCGGACCTACACGTTCGACTTTTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-12 (SEQ ID NO: 491)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGTTGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGATATTTTGGGTTCGAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCTG
TCGTGGCAGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-120 (SEQ ID NO: 492)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGTCTTATACGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATCCTATGGGTTATCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACATGGG
GTGGGGAAGGGTACTAAGCCGCATAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-121 (SEQ ID NO: 493)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCTGTATAGGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGTGGTAGTGGTTTTCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCTG
CATGATAAGACTCAGCATCATCAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-123 (SEQ ID NO: 494)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATTGAGTATCCTATGCGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTCTCCGTCTGGTGTGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAT
GAGTCTAGTACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-124 (SEQ ID NO: 495)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCGGTATGATATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGGAGTTCGGGTTATCCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAAGGATG
CCTGGTTATTTTCCTGGGTTTGCTCGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-125 (SEQ ID NO: 496)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTGGCGGTATGCTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATGATGAGGGTCGGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGCGG
GTGTCTAGTTCTGTGAATGCTCCGTATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTC

ACCGTCTCGAGC

BMS2h-126 (SEQ ID NO: 497)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAATTATAGTATGAGTTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATCGTCTTGGTACGCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAATACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTGCTG
GCTGATCTTATTGCTGGGCATGCGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-127 (SEQ ID NO: 498)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGTCGTATGATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTTCGAGGTCTGGTTCTATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
TTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGTT
GATGCGCATGTTTATTATATGGAGCCTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-128 (SEQ ID NO: 499)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGAGGTATCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTTCTGATGGTGGGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
ACTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-129 (SEQ ID NO: 500)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACATTTCCGAAGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGGTGATGGTAAGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGAT
CAGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-13 (SEQ ID NO: 501)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTTATTATTCGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCGCCTTTTGGTTGGGGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGGACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG
GAGACGAGTGGTCCGATTTCTGAGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-130 (SEQ ID NO: 502)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTACAGCCTCCGGATTCACCTTTGCGGGTTATCAGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTAATGAGGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
AAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-131 (SEQ ID NO: 503)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGTATGAGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGTCGGATGGTCTGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
ATTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-132 (SEQ ID NO: 504)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGTTGATGATGGTCTTATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
GTTGCTTTTGACTACTGGGGTCAGGGGACCCTGGTCACCGTCTCGAAC

BMS2h-133 (SEQ ID NO: 505)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATTGGTTATGCTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTTTGGGTGCGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCCT
GCTGGTACGAGTAGTCATAGTGTGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-134 (SEQ ID NO: 506)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGGATTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTCG
GTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-135 (SEQ ID NO: 507)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTAGGTATGTTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGAGGCTGATGGTCGTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTT
ACGGATCAGCATGTTATTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-136 (SEQ ID NO: 508)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGGTTATCGTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCTCCGGATGGTAATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTTGG
GGGATGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-137 (SEQ ID NO: 509)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCGTATCCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTATTGGTTTTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAATGAAG
TCGCCTTATAAGCCGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-138 (SEQ ID NO: 510)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTTGGCTTATTGGATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTCCGTCGGGTACGCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGAAATATACT
GAGCCGGGGTTGGGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-139 (SEQ ID NO: 511)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGAATTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGTGATTTCTGAGGTGGGTTCTCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCAT
GATAGTTCGATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-14 (SEQ ID NO: 512)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTGGTCTTATGATATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTATGGCTTCGGGTGATGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGGAT
CGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-15 (SEQ ID NO: 513)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGTTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTCCTATTGGTCTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATTTCCT
TTGATTATTCTTCCTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-16 (SEQ ID NO: 514)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATGGAGTATGCGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTTCTCCGCTTGGTTTGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAG
GATTCGTCTGATAGTCAGTATACGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-17 (SEQ ID NO: 515)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGAGGATTATGGGATGGGGTGGGCCCGCCAGGCTCCAGGG
AAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTCTGGGTCTTTGGACATACTACGCAGACTCCG
CGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
CCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCGCTTGAGGGTTTGATTACG
AATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-176 (SEQ ID NO: 516)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGCGTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTGATTGGGATGGTAATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
GATAATGTTGGTATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-177 (SEQ ID NO: 517)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATTATATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGATGAGTGGGGTTTTGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATTGG
GAGTTTACGTCTGATACGTCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-178 (SEQ ID NO: 518)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATTTTGATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGATCAGGGTTCTCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
CAGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-179 (SEQ ID NO: 519)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGCTTATGATATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTAGTCCTCAGGGTCAGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
GGGCAGTCGCGGATTCCTATGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-18 (SEQ ID NO: 520)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTGAGTATGATATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATATATTAGTTCTGATGGTTATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGCAT
GGGAGTCCGCGGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-180 (SEQ ID NO: 521)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGATTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTAGTTTGGGTGAGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
CGTATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-181 (SEQ ID NO: 522)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTTTTATCCTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATGCTACGGGTACGAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTAAT
TATGGGAGTTCGTATACTATGGGGGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-182 (SEQ ID NO: 523)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGAGTATCCGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTCCTTCTGGTCCGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCG
TATTTTGATGTTATTCCTAGTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-183 (SEQ ID NO: 524)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGGATTACGGTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCAGTCGTCGGGTTTGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACGGGCT
AATTCTCGTAGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-184 (SEQ ID NO: 525)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGATTATGAGATGATGTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTCATGGTGGGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAT
AAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-185 (SEQ ID NO: 526)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGCATTATCCGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTAGGCTGGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTGCT
ACGCCTGTGCCGATTAAGGGTTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-186 (SEQ ID NO: 527)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGACTCACCTTTGGGAGGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATTCGGATGGTTGGGTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACCGGAT
TCGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-187 (SEQ ID NO: 528)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTAGTTATTCTATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATCGGGGTGGTACTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTGG
AGGAGGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-188 (SEQ ID NO: 529)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGCGTTATAGGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGGATTTCGAGGGATGGTTATCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATG
ACTGCGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-189 (SEQ ID NO: 530)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCAGATGTATCCGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGAGCCGGCTGGTGATCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAG
GAGCAGCCTTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-19 (SEQ ID NO: 531)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCCCCTTTCCGCAGTATCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTACTTCTGATGGTCTTGATACATATTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAG
CCTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-190 (SEQ ID NO: 532)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTATGTATGATATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTTGTCTGATGGTACGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG

GCTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-191   (SEQ ID NO: 533)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTTGTATCCGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGCGGGGGGTCATGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATTGG
TGGGATTATCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-192   (SEQ ID NO: 534)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGCGGTATCCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATCGTTCGGGTATGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGCAT
CAGGCGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-193   (SEQ ID NO: 535)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGGGTATGCTATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGCGAATGGTATTCGGACATACTAC
GCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGGG
GTTTGGAGGTGGGGGACTGGGCATAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-194   (SEQ ID NO: 536)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCAGTATGATATGCGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGCAGAATGGTACTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGG
ACTGGTAGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-195   (SEQ ID NO: 537)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGACTTATGATATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATTGGCAGGGTGATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
TTTGGTCATTATGTTGATGGTCTTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-196   (SEQ ID NO: 538)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGGGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTGATATGGGTGATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGG
ACTGCGTTTGACTACTGGGGTCCGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-197   (SEQ ID NO: 539)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAAGTATAAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCGAAGGGTCATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGCCG
ATGACTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-198   (SEQ ID NO: 540)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATAATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCGGCCGCGGGGTGGGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCGG
CGGGAGGGGTATACTGGTTCTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-199   (SEQ ID NO: 541)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGAGGTATGGTATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTGGCCGAGGGGTCAGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAT
AGTCGGTATGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-2   (SEQ ID NO: 542)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGATTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTTCGGATGGTATTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTTCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGTGGG
AGGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-20   (SEQ ID NO: 543)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGGTTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTTCGGAGGGTCTTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
CGTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-200   (SEQ ID NO: 544)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTAATTATAGTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTCGTCCTAATGGTACTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACGGTCG
TCTGCGCATCTTCAGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-201   (SEQ ID NO: 545)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATTATTCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTCGTCATGGTGGGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGGGG
AGTACTTATCCTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-202   (SEQ ID NO: 546)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTACAGCCTCCGGATTCACCTTTTCGCATTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGAGCCTTTTGGTGGTGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTGTAT
CCTCAGGGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-203   (SEQ ID NO: 547)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATACTATGGGGTGGGTCCGTCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCGGCCTGATGGTAAGATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGTTTAT
TCTTCGTGTGCGATGTGTACTCCGCTTTTGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-204 (SEQ ID NO: 548)
GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCGGTATTCGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTGGCCGAGGGGTTTTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGGT
CGTGGTCAGCGTGATACTAGTCAGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-205 (SEQ ID NO: 549)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCTTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACTTCGGGTGGTCTTAGTACGTACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
AGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-206 (SEQ ID NO: 550)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGTGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCTTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTTCTTCTGATGGTCTGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
GTGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-207 (SEQ ID NO: 551)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCTGGATTCACCTTTGATAAGTATTTGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGAGCCTCTGGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGCT
TCGGGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-208 (SEQ ID NO: 552)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGGTTCACCTTTACTGAGTATGAGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAATGTGGGTAGTAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
AAGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-209 (SEQ ID NO: 553)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTAGGCAGGGTTTTGCTACATACTAC
GCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCTG
GAGCGGGATGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-21 (SEQ ID NO: 554)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAATTATGAGATGGGGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTTCTGAGTGGGGTTATTCTACATACTAC
GCAGACTCCGCGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTGTG
GGTGGGACTCAGTATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-22 (SEQ ID NO: 555)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCATAATTATGAGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTTCGGGTGGTTCTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
GTTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-23 (SEQ ID NO: 556)
GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCTGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACGGGTGATGGTATTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGG
AGGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-24 (SEQ ID NO: 557)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTAGTGAGGGTGGTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACACTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
AAGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-24-1 (SEQ ID NO: 558)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATCAGATGGCGTGGGTTCGCCAGGCT
CCAGGGAAGGGACTAGAGTGGGTCTCAAGTATTACTAGTGAGGGTGGTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACAGTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
AAGAATTTCGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-25 (SEQ ID NO: 559)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGTCGCAGGGTACTAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
CGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-26 (SEQ ID NO: 560)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTAGTTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGTCGGATGGTGGTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
AAGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-27 (SEQ ID NO: 561)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTTGTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
TCTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-28 (SEQ ID NO: 562)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATTATGATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTGATAATGGTAATGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-29   (SEQ ID NO: 563)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTCGTTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTGATGGTGGGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
CGGGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-30   (SEQ ID NO: 564)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAGGTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTGATGATGGTGATTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGGAT
AAGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-300   (SEQ ID NO: 565)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATGATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATACGACGGGTGGGCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
AAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-301   (SEQ ID NO: 566)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGAGTGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTCTTGATGAGGGTTCTGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
AAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-302   (SEQ ID NO: 567)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTGATGATGGTGATGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAAT
GCGGGTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-303   (SEQ ID NO: 568)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGTGTATGATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGTTAATGATGGTTCTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
AAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-304   (SEQ ID NO: 569)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATACGGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGGATGATGGTTCTAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
CAGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-31 (SEQ ID NO: 570)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGGATGATGGTTCTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
CTTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-32 (SEQ ID NO: 571)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGTGTATCAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTGTGCCTGGGGGTGATTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACGTGG
CCGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-4 (SEQ ID NO: 572)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTGATGGTACTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTAAT
CCGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-40 (SEQ ID NO: 573)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGCGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGGGAGGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCGT
CGGTATGCTATTTTTACTTTTGATCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-400 (SEQ ID NO: 574)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCAGTATCCGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTACTAATGGTGTGAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGACG
GATATTATTTCGTCTTCGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-401 (SEQ ID NO: 575)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTTTAATTATGATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTTTT
GTGTGGTCGGCTGATATTGATTTTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-402 (SEQ ID NO: 576)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGTGGTATGATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACATATTGCGAGTTGGGGTGGTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGACG
GTGAAGGATGGGGGGTATCTGATGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC

GTCTCGAGC

BMS2h-403 (SEQ ID NO: 577)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGCTGAGTATGCTATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTGGGCGGGATGGTGCGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAAGGCGGCGAAGGAGCGGGGTTCTTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-404 (SEQ ID NO: 578)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTCAGGCTTATCAGATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTTGAGTGGGTCTCAACTATTAGTCCTAATGGTCTTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTTGAGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-407 (SEQ ID NO: 579)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGCTATGTATTCGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCGCCTCGTGGTGTTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACTAATTGGAATGGTGTGGATCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-408 (SEQ ID NO: 580)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTCCTACGTATATGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATACGAATGGTCGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGATAGTAATATGTCGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-409 (SEQ ID NO: 581)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTTATTCGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGCGTCGGGTACTCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGGTAATAGGTCTGAGGTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-41 (SEQ ID NO: 582)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTTTTGAGTATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCGAATGATGGTTCGACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGATCGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-410 (SEQ ID NO: 583)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTCAGGATTATTTGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAATCAGGATGGTACTGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAAGTTCTCCGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-411 (SEQ ID NO: 584)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATGCGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTCGGGATGGTCATGTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTTCT
TCTAAGGGGGGGACGTTTGCTAGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-412   (SEQ ID NO: 585)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGCTGTTCCGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGATGATGGTCTTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCAT
ATTTATGGGGATTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-413   (SEQ ID NO: 586)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCTTTATAGGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGTGATGGTGATACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACATTGG
TTGGGTACTACGTTGTCTTTGAGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-414   (SEQ ID NO: 587)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTATCGTTATACGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCGCCTAGGGGTAATATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGGT
GTGGCGGGGGCGGAGTCGCCTGAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-415   (SEQ ID NO: 588)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGTTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTTGGGTTATTATATGAGTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGGCCGATTGGTGGTGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCAG
AATATTTATGGTCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-416   (SEQ ID NO: 589)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCAGTATGATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGTCGTGATGGTGGGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGTAT
CCTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-417   (SEQ ID NO: 590)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGCAGTATAGTATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTTGAGTGGGTCTCAACTATTTCGCCTCTGGGTTCTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGAGT
AAGTTGTTGCTGTCGAGGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-418   (SEQ ID NO: 591)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTATGTATTCGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCGCCTCGTGGTGTTGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACTAAT
TGGAATGGTGTGGATCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-419 (SEQ ID NO: 592)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGCGTCATGGTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCCTACTGGTAATACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGCT
CATGATGAGGGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-42 (SEQ ID NO: 593)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTCCGTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGTTGGTGATGGTCTGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
CGGGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-420 (SEQ ID NO: 594)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAGTACGCCTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGGGATACGGGTCTGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAGTGTTTCG
TTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-421 (SEQ ID NO: 595)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCATCTGGGGGATATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTAGTGGGACGGGTCATACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTATG
AATGATCAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-422 (SEQ ID NO: 596)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATGGATGAGGATATGTTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATTCGCTGGGTACTCATACATACTAC
GCAGACTCCGTGAAGGGCCGATTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCGTTT
ATGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-423 (SEQ ID NO: 597)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTAATTATCAGATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGCGACTGGTCGGGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAGATCTACT
AGGTCATTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-424 (SEQ ID NO: 598)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGAATGCGGATATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGGTAGTGGTGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
TTGACTTCGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-425 (SEQ ID NO: 599)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGGATTATTCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTCGGGTCTTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGTCT
CAGGCGGTTACTCGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-426 (SEQ ID NO: 600)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGATGAGGGTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAATCAGCAGGGTTCGGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGATT
GGGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-427 (SEQ ID NO: 601)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGATCAGCCGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGGGCGCGTGGTGGGCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTTT
GATATTATTGCTTGGGATCCTTTTAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-428 (SEQ ID NO: 602)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATCAGTATCCTATGATGTGGGTTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCTTCTGGTTTTTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAT
CCTTTTATTACTACGTTTGACTACTGGGGTCAGGGAACCCTGGTGACCGTCTCGAGC

BMS2h-429 (SEQ ID NO: 603)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGAT
TATTCGCTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-43 (SEQ ID NO: 604)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCTTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTAGTGATGGTGGGCCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAACCTGAT
AGGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-430 (SEQ ID NO: 605)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGCGGAGCAGATGACTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGCATGGTGATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCGG
ACTTTGGTTGATTGGCCTACGAGTGAGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-44 (SEQ ID NO: 606)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGTCTTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGCCTACTGGTATTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCAT
TTTACTGAGCTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-449 (SEQ ID NO: 607)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGGGAGCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCTGCCTGGTCCGTATACATTCTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAT
GGGACGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-45 (SEQ ID NO: 608)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATTATGCGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTGGGGCGCAGGGTCTTCATACATACTAC
GCAGGCTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGACG
ACGATGGATTATGAGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-450 (SEQ ID NO: 609)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGAGGTTGATATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGCTATTGGTAATAATGGTCTTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGCT
CTGTCGTATAGGCCTCCTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-451 (SEQ ID NO: 610)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCAGGATGATACTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCTTAAGGGTCCGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGG
GATGGGTTGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-452 (SEQ ID NO: 611)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCGTCTCCGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCGGGATGGTAGTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTTCG
CCTTATCGGCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-453 (SEQ ID NO: 612)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGATTATTCGATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGTGAGTCATGGTGGTACTACATACTAC
GCAGACTCCGTGAAGGGCCGATTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAG
GGTTATAATGCGCAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-454 (SEQ ID NO: 613)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGAT
TATTCGCTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-455 (SEQ ID NO: 614)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATGATTATGATATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTTCGCATGGTGATAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAT
GTTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-456 (SEQ ID NO: 615)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAATGGTCG
GATTCTTTTGACTACAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-457 (SEQ ID NO: 616)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTCAGTCTAATGGTAATATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTAAT
TCTCAGGTTGAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-458 (SEQ ID NO: 617)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGTGGAGCCTATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTGGTCGTGATGGTTCGATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
AAGCATGGTACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-459 (SEQ ID NO: 618)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGGAGTATCGGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGAGCGGGGTTCGCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGCGG
AAGGGTACTAAGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-46 (SEQ ID NO: 619)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGTTGTATGCTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGTGCTGTGGGTGAGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGCT
AATAATCTTTCTGATAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-460 (SEQ ID NO: 620)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTCG
GTTGAGTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-461 (SEQ ID NO: 621)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATAGTTATACGATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAATCCTTGGGGTAGTCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCTG
GTGCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-462 0 (SEQ ID NO: 622)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGGTGATATGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTCAGCTTGGTAGTAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGAAT
TGGCGGACTCTTACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-463 (SEQ ID NO: 623)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTCACCTTTAATGCTTATGGGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCTTTCTGATGGTGTTATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGCT
CGGGGTGCGAATTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-464 (SEQ ID NO: 624)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATTATATGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGCCTCATGGTACGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATTTAAT
GCTATTTTTAGTGAGGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-465 (SEQ ID NO: 625)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGGATTATTCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTCGGGTCTTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGTCT
CAGGCGGTTACTCGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-466 (SEQ ID NO: 626)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCTTTATGCGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGGGAGGGATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACGGCGGTATATTACTGTGCGAAATTGGCT
GGTTCGCTGAGGGGTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-467 (SEQ ID NO: 627)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGGCTAGTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGCCTCATGGTTCGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGCGG
TGGGGTGTTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-468 (SEQ ID NO: 628)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCAGGGGTATAGTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTGGGCGTGGTGGTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTTG
TATATTTATCATAGTCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-469 (SEQ ID NO: 629)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTGGTATGGAGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTGGGACTGGTAGTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
CATCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-470 (SEQ ID NO: 630)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGATGGTGGCTATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTCGGGATGGTAATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGTTTCG
CCGACTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-471 (SEQ ID NO: 631)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGGATATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACGGATGATGGTGAGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAT
TATGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-472 (SEQ ID NO: 632)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGTATAATATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTACGAGGGATGGTTCTAGGACATACTAC
GCAGACTCCGTGAGGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAACTGTCG
AATATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-473 (SEQ ID NO: 633)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATTCTATGATTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGCCGTATGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACTGAT
TATTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-474 (SEQ ID NO: 634)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATACGTATAGTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTTGAGTGGGTCTCAACTATTACTCCTTATGGTAGTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGGGT
CTGGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-475 (SEQ ID NO: 635)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGACTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTACGGGTCCTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGTATTGGGGGTGATACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTCTATTACTGTGCGAAATTGACT
CCGTCTAATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-476 (SEQ ID NO: 636)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCAGTATCAGATGATGTGGGTTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCTTCTGGTTTTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAT
CCTTTTATTAGTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-477 (SEQ ID NO: 637)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTAATTATGATATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGCTTTGGGTAATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAACGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTACTGTGCGAAATGGCGT
AGTGCTATTACTGGTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-478 (SEQ ID NO: 638)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGTATCAGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCGCCGTCGGGTATGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGCGG
TCGGTTGTTCGTCCTTGGCCGGGTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-479 (SEQ ID NO: 639)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGATGAGAGTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTCCTCATGGTACTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCAT
CTTAAGTTGTATGAGTCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-480 (SEQ ID NO: 640)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTGGTGAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTCCGATGGATGGTAGTGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
AGTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-481 (SEQ ID NO: 641)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATTTTATGCCGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGGATGGTGCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTGCT
TCGCCGGCGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-482 (SEQ ID NO: 642)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATGAGCCTATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGGGTACGGGTACGACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAT
CAGGGTGATTTTATTAATCGGTTTCACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG

AGC

BMS2h-483 (SEQ ID NO: 643)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCATGCGTATAATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCCGCGGGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCCG
CCGCCTTCGTCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-5 (SEQ ID NO: 644)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGGGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTGATGGTACGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
CTGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-505 (SEQ ID NO: 645)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTTATATGATGTATTGGGTCCACCAGGCT
CCGGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTCCTCAGGGTCATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTTCGT
GAGCTTCCTCGTCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-506 (SEQ ID NO: 646)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAGTTATGCTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGCGAGTGGTGGTCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGAAT
GGGAAGAAGTTTCCTTTTACTAAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-507 (SEQ ID NO: 647)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTAGTGTGCATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAATCTGACGGGTGTTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGCT
ACTACTAGGCAGGCGCATCCGTTGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-515 (SEQ ID NO: 648)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGGGTGAGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGACTAATGGTCTTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTACT
CGTGATCTGGGTTTTGCCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-516 (SEQ ID NO: 649)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGAGATGGCTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTTCTCCTCGTGGTCATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGCT
AAGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-517 (SEQ ID NO: 650)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATACGTATGAGATGCTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCTGTTGATGGTAGTATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACGCGG
ATGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-518 (SEQ ID NO: 651)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTTCGTATGCTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTTCTCGTGATGGTTCGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGCAG
TCTGGGGGGCTTCGGTCGGGTTTGACTACGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-519 (SEQ ID NO: 652)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGACTCCGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGGATGGTGCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
CCGAAGGGTATTGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-520 (SEQ ID NO: 653)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTCCGCATGCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGATGGGGGGGGTTCGATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGAT
CCTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-521 (SEQ ID NO: 654)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTCACCTTTCATGCGGGGGAGATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGCTGCCTGGTGATATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGAAT
ACTGGGTATACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-522 (SEQ ID NO: 655)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGAATTATGGTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCGTGGGATGGTTCTCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAAATACG
CGGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-523 (SEQ ID NO: 656)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCATGATGCGGATATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTTGTCTCCGGGTGAGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGGT
CTGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-524 (SEQ ID NO: 657)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTACTGATCAGATGAATTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTCCTAGTGGTGCGTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCTT
GGTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-525 (SEQ ID NO: 658)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCATCTTTGAGCAGTATCAGATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTTCGCCTGATGGTACGCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTAGT
TTGCGTAAGATGGAGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-526 (SEQ ID NO: 659)
GAGGTGCAGCTGTTGGAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCAGGATGAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCGTCTGATGGTATGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACCTGGG
AAGAATTTTGACCACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-527 (SEQ ID NO: 660)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTACTGGGGGTGAGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTTGG
AATCTGTATACGGAGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-528 (SEQ ID NO: 661)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGGTCAGCCGATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTCCTGATGGTATTCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATTTG
GGTCAGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-529 (SEQ ID NO: 662)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATCAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTCCTAGTGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAG
GCGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-530 (SEQ ID NO: 663)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTCATTCGACTATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTTGCCGTCGGGTAGTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTTCT
GATGAGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-531 (SEQ ID NO: 664)
GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATGGGAATATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCTAGTGATGGTGTGACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGG
GGTCAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-532 (SEQ ID NO: 665)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCTTCCGGATTCACCTTTGATGATTATATGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTCCGCATGGTGTTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGTTG
CATACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-533 (SEQ ID NO: 666)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGAATTATACGATGGCGTGGGCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTGCTGGTCCGGGTAATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
AGTACTGCGACGTATAATAATGGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-534 (SEQ ID NO: 667)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGAGTATAGTATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTGGGAGTGGTCGTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCTT
AAGCTGGTTAGGGCTCCTAATCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-535 (SEQ ID NO: 668)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCTAAGACTGGTCATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTCG
CATTCGTTGGGGCCTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-54 (SEQ ID NO: 669)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGCGTATAGGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTTCGCCTTCTGGTTCGGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACTTTG
ACGGATTCGCCGTCGGGGCATTATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-55 (SEQ ID NO: 670)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGCGGTATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTACTGCTCAGGGTCTTGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATCTT
ACTGATTTTAGTAGTGGGCATCAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-553 (SEQ ID NO: 671)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGATTATGGTATGTCGTGGGTCCGCCAGGTT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTAGTCATAATGGTATGTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATTGG
CCGTCTACTAGTTGGGAGACTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC

TCGAGC

BMS2h-554 (SEQ ID NO: 672)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGAATGAGCCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGAGATGCAGGGTAAGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGG
GGTCAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-555 1 (SEQ ID NO: 673)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGTATTGATAATCTGGGTAGTCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAACGATT
TCTCATCAGTATGATAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-556 (SEQ ID NO: 674)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGAGGGGGGTCGGTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGACG
CCGCATAAGCAGTTGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-557 (SEQ ID NO: 675)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCAGCTTTGCTGATGAGTATATGGTTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGATCCGTTGGGTACTGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG
ACGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-558 (SEQ ID NO: 676)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTACGCATGATATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGATGATGGTATTAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAT
ATGTCTCTTATTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-559 (SEQ ID NO: 677)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGGTACTCCGATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAGTGGTGATGGTAGGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCTTAT
GCGCTTACTTCGTCTAAGCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-56 (SEQ ID NO: 678)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATGATTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTCATGGGACTGGTGGTCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTTG
GCTGATAGGAGTGGGGGGGTTGTTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-560 (SEQ ID NO: 679)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGGAGACGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGTATTAGTAATGATGGTAATACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTCT
CTGATTAGTCCTGGTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-561 (SEQ ID NO: 680)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGGTGAGTATATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGAGACTGGTTATATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTTCT
ACGAGGGGGGTGCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-562 (SEQ ID NO: 681)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGTCGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGCCTATGGGTGTTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTAAT
CAGCATGCTCATGATCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-563 (SEQ ID NO: 682)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTCGCCTATGGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGCT
TTGACTGAGCCTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-564 (SEQ ID NO: 683)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTGATTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTCTTGGTCATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTCCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTGAG
GAGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-565 (SEQ ID NO: 684)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCGCCTTTCCTAGGTATGGTATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTGATCAGTTTGGTATGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGTAT
GCTTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-566 (SEQ ID NO: 685)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAAGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGCCTATGGGTGTTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGG
GGTAATACTTCGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-567 (SEQ ID NO: 686)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATGATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGGGGCGGGTCATTTTACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTTT
CCGCGTGATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-568 (SEQ ID NO: 687)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGAAGTATGAGATGAGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGGTCTGGATGGTTCGCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
GATCCGAATGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-569 (SEQ ID NO: 688)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGACTAGTGAGATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGGGCCTGATGGTTTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCG
GATTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-57 (SEQ ID NO: 689)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGAGTATGATATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATACTGATGGTGGGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
CTGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-570 (SEQ ID NO: 690)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTACAGCCTCCGGATTCACCTTTGAGAATGCTTCTATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGGGGCAGGGTAATGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTCG
TCTTGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-571 (SEQ ID NO: 691)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGCGTAATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGCCGACTGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGAT
CCTGGTAATAGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572 (SEQ ID NO: 692)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-1 (SEQ ID NO: 693)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGTTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGGACCCTGGTCACCGTCTCGAGC

BMS2h-572-10 (SEQ ID NO: 694)
GAGGTGCAGCTGTTGGAGTCTGGTGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-11 (SEQ ID NO: 695)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCAGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGATTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-572-12 (SEQ ID NO: 696)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-13 (SEQ ID NO: 697)
GAGGTGCAGTTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGACCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCTAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTAGGG
AAGGAGAGTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-14 (SEQ ID NO: 698)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGCATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCAGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-15 (SEQ ID NO: 699)
GAGGTGCGGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCAACTTTAATTGGCAGCTGATGGGTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCAGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-16 (SEQ ID NO: 700)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCACTGCGTCTC
TCCTGTGTAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-17 (SEQ ID NO: 701)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGACTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTATAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGATGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCACGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-18 (SEQ ID NO: 702)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCAAGGCT
CCTGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-19 (SEQ ID NO: 703)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-2 (SEQ ID NO: 704)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTTGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAAGTTTGACTACCTGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-21 (SEQ ID NO: 705)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGAATCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATCTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-22 (SEQ ID NO: 706)
GAGGTGCAGCTGTTTGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGGACCCTGGTCACCGTCTCGAGC

BMS2h-572-23 (SEQ ID NO: 707)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
ACCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCGGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCATCATCTCCCGCGACAATTCCAAGAACACGCTATAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-24 (SEQ ID NO: 708)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCACGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTGAATTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-3 (SEQ ID NO: 709)
GAGGTGCGGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCACCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATCTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-4 (SEQ ID NO: 710)
GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-5 (SEQ ID NO: 711)
GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-6 (SEQ ID NO: 712)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-601 (SEQ ID NO: 713)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTCATGGGGTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-602 (SEQ ID NO: 714)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCACCTGATGGGGTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAGTTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-603 (SEQ ID NO: 715)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGCACCTGATGGCCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-604 (SEQ ID NO: 716)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTCGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-605 (SEQ ID NO: 717)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGCCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-606 (SEQ ID NO: 718)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGCACTTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-607 (SEQ ID NO: 719)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTCATGGGGTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-608 (SEQ ID NO: 720)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-609 (SEQ ID NO: 721)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGCAGCTCATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-610 (SEQ ID NO: 722)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-611 (SEQ ID NO: 723)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCGGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTCGGG
AAGGACAGCAAGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-612 (SEQ ID NO: 724)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTCGGG
AAGGACAGCAACTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-613 (SEQ ID NO: 725)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGCACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-614 (SEQ ID NO: 726)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACGCCAAGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-615 (SEQ ID NO: 727)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGCCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACAAGAACTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-616 (SEQ ID NO: 728)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGAGAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-617 (SEQ ID NO: 729)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AGGGACAGCAAGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-618 (SEQ ID NO: 730)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTCGGG
AAGTACAGCAACTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-619 (SEQ ID NO: 731)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAGGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-620 (SEQ ID NO: 732)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACGACAGCTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-621 (SEQ ID NO: 733)
GAGGTGCAGCTGTTGGAGTTTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCTTGCGTTTT
TCCTGTGCAGCTTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGTTCCGGCAGGCT
CCAGGGAAGGGTTTAGAGTGGGTTTCAGGTATTGAGGGTCCAGGTGATGTTACATATTAC
GCAGATTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCTTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AGGGACAGCAATTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-622 (SEQ ID NO: 734)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACAGCACCTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-623 (SEQ ID NO: 735)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGAGAGCAGCTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-624 (SEQ ID NO: 736)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTTCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCGCGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-625 (SEQ ID NO: 737)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTCGGC
AACGACAGCTACTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-626 (SEQ ID NO: 738)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCTGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACAGCAGCTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-627 (SEQ ID NO: 739)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGATATATTACTGTGTGAAAGTGGGC
AAGGACAGCGCGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-630 (SEQ ID NO: 740)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACGCCAAGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-631 (SEQ ID NO: 741)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAGGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-632 (SEQ ID NO: 742)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-633 (SEQ ID NO: 743)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACGCCAAGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-634 (SEQ ID NO: 744)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAGGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-635 (SEQ ID NO: 745)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-7 (SEQ ID NO: 746)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGATGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC

GCAGACTCCGTGAAGGGTCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTACAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTGACTACCTGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-8 (SEQ ID NO: 747)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGTAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCG
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTCGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTTTCGAGC

BMS2h-572-9 (SEQ ID NO: 748)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-573 (SEQ ID NO: 749)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGGGTGGGAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGAGTCTGGTCTTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTGCG
CCGCAGTATCAGATTACATTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-574 (SEQ ID NO: 750)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTAATTATGGGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTTCGCGGAGGGGTTTGTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGTCG
CATTATATGAATAATGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-575 (SEQ ID NO: 751)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTGGATTATACGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTCCGATTGGTACTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCCT
TATGGGATGGAGGATGGTCTGACGTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-576 (SEQ ID NO: 752)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGCGTATGATATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTACGTCGGAGGGTCTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTAGT
GATTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-577 (SEQ ID NO: 753)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGGGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCGTGGGGGTTGGTTCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGACG
AGTCAGTCGTCTACGGGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG

AGC

BMS2h-578 (SEQ ID NO: 754)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTCGGTATGATATGCTTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTCGCCTACGGGTGCTCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTGGT
TCGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-579 (SEQ ID NO: 755)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTTTCCGTATTATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGGGTACGGGTGGGCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGACG
CAGAATGCGACGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-58 (SEQ ID NO: 756)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGTTTATACTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTGATGAGTCTGGTCGTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
GTTTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-580 (SEQ ID NO: 757)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGTTTTATAAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTCCTAAGGGTCATCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTTTT
AAGGGTAAGGGTTGGACTCGTCCGAGTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-581 (SEQ ID NO: 758)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATGAGTATAGTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGCGTGGTTGGCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGTG
CTGCTGGATTCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-582 (SEQ ID NO: 759)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGAGTATCCGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGCGCGTGGTCCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGG
CATTGGCTTCGTAATGGTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-583 (SEQ ID NO: 760)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTATGCAGTCGATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTGATGATGGTACTAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
CGGGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-584 (SEQ ID NO: 761)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGCGGCTGATATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTACTAATGATGGTATTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
GATCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-586 (SEQ ID NO: 762)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGTATAGGATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAGTTCTGGTGAGCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGGTT
CCGATGGGGAATCAGACTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-587 (SEQ ID NO: 763)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGATTATACTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGTCTCAGGGTGCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTACG
GGTACGGATTCGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-588 (SEQ ID NO: 764)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATTATGAGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATGTATTGGGCCGGGGGGTAAGCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGAT
GGGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-589 (SEQ ID NO: 765)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTCAGTATGATATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTTCGAGGGGTTGGCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCCG
GGGGGTCGTCGGCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-59 (SEQ ID NO: 766)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTGGATTATGCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTCCGATGGGTATGGGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGT
GCTATTTCGTTTACTTCTGATATTTCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-590 (SEQ ID NO: 767)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATCCGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTTGGTCTGGTTTTCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGT
GTTGCGAGGATGCCTACTGGGATTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-591 (SEQ ID NO: 768)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGCTTATGAGATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAGTGCTGGTACTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTCTATTACTGTGCGGAACCTTTT
GGGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-592 (SEQ ID NO: 769)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGAGTATCCGATGAAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCGGCAGGGTGATCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGTG
CGGAGGGGTCTTCCTCGTCCGAGTCGTTATTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-593 (SEQ ID NO: 770)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTCGCCTATGGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTG
AGTGTGTATTCGGGTCTTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-594 (SEQ ID NO: 771)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTCACCTTTTCTCATTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGATATTGATTATATTGGTAAGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCTCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTCG
GATGAGGTGGGTGTTAATACTTCCAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-595 (SEQ ID NO: 772)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGCGGTATGATATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTACTGGTGTGTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTTT
GAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-596 (SEQ ID NO: 773)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCTTATCCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTTCTCATACGGGTCATGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAT
TGGCCTTTTGACTACCGGGGTCAGGGAACCCTGATCACCGTCTCGAGC

BMS2h-597 0 (SEQ ID NO: 774)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATGAGTGGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTAGCCCGGGTGGTTGGACTACATACTAC
GCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
CGTCCGTTTGATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-598 (SEQ ID NO: 775)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

TCCTGTGCAGCCTCCGGAGTCACCTTTGATGCTATTGAGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTCGCGTCATGGTGAGTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATGCT
TGGTCTCGGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-599 (SEQ ID NO: 776)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAGTACGGATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTTGGATAATGGTAGTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGGCG
AGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-600 (SEQ ID NO: 777)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCTTCCGGATTCACCTTTGGTAGGCAGAGTATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGATGATGGTTTTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAT
CCGTGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-601 (SEQ ID NO: 778)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTACAGCCTCCGGATTCACCTTTAGTGATACGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGATGGGGGTGTGAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
CGTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-602 (SEQ ID NO: 779)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGAGTACGACGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGTGATTTCGGATGATGGTGGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGAT
GGTTATGGTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-603 (SEQ ID NO: 780)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGGAGTGGGGATATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGAATGATGGTACGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAATACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTGAT
TCTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-61 (SEQ ID NO: 781)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGCTTATGCTATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTAGTCCGAATGGTACGGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATATGTG
GGGATGCGTTGGAATTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-62 (SEQ ID NO: 782)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGAGTTATGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTCTTGGTACTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT

AGGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-65 (SEQ ID NO: 783)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATGAGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTAGTGAGGGTAGTGGGACATACTAC
GCAGACTCCGTAAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAAT
GGTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-66 (SEQ ID NO: 784)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGATTATGAGATGTTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTACTAGTGAGGGTCATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGG
ACTTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-67 (SEQ ID NO: 785)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGAGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATTCTGATGGTAGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
GTGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-68 (SEQ ID NO: 786)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGATTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTACTGGTCAGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
AATAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-69 (SEQ ID NO: 787)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTTGATTATGGTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCGCCTCTTGGTCTTAGTACATACTAC
GCAGACTCCGTGAAGAGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGGTG
AGGGTGGGTAGGGGTGTTCATCCTCCGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-7 (SEQ ID NO: 788)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTTGTATGAGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGG
GTGATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-70 (SEQ ID NO: 789)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGAATTATGCTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGCTCCGCTGGGTGTTCCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAAGAAG
GTTGGGGCGTGGCTGCAGTCGCGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-701   (SEQ ID NO: 790)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATGGATTATGAGATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTGCTTCTGGTCATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCTT
GATATGCTGCTGTTTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-702   (SEQ ID NO: 791)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGAGTATGAGATGATGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCTGGTAATGGTTCTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATAATGCTT
TCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-703   (SEQ ID NO: 792)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTATAATTATGATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATTCGATGGGTCTTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGTCT
AATGCGAGTGATTGGGTTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-704   (SEQ ID NO: 793)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGTCGTATCATATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGGATACGGGTGATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTACTGTGCGAAATTGCGT
GGGATGGCTCGGGTTTGGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-705   (SEQ ID NO: 794)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTTATTATGATATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGATCTCATCTATTTCGGATCGTGGTCTTCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTACG
GAGATTCCGTTGGATTGGTTGGAGGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-706   (SEQ ID NO: 795)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGAGTTATAAGATGTTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTAATTCTGGTACTGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGATG
TATCCGGATTTGGAGATTGTGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-707   (SEQ ID NO: 796)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGACTTATCGTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATCAGGAGGGTTCTGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATAGT
GGGACGAGGCCGGGGCTTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-708 (SEQ ID NO: 797)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAGTTATGATATGCTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATGCGAGTGGTTATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAATTGTTG
AAGCTGTCGTTGAATCCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-709 1 (SEQ ID NO: 798)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCATAATACTGGTTTGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGACT
CAGCATCGTTTTGTTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-71 (SEQ ID NO: 799)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTTATCCTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTCCTTTGGGTCCTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTGTTG
ATGGGGGAGTATTTGAATTCTAGGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-710 (SEQ ID NO: 800)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATACGTATAGTATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGCTGATGGTTGGGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAACTGGG
CATACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-711 (SEQ ID NO: 801)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGATGGGGAGATGGGTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGTGGATCCTGGTGATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
GATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-712 (SEQ ID NO: 802)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTGAGTATGAGATGAAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTCGGGTGGTCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGATACCTCTT
TCTAGTTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-713 (SEQ ID NO: 803)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTAATTATGTGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTAATGGTGCTGGTGATATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGGGT
GCGCGTTCGTTTGGGGTTCCGCCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-714 (SEQ ID NO: 804)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGATGGGGAGATGGGTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGTGGATCCTGGTGATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
GATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-715 (SEQ ID NO: 805)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGTAGCCTCCGGATTCACCTTTACGCTGTATAATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGTTATTTCTAGTAAGGGTGATAGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAACGAGT
AGTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-716 (SEQ ID NO: 806)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGTATTATATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGTTAATAATGGTTTGTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGCT
GTTCATCCTTCGTATAGGGCGGAGTTGTTCGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-717 (SEQ ID NO: 807)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTTCGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGAGCCTGATGGTAGTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCCG
GATAATTTTACTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-718 (SEQ ID NO: 808)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGTATATGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAGTCTTGGTCATTATACATACTAC
GCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGGAG
TTTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719 (SEQ ID NO: 809)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-1 (SEQ ID NO: 810)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCATGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-719-10 (SEQ ID NO: 811)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCATGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-11 (SEQ ID NO: 812)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCAAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCGAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGTTTGACTATTGGGGTCAGGGTACCCTGGTCACCGTCTCGAGC

BMS2h-719-12 (SEQ ID NO: 813)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGACCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-13 (SEQ ID NO: 814)
GAGGTGCAGCTGTTGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCGTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTACAGATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGACCCGTTT
ACTGAGCTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-14 (SEQ ID NO: 815)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTTCTGTGCAGATCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-15 (SEQ ID NO: 816)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCGCCTTTAAGAGGTATGAGATGACATGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCATATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGATTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-16 (SEQ ID NO: 817)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCCCCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACCGGGCTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-17 (SEQ ID NO: 818)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCTTCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGATTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-719-18 (SEQ ID NO: 819)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACATCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCTTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGACGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-19 (SEQ ID NO: 820)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCAGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-2 (SEQ ID NO: 821)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-20 (SEQ ID NO: 822)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACTCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGATTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-202 (SEQ ID NO: 823)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAAGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-203 (SEQ ID NO: 824)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACAGCTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-21 (SEQ ID NO: 825)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCATTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-213 (SEQ ID NO: 826)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGACCCGTTC
ACGGAGATGGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-214 (SEQ ID NO: 827)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGACCCGTTC
ACGGAGTTCGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-215 (SEQ ID NO: 828)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTA
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAGCCGTTC
ACGGAGTTGGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-218 (SEQ ID NO: 829)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTCGTCCGACGGTTCCTTCACGTACTAC
GCCGAGTCGGTCAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-225 (SEQ ID NO: 830)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACACGTATGAGATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-226 (SEQ ID NO: 831)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACAAGTATGAGATGATGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-3 (SEQ ID NO: 832)
GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAATACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-4 (SEQ ID NO: 833)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGACT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGGCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCAGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCAAGC

BMS2h-719-5 (SEQ ID NO: 834)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGGAAATGAACAGCATGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACAACTGGGGTCAGGGAACCCTCGTCACCGTCTCGAGC

BMS2h-719-6 (SEQ ID NO: 835)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCAGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-719-7 (SEQ ID NO: 836)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCAACTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCAGACCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-8 (SEQ ID NO: 837)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-9 (SEQ ID NO: 838)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-72 (SEQ ID NO: 839)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGTATCCTATGTCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCCCCTCTTGGTTTGTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTAGT
GCTGGGGCGGAGACTCATGTTTATCGGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-720 (SEQ ID NO: 840)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGGTGTTGGGTCATACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTATG
TCGTTGAGGACGTTTGAGAATCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-722 (SEQ ID NO: 841)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGAAGTATCCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGCTAATGGTAATAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGACT
TGGCGTAGGCATTTTGCGATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-723 (SEQ ID NO: 842)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCTGTATGATATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTGATCTGGGTACGCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATGGT
TTTAGGGTTACGAGTAATGATCGTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-724 (SEQ ID NO: 843)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTGGTGGGGATATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGAGGGTGGTGGTGTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTTGAT
CTTCGGACGGGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725 (SEQ ID NO: 844)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-1 (SEQ ID NO: 845)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCATCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTTCTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-10 (SEQ ID NO: 846)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-11 (SEQ ID NO: 847)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAGCAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-12 (SEQ ID NO: 848)
GAGGTGCAGCTGTTGGAGTCTGGGGGTGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTCCCGGCTTATACTATGGGTTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTTGTCACCGTCTCGAGC

BMS2h-725-13 (SEQ ID NO: 849)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCTCTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-14 (SEQ ID NO: 850)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCATCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCA
GATCCTACTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-15 (SEQ ID NO: 851)
GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCATGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCATGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-16 (SEQ ID NO: 852)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCACACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-17 (SEQ ID NO: 853)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACACTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGAACCGTCG
GATCCTACTAAGTTAGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-18 (SEQ ID NO: 854)
GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
ACCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-19 (SEQ ID NO: 855)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCAGATCCGTCG
GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-2 (SEQ ID NO: 856)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGAACCGTCGGATCCTACTAAGTTTGTCT
ACTGGGGTCAGGGAACCCCGGTCACCGTCTCGAGC

BMS2h-725-3 (SEQ ID NO: 857)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCGCTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACATGCTGTAT
CTGCAAATGAAAAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGATCCGTCG
GATCCTACTAAGTTTGTCTACTGGGGTCAAGGAACCCAGGTCACCGTCTCGAGC

BMS2h-725-4 (SEQ ID NO: 858)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTTCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-5 (SEQ ID NO: 859)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGTTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGATTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTCGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-6 (SEQ ID NO: 860)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCC
GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-7 (SEQ ID NO: 861)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTACTTGGACATATTAC
GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACACTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTATTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-8 (SEQ ID NO: 862)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-9 (SEQ ID NO: 863)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT

CCAGGGATGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-726 (SEQ ID NO: 864)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCCGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATAAGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTCGGAGATAGGTAATCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATAGCTCTG
ACGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-727 (SEQ ID NO: 865)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAGTTATCGTATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATATATTGATCCGCCGGGTAGTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTTG
AATTTGTCGTTTCCTTATATTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-728 (SEQ ID NO: 866)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATGAGATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCTCATTCGGGTCGGACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAATTGGAT
GGTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-729 (SEQ ID NO: 867)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATTATATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATCATAATGGTTCTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGCCG
CAGGGTACTTCTGATTGGTATTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-73 (SEQ ID NO: 868)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTAAGTATGATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTCTGGAGGATGGTCTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
CGTTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-74 (SEQ ID NO: 869)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGATTATCCTATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTCTGTCTCCGGGTACGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGAG
AAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-741 (SEQ ID NO: 870)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTGGTGAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTCCGATGGATGGTAGTGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
GAGGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-742 (SEQ ID NO: 871)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGGAGTATCATATGAAGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAGTAGGGATGGTATGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATACAGCTT
GCTTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-743 (SEQ ID NO: 872)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGTGATTATGAGATGCTTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTCTTCCGTCGGGTGGGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGT
TCGGGGAATGGGCCTATTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-744 (SEQ ID NO: 873)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGCATGATATGTTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGGGCTGAGGGTGTTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGACG
ATGTCTAATGGTTCTCAGTCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-745 (SEQ ID NO: 874)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-1 (SEQ ID NO: 875)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTTTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-10 (SEQ ID NO: 876)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAACCTGCGTGCCGAAGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-11 (SEQ ID NO: 877)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTTCAAGAACACGCTGTAT
CTGCAGATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-12   (SEQ ID NO: 878)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGATTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCATGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-13   (SEQ ID NO: 879)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCTTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAACACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-14   (SEQ ID NO: 880)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGGTTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-15   (SEQ ID NO: 881)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCTGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACGCGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCTGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-16   (SEQ ID NO: 882)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-17   (SEQ ID NO: 883)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCCTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACAGGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGCACCCTGGTCACC
GTTTCGAGC

BMS2h-745-18   (SEQ ID NO: 884)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTCGTCACC
GTCTCGAGC

BMS2h-745-19   (SEQ ID NO: 885)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGAGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-2   (SEQ ID NO: 886)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCAGAGGACTCCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-3   (SEQ ID NO: 887)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAGAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCTGGGAAGGGTCTCGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAGCAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-4   (SEQ ID NO: 888)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-5   (SEQ ID NO: 889)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCTGACTCCGTGAAGGGCCGGTTCATCATCTCCCGCGACAATTCCAAGAACACGCTGAAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-6   (SEQ ID NO: 890)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAGGGGTCTAGAGTGGGTCTCAGGTGTTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAATTTGACTACTGGGGTCAGGGAACCCTGGTCACC

GTCTCGAGC

BMS2h-745-7 (SEQ ID NO: 891)
GAGGTGCAGCTGTTGGAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGAAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGT

BMS2h-745-8 (SEQ ID NO: 892)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTGATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAGCTCGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCCAGC

BMS2h-745-9 (SEQ ID NO: 893)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACTCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-746 (SEQ ID NO: 894)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGTCGGCTGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCGAGGCCTGGTCAGGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-747 (SEQ ID NO: 895)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGATGGTACTATGGGGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTTGCCGTCGGGTAGTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATTCG
CTGACTAATCGTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-748 (SEQ ID NO: 896)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAAGTATGATATGCGGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTGATGCTGTTGGTACTCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATACCGGGG
GGGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-749 (SEQ ID NO: 897)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGATGTATGGTATGATGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGGGTGCGGGTCATGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTACTGTGCGATAGTGCTT

GGTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-75   (SEQ ID NO: 898)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCGGGATTCACCTTTTTGCAGTATCCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTGTTGGTTTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTGTTT
GAGGGGTCGAGGATTCAGCGTGATGTGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-750   (SEQ ID NO: 899)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGAAGTATCAGATGGGTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCGGGGGTCTGGTCTTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGCAT
ACTACGCTGCATACGGAGGTGATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-751   (SEQ ID NO: 900)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCGGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTCAGTATACGATGTATTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTCTCATAGTGGTTCTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATATCGGGG
CTGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-752   (SEQ ID NO: 901)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGATTATGCGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACGTATTGGTGTGGAGGGTGGGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGTTG
CGGCTTTATCGTCTGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-753   (SEQ ID NO: 902)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTAAGTATGATATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTAATTCTGATGGTGGTCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTG
CATGGTAGGGGGTTTGTTATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-754   (SEQ ID NO: 903)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGCGGTATGATATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTAATTCTATGGGTCTGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATTAT
TCGGTTGCGCCGCATGGGTATCCTTTGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-755   (SEQ ID NO: 904)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGATTATTCGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTGATAATGGTACGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATATG

TCGCTTGCTACTTATCTGCAGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-756   (SEQ ID NO: 905)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTATGGAGTATGATATGCTTTGGGTCCGCCAGGCT
CCAGGGAAGGCTCTAGAGTGGGTCTCACGTATTTCGTCGGATGGTCTTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTG
AGTGCGCTTGCTCCTTTTGATATTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-757   (SEQ ID NO: 906)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGTATAATATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTAATTTTGCTGGTCGGACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGTCT
CTTCCTTTGGATATTTTTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-758   (SEQ ID NO: 907)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-1   (SEQ ID NO: 908)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
CTGCGAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTATTATGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-2   (SEQ ID NO: 909)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-3   (SEQ ID NO: 910)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
AGTTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-4   (SEQ ID NO: 911)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGGTTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTTT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTATTATGAGTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-5 (SEQ ID NO: 912)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCTGCCTCCGGATTCGCCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-6 (SEQ ID NO: 913)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTATATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
GGTTACTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-759 (SEQ ID NO: 914)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGGAGTATGTTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGGTTTGGGTAATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGAGACCGCGGTATATTACTGTGCGATACAGCTG
CCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-760 (SEQ ID NO: 915)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATGATGGGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTAATGTTGATGGTAGGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAATGGTCT
CCTGGGCGGGTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-761 (SEQ ID NO: 916)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGGTTGGGATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCTCATGAGGGTGGTGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGTT
CCTGGGTCTCCTCTGTTTGACTACTGGGGTCAGAGAACCCTGGTCACCGTCTCGAGC

BMS2h-762 (SEQ ID NO: 917)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCAGGGTTGGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTTCGAATGGTCCTCGGACATCCTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGGG
GAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-763 (SEQ ID NO: 918)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGCAGAGTGATATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTGGTAATAATGGTGAGTTTACATACTAC
GCAGACTCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAAT
TGGCTGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-764 (SEQ ID NO: 919)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCTTAGTACTATGTATTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTGGGGATGGTAGTCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAAGGTACG
CAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-765 (SEQ ID NO: 920)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCGTATACGATGGAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGGGTTACGGGTTATGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGT
CAGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-766 (SEQ ID NO: 921)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGGGATTATGGGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTGATCCTCTGGGTCGTCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATTTG
TCGTCGCTGCAGTATGGGGTGTCGCCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-767 (SEQ ID NO: 922)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTTTCATTATTCTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGTCCGGTTGGTCGGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGATT
CAGTCGCCGTTGTTTAAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-768 (SEQ ID NO: 923)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGATATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAGTGGGGGTAATCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGTCG
CTTTGGAAGTGGAGGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-77 (SEQ ID NO: 924)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGGTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCGCTGGGTATTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCT
ACGTCTCAGGAGTCTTTGCGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-770 (SEQ ID NO: 925)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAAGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCCT
CTGCCTGATGCGTTTTGGACTAGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-771 (SEQ ID NO: 926)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTACTTATTCTATGGCGTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGATCGGCATGGTTTGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACTCCT
GGTTCTTCTTGGCAGACTGTTTTTGGCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-772 (SEQ ID NO: 927)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGTCGTATCCTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATCATCATGGTCATTCGACATACTAC
GCAGACTCCGCGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCTT
AGGGTTTCGATGATTTTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-773 (SEQ ID NO: 928)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTGCAGTATGGGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTAGTAGTAGTGGTACGTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTACGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACGTCT
AGGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-774 (SEQ ID NO: 929)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCGGCCTCCGGATTCACCTTTCGGGAGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTCGCCTCCTGGTCGTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTTGTG
ATTCTGGGTTATACGAATAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-775 (SEQ ID NO: 930)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCTAATTACGGGATGTTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTAATTCTTCGGGTATGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTTTT
CGTCTGAATGATCATAATTCTGTGTTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-776 (SEQ ID NO: 931)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGATTATAAGATGATGTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGTTGGGTCTGGTTCGATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCCT
GGTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-777 (SEQ ID NO: 932)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCATAATTATGCTATGGGGTGGGTCCGCCGGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGAGCATGGTACTATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGT
CTGGATCGGGTTTGGATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-778 (SEQ ID NO: 933)
GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATCCGATGACTTGGGTCCGCCAGGCT

CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTATTCTGCGGGTTCTCCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTTATCATCGGGAGCCGATTCTTTTTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-78   (SEQ ID NO: 934)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGAGAGGTATCAGATGGCGTGGGTCCGCCAGGCTCCGGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTTCTGATGGTGGGGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGTCATCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-780   (SEQ ID NO: 935)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGGTTCTTATACTATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGATCGGACGGGTGAGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCTGGGTTTGCTTCTCTTCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-781   (SEQ ID NO: 936)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTACGGATTATACTATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTTCTCCGAGTGGTCGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCGTTTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-782   (SEQ ID NO: 937)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGATGATGCGGAGATGTTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGCTCGTGGTTTGACGACATACTACGCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGACGTCGGCTATGTATCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-783   (SEQ ID NO: 938)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTCGTGATTATGATATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTCTTGGTCATTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCTGGGTTTCATGAGTATACTGAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-784   (SEQ ID NO: 939)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGATCGTGCGGGTATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTGGGCGTGGTGGTGATATTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGTAATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-80   (SEQ ID NO: 940)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCACCTTTGGTCGTTATCAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTGATGGTGGGGGGACATACTAC

GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTCT
CGTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-81 (SEQ ID NO: 941)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTTCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGTTGTATCCGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTCTCCGGTTGGTTTTCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGCAT
GAGGGGTCGTATACTCCGCGGTCGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-82 (SEQ ID NO: 942)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTGGCGTATCCTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTGCGCCTCTGGGTGGTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGCCG
GAGGGGCTGCAGATTGATTCTCAGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-83 (SEQ ID NO: 943)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGTTGTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTCTTCTGGTAGTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAG
CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-84 (SEQ ID NO: 944)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGCAGTACCAGATGGCTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGCGTCGGATGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGT
CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-85 (SEQ ID NO: 945)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCAGTATGATATGAGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATGAGGCGGGTCATGAGACATACTAT
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATG
GATGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-92 (SEQ ID NO: 946)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTTGATTATCCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTACGGGGGGTTTTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGCGG
TATTATTATCTTAGTCAGATTAAGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-93 (SEQ ID NO: 947)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATATTTATGGGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTCGCCTCTTGGTCTTGTTACATACTAC
GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGAAG
GAGCATGGGGATGTTCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-94 (SEQ ID NO: 948)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCTTTATCCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTACGGGTTTGTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTAAG
AGGAGTGGGAAGACTGATGATACTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-95 (SEQ ID NO: 949)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCGGGAGTATGATATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGTGGGGGATGGTAATGGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGAT
CGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-97 (SEQ ID NO: 950)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGGTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGCCTATTGGTGTTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATGCT
TATGATCGGAAGTCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-98 (SEQ ID NO: 951)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCGGTATGTGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGATCTAGAGTGGGTCTCAGGTATTACTCCGAGTGGTAGGAGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGGACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTTG
GGGCGTCATTTTGATCCTCTTCTGCCTTCGTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

BMS2h-99 (SEQ ID NO: 952)
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATTATGCTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGGGTGGTTTTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACGTCT
AGTGGGGAGTTGCAGTTGGTTGAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

TABLE 3

Anti-human CD40L VK Domain Amino Acid Sequences

BMS2h-100 (SEQ ID NO: 953)
DIQMTQSPSS LSASVGDRVT ITCRASQNIK HSLRWYQQKP GKAPRLLIYH RSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRHRPYTFGQ GTKVEIKR

BMS2h-101 (SEQ ID NO: 954)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VALFPYTFGQ GTKVEIKR

BMS2h-102 (SEQ ID NO: 955)

DIQMTQSPSS LSASVGDRVT ITCRASQHIG HHLRWYQQKP GKAPKLLIYH RSHLQSGVPS RFSGSGSGTD FTLTISSLQP EDSATYYCQQ WDRPPYTFGQ GTKVEIKR

BMS2h-103 (SEQ ID NO: 956)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRAVPYTFGQ GTKVEIKR

BMS2h-104 (SEQ ID NO: 957)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRFSPYTFGQ GTKVEIKR

BMS2h-105 (SEQ ID NO: 958)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYARPVTFGQ GTKVEIKR

BMS2h-106 (SEQ ID NO: 959)
DIQMTQSPSS LSASVGDRVT ITCRASQSIN HRLYWYQQKP GKAPKLLIYH RSRLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YKVRPNTFGQ GTKVEIKR

BMS2h-107 (SEQ ID NO: 960)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TYSSPHTFGQ GTKVEIKR

BMS2h-108 (SEQ ID NO: 961)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RAVRPFTFGQ GTKVEIKR

BMS2h-109 (SEQ ID NO: 962)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TYYRPLTFGQ GTKVEIKR

BMS2h-110 (SEQ ID NO: 963)
DIQMTQSPAS LSASVGDRVT ITCRASQDID PMLRWYQQKP GKAPKLLIYA GSILQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TSIRPYTFGQ GTKVEIKR

BMS2h-116 (SEQ ID NO: 964)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-1 (SEQ ID NO: 965)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDILWYQQKP GKAPKLLIYQ TSILQSGVPS RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-10 (SEQ ID NO: 966)
DIQITQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-11 (SEQ ID NO: 967)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-12 (SEQ ID NO: 968)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR

BMS2h-116-13 (SEQ ID NO: 969)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGQ GTKVVIKR

BMS2h-116-1312 (SEQ ID NO: 970)

DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDLATYYCQQ YWAFPVTFGK GTKVVIKR

BMS2h-116-1313 (SEQ ID NO: 971)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGR GTKVVIKR

BMS2h-116-1314 (SEQ ID NO: 972)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYRQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGQ GTKVVIKR

BMS2h-116-1319 (SEQ ID NO: 973)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSIMRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR

BMS2h-116-1320 (SEQ ID NO: 974)
DIQMTQSPSS LSAYVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFAKYYCQQ YWAFPVTFGQ GTKVVIKR

BMS2h-116-138 (SEQ ID NO: 975)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP VDFATYYCQQ YWAFPVTFGQ GTKVVIKR

BMS2h-116-14 (SEQ ID NO: 976)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWFQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-15 (SEQ ID NO: 977)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYRQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR

BMS2h-116-16 (SEQ ID NO: 978)
DIQMTQSPSS LSASVGDRVT ITCRASQPID PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTV FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-17 (SEQ ID NO: 979)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-2 (SEQ ID NO: 980)
DIQMTQSPSS LSASVGDRVT ITCRASQPIE PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWASPVTFGQ GTKVEIKR

BMS2h-116-3 (SEQ ID NO: 981)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ
TSILQSGVPS RFSGSESGTD FTLTISSLQP EDIATYYCQQ YWAFPVTFGQ GTRVEIKR

BMS2h-116-4 (SEQ ID NO: 982)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-5 (SEQ ID NO: 983)
DIQMTQSPSS LSASVGDRVA ITCRASQPIG PDILWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSGTD FTLTISSLQP EDSATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-6 (SEQ ID NO: 984)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSVTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVGIKR

BMS2h-116-7 (SEQ ID NO: 985)

DIQMTQSPSS LSASVGDRVT ITCRASQPID PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSRTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-8 (SEQ ID NO: 986)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTD FTLTISGLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-9 (SEQ ID NO: 987)
DIQMTQSPSS LSASVGDRVT ITCRASMPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR

BMS2h-141 (SEQ ID NO: 988)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG DTLTWYQQKL GKAPKLLIYG GSELQSGVPP
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ CISSPCTFGQ GTKVEIKR

BMS2h-142 (SEQ ID NO: 989)
DIQMTQSPSS LSASVGDRVT ITCRASQFIG DSLSWYQQKP GKAPKLLIYF SSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHTSPTTFGR GTKVKIKR

BMS2h-143 (SEQ ID NO: 990)
DIQMTQSPSS LSASVGDRVT ITCRASQTIE TNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YHGYPTTFGQ GTKVEIKR

BMS2h-144 (SEQ ID NO: 991)
DIQMTQSPSS LSASVGDRVT ITCRASQMID QDLEWYQQKP GKAPKLLIYN ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHGYPITFGQ GTKVEIKR

BMS2h-145 (SEQ ID NO: 992)
DIQMTQSPSS LSASVGDRVT ITCRASQTIY TSLSWYQQKP GKAPKLLIHY GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDSATYYCQQ VHQAPTTFGQ GTKVEIKR

BMS2h-146 (SEQ ID NO: 993)
DIRMTQSPSS LSASVGDRVT ITCRASQWIG DSLAWYQQKP GKAPKLLIYG ISELQSGVPS
RFSGSGSGTD FTLTISSLQP EDSATYYCQL SSSMPHTFGQ GTKVEIKR

BMS2h-147 (SEQ ID NO: 994)
DIQMTQSPSS LSASVGDRVT ITCRASQEIE TNLEWYQQKP GKAPKLLIYD SSHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHQNPPTFGQ GTKVEIKR

BMS2h-149 (SEQ ID NO: 995)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG RQLVWYQQKP GKAPKLLIYG ATELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ QSKGPLTFGH GTKVEIKR

BMS2h-150 (SEQ ID NO: 996)
DIQMTQSPSS LSASVGDRVT ITCRASQGIG TDLNWYQQKP GKAPKLLIYM GSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IYSFPITFGQ GTKVEIKR

BMS2h-154 (SEQ ID NO: 997)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE EMLHWYQQKP GKAPKLLIYF GSLLQSGVPS
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HHTRPYTFGQ GTKVEIKR

BMS2h-155 (SEQ ID NO: 998)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG MDLEWYQQIP GKVPKLLIYD ASYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHKLPATFGQ GTKVEIKR

BMS2h-156 (SEQ ID NO: 999)
DIQMTQSPSS LSASVGDRVT ITCRASQDIM DNLEWYQQKP GKAPKLLIYA ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHKLPVTFGQ GTKVEIKR

BMS2h-157 (SEQ ID NO: 1000)

DIQMTQSPSS LSASVGDRVT ITCRASQNIG EDLEWYQQKP GNAPKLLIYS ASHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSSYPVTFGQ GTKVEIKR

BMS2h-158 (SEQ ID NO: 1001)
DIQMTQSPSS LSASVGDRVT ITCRASQPID EDLEWYQQKP GNAPKLLIYS ASYLQSGVPS
RFSGSGSGTD FTLTISRLQP EDFATYYCQQ YHLLPATFGQ GTKVEIKR

BMS2h-159 (SEQ ID NO: 1002)
DIQMIQSPSS LSASVGDRVT ITCRASQDIN EDLEWYQQKP GKAPKLLIYN ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP KDFATYYCQQ YHTNPTTFGQ GTKVEIKR

BMS2h-160 (SEQ ID NO: 1003)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE ADLEWYQQKP GKAPKLLIYH SSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHMSPVTFGQ GTKVEIKR

BMS2h-161 (SEQ ID NO: 1004)
DIQMTQSPSS LSASVGDRVT ITCRASQDID SDLEWYQQKP GKAPMLLIYS SSDLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSLPVTFGQ GTKVEIKR

BMS2h-162 (SEQ ID NO: 1005)
DIQMTQSPSS LSASVGDRVT ITCRASQDIS DDLEWYQQKP GKAPKLLIYN SSFLQSGVPS
RFSGSGSGAD FTLTISSLQP EDFATYYCQQ YHSLPVTFGQ GTKVEIKR

BMS2h-163 (SEQ ID NO: 1006)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE GNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHHLPTTFGQ GTKVEIKR

BMS2h-164 (SEQ ID NO: 1007)
DIQMTQSPSS LSASVGDRVT ITCRASQSID TDLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRWIPVTFGQ GTKVEIKR

BMS2h-165 (SEQ ID NO: 1008)
DIQMTQSPSS LSASVGDRVT ITCRASQSIS TDLEWYQQKL GKAPKLLIYD ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSSLPVTFGQ GTKVEIKR

BMS2h-166 (SEQ ID NO: 1009)
DIQMTQSPSS LSASVGDRVT ITCRASQPIT TSLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWVTPVTFGQ GTKVEIKR

BMS2h-167 (SEQ ID NO: 1010)
DIQMTQSPSS LSASVGDRVT ITCRASQNIH TNLEWYQQKP GKAPKLLIYD GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSANPVTFGQ GTKVGIKR

BMS2h-168 (SEQ ID NO: 1011)
DIQMTQSPSS LSASVGDRVT ITCRASQWIH TDLEWYQQKP GKAPKLLIYD GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSVSPVTFGQ GTKVEIKR

BMS2h-169 (SEQ ID NO: 1012)
DIQMTQSPSS LSASVGDRVT ITCRASQSID NNLEWYQQKP GEAPKLLIYD GSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHLHPVTFGQ GTKVEIKR

BMS2h-170 (SEQ ID NO: 1013)
DIQMTQSPSS LSASVGDRVT ITCRASQDID TNLEWYQQKP GEAPKLLIYD RSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDSYPVTFGQ GTKVEIKR

BMS2h-171 (SEQ ID NO: 1014)
DIQMTQSPSS LSASVGDRVT ITCRASQSIE SNLEWYQQKP GKAPKLLIYN ASELQSGVPS
RFSGSGSGTD FTLTISSLRP EDFATYYCQQ YDQWPTTFGQ GTKVEIKR

BMS2h-172 (SEQ ID NO: 1015)

DIQMTQSPSS LSASVGDRVT ITCRASQAIG NTLRWYQQKP GKAPKLLIYL SSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LKKPPYTFGQ GTKVEIKR

BMS2h-173 (SEQ ID NO: 1016)
DIQMTQSPSS LSASVGDRVT ITCRASQKIK NRLAWYQQKP GKAPKLLIYE VSHLQSGVPS
RFSGSGSGTD FTLTIGSLQP EDFATYYCQQ RRQSPYTFGQ GTKVEIKR

BMS2h-174 (SEQ ID NO: 1017)
DIQMTQSPSS LSASVGDRVT ITCRASEDIG EELFWYQQKP GKAPKLLIYS ASTLQSEVPS
RFSGSGSGTD FTLTISSLQH EDFATYYCQQ VYEWPYTFGQ GTKVEIKR

BMS2h-175 (SEQ ID NO: 1018)
DIQMTQSPSS LSASVGDRVT ITCRASQPIS GGLRWYQQKP GKAPKLLIYS TSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYSAPYTFGQ GTKVEIKR

BMS2h-305 (SEQ ID NO: 1019)
DIQMTQSPSS LSASVGDRVT ITCRASQDID QDLEWYQQKP GKAPKLLIYN VSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSMNPVTFGQ GTKVEIKR

BMS2h-306 (SEQ ID NO: 1020)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG NQLKWYQQKP GKAPKLLIYQ ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDLRPQTFGQ GTKVEIKR

BMS2h-307 (SEQ ID NO: 1021)
DIQMTQSPSF LSASVGDRVT ITCRASQKIS TSLEWYQQKP GKAPRLLIYD SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YEYNPITFGQ GTKVEIKR

BMS2h-33 (SEQ ID NO: 1022)
DIQMTQSPSS LSASVGDRVT ITCRASQTIG ESLHWYQQKP GKAPRLLIYF ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HHMLPSTFGQ GTKVEIKR

BMS2h-35 (SEQ ID NO: 1023)
DIQMTQSPSS LSASVGDRVT ITCRASQFIG DSLSWYQQKP GKAPKLLIYF SSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YMDIPITFGQ GTKVEIKR

BMS2h-36 (SEQ ID NO: 1024)
DIQMTQSPSS LSASVGDRVT ITCRASQDID HNLEWYQQKP GKAPKLLIYD SSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSIPVTFGQ GTKVEIKR

BMS2h-37 (SEQ ID NO: 1025)
DIQMTQSPSS LSASVGDRVT ITCRASQQIE TNLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSLPATFGQ GTKVEIKR

BMS2h-38 (SEQ ID NO: 1026)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG NNLEWYQQKP GKAPRLLIYH GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDFNPTTFGQ GTKVEIKR

BMS2h-39 (SEQ ID NO: 1027)
DIQMTQSPSS LSASVGDCVT ITCRASQNID GLLWWYQQKP GKAPKLLIYA GSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ KAFEPFTFGQ GTKVEIKR

BMS2h-405 (SEQ ID NO: 1028)
DIQMTQTPSS LSASVGDRVT ITCRASQSIG HDLEWYQQKP GKAPKLLIYN VSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSHNPPTFGQ GTKVEIKR

BMS2h-406 (SEQ ID NO: 1029)
DIQMTQSPSS LSASVGDRVT ITCRASQHIE NDLEWYQQKP GKAPKLLIYS ASHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHLQPTTFGP GTKVEIKR

BMS2h-431 (SEQ ID NO: 1030)

DIQMTQSPSS LSASVGDRVT ITCRASQVIE GSLNWYQQKP GKAPKLLIYH RSILQSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ TYQLPLTFGQ GTKVEIKR

BMS2h-432 (SEQ ID NO: 1031)
DIQMTQSPSS LSASVGDRVT ITCRASRPIN GKLFWYQQKP GKAPKLLIAF ASALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ QAVYPITFGQ GTKVEIKR

BMS2h-433 (SEQ ID NO: 1032)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE TNLEWYQQKP GKAPKLLIYD GSLLQSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YHYQPATFGQ GTKVEIKR

BMS2h-434 (SEQ ID NO: 1033)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE HDLEWYQQKP GKAPKLLIYS ASQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YQQQPTTFGQ GTKVEIKR

BMS2h-435 (SEQ ID NO: 1034)
DIQMTQSPSS LSASVGDRVT ITCRASSQIE ESLWWYQQKP GKAPKLLIAD VSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ GVVEPRTFGQ GTKVEIKR

BMS2h-436 (SEQ ID NO: 1035)
DIQMTQSPSS LSASVGDRVT ITCRASQYIG LDLEWYQQKP GKAPKLLIYA ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFRQPITFGQ GTKVEIKR

BMS2h-437 (SEQ ID NO: 1036)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

BMS2h-437-1 (SEQ ID NO: 1037)
DIQLTQSPTS LSATVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRHPATFGQ GTKVEIKR

BMS2h-437-2 (SEQ ID NO: 1038)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVGIKR

BMS2h-437-3 (SEQ ID NO: 1039)
DIQMTQSPSS LSASVGDRVT ITCRVSTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPP
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

BMS2h-437-4 (SEQ ID NO: 1040)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGCGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

BMS2h-437-5 (SEQ ID NO: 1041)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMIDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGK GTKVEIKR

BMS2h-438 (SEQ ID NO: 1042)
DIQMTQSPSS LSASVGDRVT ITCRASQYID TNLEWYQQKP GKAPRLLIYD GSQLQSGVPS
RFSGSGSGTD FTLIISSLQP EDFATYYCQQ YQVVPVTFGQ GTKVEIKR

BMS2h-439 (SEQ ID NO: 1043)
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPRLLIVD SSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ DRWSPATFGQ GTKVEIKR

BMS2h-440 (SEQ ID NO: 1044)
DIQMTQSPSS LSASVGDRVT ITCRASSRIQ HMLSWYQQKP GKAPKLLIGG HSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ SCAWPLTFGQ GTKVEIKR

BMS2h-441 (SEQ ID NO: 1045)

DIQMTQSPSS LSASVGDRVT ITCRASRGID GDLWWYQQKP GKAPKLLIAD SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVRPMTFGQ GTKVEIKR

BMS2h-442 (SEQ ID NO: 1046)
DIQMTQSPSS LSASVGDRVT ITCRASRGID TDLWWYQQKP GKAPKLLIAD SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVRPMTFGQ GTKVEIKR

BMS2h-443 (SEQ ID NO: 1047)
DIQMTQSPSS LSASVGDRVT ITCRASYTIP VALDWYQQKP GKAPKLLIAD ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ GWPGPQTFGQ GTKVEIKR

BMS2h-444 (SEQ ID NO: 1048)
DIQMTQSPSS LSASVGDRVT ITCRASQSIA TDLEWYQQKP GKAPKLLIYD TSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSYNPSTFGQ GTKVEIKR

BMS2h-445 (SEQ ID NO: 1049)
DIQMTQSPSS LSASVGDRVT ITCRASVPIT EGLSWYQQKP GKAPKLLIQA NSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WEHVPATFGQ GTKVEIKR

BMS2h-446 (SEQ ID NO: 1050)
DIQMTQSPSS LSASVGDRVT ITCRASSMIL YGLDWYQQKP GKAPKLLIGG TSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WETVPATFGQ GTKVEIKR

BMS2h-447 (SEQ ID NO: 1051)
DIQMTQSPSS LSASVGDRVT ITCRASQPIN GLLIWYQQKP GKAPKLLIYA MSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LARIPFTFGQ GTKVGIKR

BMS2h-448 (SEQ ID NO: 1052)
DIQMTQSPSS LSASVGDRVT ITCRASQLIR TYLAWYQQKP GKAPKLLIYQ SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPDTFGQ GTKVEIKR

BMS2h-47 (SEQ ID NO: 1053)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG DSLSWYQQKP GKAPKLLIYF GSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLHTPSTFGQ GTKVEIKR

BMS2h-484 (SEQ ID NO: 1054)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE ADLEWYQQKP GKAPKLLIYH SSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YGFNPPTFGQ GTKVEIKR

BMS2h-485 (SEQ ID NO: 1055)
DIQMTQSPSS LSASVGDRVT ITCRASSPIE YGLDWYQQKP GKAPKLLIGG GSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WEVQPATFGQ GTKVEIKR

BMS2h-486 (SEQ ID NO: 1056)
DIQMTQSPSS LSASVGDRVT ITCRASQRID TDLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSAPATFGQ GTKVEIKR

BMS2h-487 (SEQ ID NO: 1057)
DIQMTQSPSS LSASVGDRVT ITCRASGWIG MSLEWHQQKP GKAPKLLIRG ASSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCSQ SRWPPVTFGQ GTKVEIKR

BMS2h-488 (SEQ ID NO: 1058)
DIQMTQSPSS LSASVGDRVT ITCRASRNIS NALSWYQQKP GKAPKLLILG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCTQ VWDRPFTFGQ GTKVEIKR

BMS2h-489 (SEQ ID NO: 1059)
DIQMTQSPSS LSASVGDRVT ITCRASQDIM SALSWYQQKP GKAPKLLIYS TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VYLLPVTFGQ GTKVEIKR

BMS2h-490 (SEQ ID NO: 1060)

DIQMTQSPSS LSASVGDRVT ITCRASQEIG IDLEWYQQKP GKAPKLLIYA ASYLQSGVPS RFSSSGSGTD FTLTISSLQP EDFATYYCQQ YASNPPTFGR GTKVEIKR

BMS2h-491 (SEQ ID NO: 1061)
DIQMTQSPSS LSASVGDRVT ITCRASQMIG DWLNWYQQKP GKAPKLLIYR SSELQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYFWPRTFGQ GTKVEIKR

BMS2h-492 (SEQ ID NO: 1062)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE LNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-1 (SEQ ID NO: 1063)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YDAYPPTYGQ GTKVEIKR

BMS2h-492-2 (SEQ ID NO: 1064)
DIQMTQSPSS LSASVGDRVT ITCRASRAIE TNLEWYQQKP GKAPKLLFYD ASMLQSGVPS RFGGSGSGTD FTLTISSLQP EDFATYYCLQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-3 (SEQ ID NO: 1065)
DIQMTQSPSS LSATVGDRVT ITCRASQAIE TNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-4 (SEQ ID NO: 1066)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-5 (SEQ ID NO: 1067)
DIQMNQSPSS LSASVGDRVS ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-6 (SEQ ID NO: 1068)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE SNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-7 (SEQ ID NO: 1069)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-493 (SEQ ID NO: 1070)
DIQMTQSPSS LSASVGDRVT ITCRASQGID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494 (SEQ ID NO: 1071)
DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494-1 (SEQ ID NO: 1072)
DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSQYPPTFGQ GTKVEIKR

BMS2h-494-2 (SEQ ID NO: 1073)
DIQMTQSPSS LSASVGDRVT ITCRASQSIE EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGH GTKVEIKR

BMS2h-494-3 (SEQ ID NO: 1074)
DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYFCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494-4 (SEQ ID NO: 1075)

EIQMTQSPSS LSASVGDRVT MTCRASQSID KDLEWYQQKP GKAPRLLIYS SSWLQRGVPS
RFSGSGSGTD FTLTISSLRP EDFATYYCQQ YFQYPPTLGQ GTKVEIKR

BMS2h-494-5 (SEQ ID NO: 1076)
DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISGLQP EDIATYYCKQ YSQYPPTFGQ GTKVEIKR

BMS2h-494-6 (SEQ ID NO: 1077)
DIQMTQSPPS LSASVGDRVT ITCRASQSID KDLEWYQQKP GKAPRLLIYS SSWLQRGVPS
RFSGSGSGTD FTLTISSLQP EDFATYHCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-495 (SEQ ID NO: 1078)
DIQMTQSPSS LSASVGDRVT ITCRASEYIN AELAWYQQKP GKAPKLLIYG SSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCLQ NAMWPITFGQ GTKVEIKR

BMS2h-496 (SEQ ID NO: 1079)
DIQMTQSPSS LSASVGDRVT ITCRASLDIN NGLIWYQQKP GKAPRLLILG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCSQ VRSRPFTFGQ GTKVEIKR

BMS2h-497 (SEQ ID NO: 1080)
DIQMTQSPSS LSASVGDRVT ITCRASQDIL SALAWYQQKP GKAPKLLIYG SSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NYSLPITFGQ GTKVEIKR

BMS2h-498 (SEQ ID NO: 1081)
DIQMTQSPSS LSASVGDRVT ITCRASSPIE SYLRWYQQKP GKAPKLLIRY VSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WFRAPVTFGQ GTKVEIKR

BMS2h-499 (SEQ ID NO: 1082)
DIQMTQSPSS LSASVGDRVT ITCRVSESIN AELHWYQQKP GKAPKLLISG FSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ FAMWPFTFGQ GTKVEIKR

BMS2h-500 (SEQ ID NO: 1083)
DIQMTQSPSS LSASVGDRVT ITCRASMMIR FGLDWYQQKP GKAPKLLIGG GSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HERWPATFGQ GTKVEIKR

BMS2h-501 (SEQ ID NO: 1084)
DIQMTQSPSS LSASVGDRVT ITCRASQSIG TLLRWYQQKP GKAPKLLIYL TSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ MVYRPYTFGQ GTKVEIKR

BMS2h-502 (SEQ ID NO: 1085)
DIQMTQSPSS LSASVGDRVT ITCRASQTIE TNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDKVPATFGQ GTKVEIKR

BMS2h-503 (SEQ ID NO: 1086)
DIQMTQSPSS LSASVGDRVT ITCRASHHIQ RYLSWYQQKP GKAPKLLILW GSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPPTFGQ GTKVEIKR

BMS2h-503-1 (SEQ ID NO: 1087)
DIQMTQSPSS LSASVGDRVT ITCRASHHIQ RYLSWYQQKP GKAPKLLILW GSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPQTFGQ GTKVEIKR

BMS2h-503-2 (SEQ ID NO: 1088)
DIQMTQSPSS LSASVGDRVT ITCRASHDIQ RYLSWYQQKP GKAPKLLILW GSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPQTFGQ GTKVEIKR

BMS2h-504 (SEQ ID NO: 1089)
DIQMTQSPSS LSASVGDRVT ITCRASQYID TNLEWYQQKP GKAPKLLIYD GSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVVPVTFGQ GTKVEIKR

BMS2h-508 (SEQ ID NO: 1090)

DIQMTQSPSS LSASVGDRVT ITCRASQDIA FDLEWYQQKP GKAPKLLIYS ASMLQSGVPS
RFSGSGSGSD FTLTISSLQP EDFATYYCQQ YNLQPPTFGQ GTKVEIKR

BMS2h-509 (SEQ ID NO: 1091)
DIQMTQSPSS LSASVGDRVT ITCRASQNIA TLLRWYQQKP GKAPKLLIYA GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ MWQRPYTFGQ GTKVEIKR

BMS2h-51 (SEQ ID NO: 1092)
DIQMTQSPSS LSASVGDRVT ITCRASQPIV DELDWYQQKP GKAPKLLIYA ASILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCHQ WSTYPTTFGQ GTKVEIKR

BMS2h-510 (SEQ ID NO: 1093)
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIDG VSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ DWDWPRTFGQ GTKVEIKR

BMS2h-511 (SEQ ID NO: 1094)
DIQMTQSPSS LSASVGDRVT ITCRASRNIR DWLRWYQQKP GKAPKLLIDW GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ TWDDPLTFGQ GTKVEIKR

BMS2h-511-1 (SEQ ID NO: 1095)
DIQMTQSPSS LSAFVGDRVT ITCRASRNIR DWLRWYQQKP GKAPKLLIDW GSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ TWYDPLTFGH GTKVEIKR

BMS2h-512 (SEQ ID NO: 1096)
DIQMTQSPSS LSASVGDRVT ITCRASIDIH GGLTWYQQKP GKAPKLLIVG VSGLQSGVPS
RFSGSGSGTD FTLTISNLQP EDFATYYCAQ VWRRPFTFGQ GTKVEIKR

BMS2h-513 (SEQ ID NO: 1097)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG SSLSWYQQKP GKAPKLLIYA SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TYALPVTFGQ GTKVEIKR

BMS2h-514 (SEQ ID NO: 1098)
DIQMTQSPSS LSASVGDRVT ITCRASQQIE TNLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YKYLPVTFGQ GTKVEIKR

BMS2h-52 (SEQ ID NO: 1099)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG SALRWYQQKP GKAPKLLIYL GSDLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TQYFPTTFGQ GTKVEIKR

BMS2h-53 (SEQ ID NO: 1100)
DIQMTQSPSS LSASVGDRVT ITCRASQAIY GGLRWYQQKP GKAPKLLIYG ESMLQSGVPS
RFSGSGSGTD FTLTISSLHP EDFATYYCQQ VYHKPFTFGQ GTKVEIKR

BMS2h-536 (SEQ ID NO: 1101)
DIQMTQSPSS LSASVGDRVT ITCRASQRIG VWLDWYQQKP GKAPKLLIYD GSFLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TFSSPSTFGQ GTKVEIKR

BMS2h-537 (SEQ ID NO: 1102)
DIQMTQSPSS LSASVGDRVP ITCRASQWIG DELYWYQQKP GKAPKLLIYS SSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SFQFPYTFGQ GTKVEIKR

BMS2h-538 (SEQ ID NO: 1103)
DIQMTQSPSS LSASVGDRVT ITCRASSNIT GPLEWYQQKP GKAPKLLIPG WSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ VWGEPVTFGQ GTKVEIKR

BMS2h-539 (SEQ ID NO: 1104)
DIQMTQSPSS LSASIGDRVT ITCRASQRIA YGLHWYQQKP GKAPRLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ PGMPPDTFGQ GTKVEIKR

BMS2h-540 (SEQ ID NO: 1105)

DIQMTQSPSS LSASVGDRVT ITCRASKQIV GGLSWYQQKP GKAPKLLIGR HSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ GVWAPGTFGQ GTKVEIKR

BMS2h-541 (SEQ ID NO: 1106)
DIQMTQSPSS LSASVGDRVT ITCRASPAIA AKLDWYQQKP GKAPKLLIGA DSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWAGPPTFGQ GTKVEIKR

BMS2h-542 (SEQ ID NO: 1107)
DIQMTQSPSS LSASVGDRVT ITCRASRTIA DGLDWYQQKP GKAPKLLIGA YSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWEGPPTFGQ GTKVEIKR

BMS2h-543 (SEQ ID NO: 1108)
DIQMTQSPSS LSASVGDRVT ITCRASQRIY GFLDWYQQKP GKAPKLLIYG VSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TLAWPFTFGQ GTKVEIKR

BMS2h-544 (SEQ ID NO: 1109)
DIQMTQSPSS LSASVGDRVT ITCRASQDIR DWLMWYQQKP GKAPKLLIYW GSFLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYDTPYTFGQ GTKVEIKR

BMS2h-545 (SEQ ID NO: 1110)
DIQMTQSPSS LSASVGDRVT ITCRASQNIN TGLDWYQQKP GKAPKLLIYD SSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TSYYPYTFGQ GTKVEIKR

BMS2h-546 (SEQ ID NO: 1111)
DIQMTQSPSS LSASVGDRVT ITCRASQKIF GWLDWYQQKP GKAPKLLIYG TSKLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VYSLPYTFGQ GTKVEIKR

BMS2h-547 (SEQ ID NO: 1112)
DIQMTQSPSS LSASVGDRVT ITCRASSNIG ADLDWYQQKP GKAPKLLIGG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWNGPPTFGQ GTKVEIKR

BMS2h-548 (SEQ ID NO: 1113)
DIQMTQSPSS LSASVGDRVT ITCRASSPIY DGLDWYQQKP GKAPKLLISG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWLGPPTFGQ GTKVEIKQ

BMS2h-549 (SEQ ID NO: 1114)
DIQMTQSPSS LSASVGDRVT ITCRASSRIY NGLHWYQQKP GKAPKLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ VGEAPSTFGQ GTKVEIKR

BMS2h-550 (SEQ ID NO: 1115)
DIQMTQSPSS LSASVGDRVT ITCRASRFIN EELDWYQQKP GKAPKLLISW SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ PGGGPGTFGQ GTKVEIKR

BMS2h-551 (SEQ ID NO: 1116)
DIQMTQSPSS LSASVGDRVT ITCRASRDIL DELDWYQQKP GKAPRLLIGG GSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWHGPPTFGQ GTKVEIKR

BMS2h-552 (SEQ ID NO: 1117)
DIQMTQSPSS LSASVGDRVT ITCRASSPIY TGLHWYQQKP GKAPKLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCMQ VGTAPATFGQ GTKVEIKR

BMS2h-585 (SEQ ID NO: 1118)
DIRMTQSPSS LSASVGDRVT ITCRASQNIS RRLLWYQQKP GKAPKLLIYS SSRLQSGVPS
RFGGSGSGTD FTLTISSLQP EDFATYYCQQ TYSYPHTFGQ GTKVEIKR

BMS2h-604 (SEQ ID NO: 1119)
DIQMTQSPSS LSASVGDRVT ITCRASSPIP QDLYWYQQKP GKAPKLLIVG ISQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWSAPATFGQ GTKVEIKR

BMS2h-605 (SEQ ID NO: 1120)

DIQMTQSPSS LSASVGDRVT ITCRASKSID GMLDWYQQKP GKAPKLLIPG FSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SVEAPWTFGQ GTKVEIKR

BMS2h-606 (SEQ ID NO: 1121)
DIQMTQSPSS LSASVGDRVT ITCRASRYIA HPLDWYQQKP GKAPKLLIPG SSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SVVVPWTFGQ GTKVEIKR

BMS2h-607 (SEQ ID NO: 1122)
DIQMTQSPSS LSASVGDRVT ITCRASRTIE GGLDWYQQKP GKAPKLLIMG GSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWVGPPTFGQ GTKVEIKR

BMS2h-608 (SEQ ID NO: 1123)
DIQMTQSPSS LSASVGDRVT ITCRASKFIR DELYWYQQKP GKAPRLLIGG SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWRAPATFGQ GTKVEIKR

BMS2h-609 (SEQ ID NO: 1124)
DIQMTQSPSS LSASVGDRVT ITCRASKPIY GGLEWYQQKP GKAPRLLIGG GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ VWGGPVTFGQ GTKVEIKR

BMS2h-610 (SEQ ID NO: 1125)
DIRMTQSPSS LSASVGDRVT ITCRASRPIS GCLDWYQQKP GKAPKLLIDG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWEYPPTFGQ GTKVEIKR

BMS2h-611 (SEQ ID NO: 1126)
DIQMTQSPSS LSASVGDRVT ITCRASKPIV RDLEWYQQKP GKAPKLLIHG VSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LEAAPATFGQ GTKVEIKR

BMS2h-612 (SEQ ID NO: 1127)
DIQMTQSPSS LSASVGDRVT ITCRASRDIG DWLYWYQQKP GKAPRLLIVW ASVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ WGTPPTTFGQ GTKVEIKR

BMS2h-613 (SEQ ID NO: 1128)
DIQMTQSPSS LSASVGDRVT ITCRASNRIE YGLDWYQQKP GKAPKLLISG SSRLQSGVPS
RFSSSGSGTD FTLTISSLQP EDFATYYCGQ LEAAPATFGQ GTKVEIKR

BMS2h-614 (SEQ ID NO: 1129)
DIQMTQSPSS LSASVGDRVT ITCRASRNIG HFLDWYQQKP GKAPKLLILG GSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LVEPPATFGQ GTKVEIKR

BMS2h-615 (SEQ ID NO: 1130)
DIQMTQSPSS LSASVGDRVT ITCRASSSIY SDLYWYQQKP GKAPKLLIDG WSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LHRAPATFGQ GTKVEIKR

BMS2h-616 (SEQ ID NO: 1131)
DIQMTQSPSS LSASVGDRVT ITCRASRFIT DRLDWYQQKP GKAPKLLIGG VSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SSELPWTFGQ GTKVEIKR

BMS2h-617 (SEQ ID NO: 1132)
DIQMTQSPSS LSASVGDRVT ITCRASRKIG SELYWYQQKP GKAPKLLIGG RSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWEPPATFGQ GTKVEIKR

BMS2h-618 (SEQ ID NO: 1133)
DIQMTQSPSS LSASVGDRVT ITCRASRNIG NGLDWYQQKP GKAPKLLIGE GSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWHTPPTFGQ GTKVEIKR

BMS2h-619 (SEQ ID NO: 1134)
DIQMTQSPSS LSASVGDRVT ITCRASRNIY GWLSWYQQKP GKAPRLLIGG WSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ DYTLPGTFGQ GTKVEIKR

BMS2h-730 (SEQ ID NO: 1135)

DIQMTQSPSS LSASVGDRVT ITCRASQDIK DWLHWYQQKP GKAPKLLIYF ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDSATYYCQQ HYSTPYTSGQ GTKVEIKR

BMS2h-731 (SEQ ID NO: 1136)
DIQMTQSPPS LSASVGDRVT ITCRASQLIS SHLDWYQQKP GKAPKLLVYD ASELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HRSLPFTFGQ GTKVEIKR

BMS2h-732 (SEQ ID NO: 1137)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG GALAWYQQKP GKAPRLLIYQ ISVLQSGIPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YIRSPFTFGQ GTKVEIKR

BMS2h-733 (SEQ ID NO: 1138)
DIQMTQSPSS LSASVGDRVT ITCRASQSIG AALNWYQQKP GKAPKLLIYG LSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LFRLPLTFGQ GTKVEIKR

BMS2h-734 (SEQ ID NO: 1139)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG GRLVWYQQKP GKAPKLLIYG SSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YAEAPITFGQ GTKVEIKR

BMS2h-735 (SEQ ID NO: 1140)
DIQMTQSPSS LSASVGDRVT ITCRASQNIG SSLIWYQQKP GKAPTLLIYY SSKLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SLSSPYTVGQ GTKVEIKR

BMS2h-736 (SEQ ID NO: 1141)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG SELAWYQQKP GKAPKLLIYW TSNLQSGVPS
RFSGSGSGTD FTLTISNLQP EDFATYYCQQ ILETPLTFGQ GTKVEIKR

BMS2h-737 (SEQ ID NO: 1142)
DIQMTQSPSS LSASVGDRVT ITCRASQKIW DALYWYQQKP GKAPKLLIYR GSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ FYRWPHTFGQ GTKVEIKR

BMS2h-738 (SEQ ID NO: 1143)
DIQMTQSPSS LSASVGDRVT ITCRASQHIE DSLRWYQQKP GKAPKLLIYY GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ MYKFPITFGQ GTKVEIKR

BMS2h-739 (SEQ ID NO: 1144)
DIQTTQSPSS LSASVGDRVT ITCRASQRIN SSLLWYQQKP GKAPKLLIYD TSTLQSGVPS
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ IWGSPPTFGQ GTKVEIKR

BMS2h-740 (SEQ ID NO: 1145)
DIQMTQSPSS LSASVGDRVT ITCRASQSIP VGLNWYQQKP GKAPRLLIYS GSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ DWYYPNTFGQ GTKVEIKR

BMS2h-785 (SEQ ID NO: 1146)
DIQMTQSPSS LSASVGDRVT ITCRASQPIY GWLNWYQQKP GKAPKLLIYL TSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IHSSPFTFGQ GTKVEIKR

BMS2h-8 (SEQ ID NO: 1147)
DIQMTQSPSS LSASVGDRVT ITCRASQFID TSLEWYQQKP GKAPKLLIYD GSHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YWVLPLTFGQ GTKVEIKR

BMS2h-86 (SEQ ID NO: 1148)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG DALFWYQQKP GKAPKLLIYY SSMLQSGVPS
RFSGGGSGTD FTLTISSLQP EDFATYYCQQ RHSTPATFGQ GTKVEIKR

BMS2h-87 (SEQ ID NO: 1149)
DIQMTQSPSS LSASVGDRVT ITCRASQDID ESLMWYQQKP GKAPRLLIYG VSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RWKAPFTFGQ GTKVEIKR

BMS2h-88 (SEQ ID NO: 1150)

DIQMTQSPSS LSASVGDRVT ITCRASQEIV EDLYWYQQKP GKAAKLLIYG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TRRRPYTFGQ GTKVEIKR

BMS2h-89 (SEQ ID NO: 1151)
DIQMTQSPAS LSASVGDRVT ITCRASQDID PMLRWYQQKP GKAPKLLIYA GSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TLVTPYTFGQ GTKVEIKR

BMS2h-90 (SEQ ID NO: 1152)
DIQMTQSPSS LSASVGDRVT ITCRASQSIS DALFWYQQKP GKAPRLLIYY GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RFQEPVTFGQ GTKVEIKR

BMS2h-91 (SEQ ID NO: 1153)
DIQMTQSPSS LSASVGDRVT ITCRASQQIS DELNWYQQKP GKAPKLLIYA VSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ WLSFPSTFGQ GTKVEIKR

TABLE 4

Human Anti-CD40L VK Domain Encoding Nucleotide Sequences

BMS2h-100 (SEQ ID NO: 1154)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGAGCAAGTCAGAATATTAAGCATTCGTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATCATCGTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTAGGCATCGTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-101 (SEQ ID NO: 1155)
GACATCCAGATGACCCAGTCTCCATCCTCTCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTGCTTTGTTTCCCTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-102 (SEQ ID NO: 1156)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCATATTGGTCATCATTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCCAAGCTCCTGATCTATCATAGGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGTGGGATAGGCCGCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-103 (SEQ ID NO: 1157)
GACATCCAGATGACCCAGTCCCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTGCGGGCTGTGCCTTATACGTTTGGCCAA
GGGACCAAGGTGGAAATTAAACGG

BMS2h-104 (SEQ ID NO: 1158)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTCGTTTTTCTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-105   (SEQ ID NO: 1159)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTCTTATGCTAGGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-106   (SEQ ID NO: 1160)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAAAGTATTAATCATAGGTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAGGATTTTGCTACGTACTACTGTCAACAGTATAAGGTTAGGCCTAATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-107   (SEQ ID NO: 1161)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATTTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTATTCGTCTCCTCATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-108   (SEQ ID NO: 1162)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGAGGGCGGTGAGGCCTTTTACGTTCGGCCAA
GGGACCAAAGTGGAAATCAAACGG

BMS2h-109   (SEQ ID NO: 1163)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTATTATCGTCCTCTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-110   (SEQ ID NO: 1164)
GACATCCAGATGACCCAGTCTCCAGCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATCCTATGTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTAGTATTAGGCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116   (SEQ ID NO: 1165)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-1   (SEQ ID NO: 1166)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATATACTGTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATCTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-10 (SEQ ID NO: 1167)
GACATCCAGATAACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATATTGCGAAGTGGAGTCCCATCA
CGTTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATCTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-11 (SEQ ID NO: 1168)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTTCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-12 (SEQ ID NO: 1169)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAACCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCTTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGCGGATCTGGGACTGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-13 (SEQ ID NO: 1170)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1312 (SEQ ID NO: 1171)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATCTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCAAA
GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1313 (SEQ ID NO: 1172)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCGA
GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1314 (SEQ ID NO: 1173)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGAGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCGGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGTGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1319 (SEQ ID NO: 1174)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTATGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-1320 (SEQ ID NO: 1175)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATATGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACCCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTAAGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGTGATCAAACGG

BMS2h-116-138 (SEQ ID NO: 1176)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GTAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTAGTAATCAAACGG

BMS2h-116-14 (SEQ ID NO: 1177)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTTCCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-15 (SEQ ID NO: 1178)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATCGGTCCTGATTTACTGTGGTACCGGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-16 (SEQ ID NO: 1179)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGATCCTGACTTACTGTGGTACCAGCAGAAACCA
GGTAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGTTTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCATTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-17 (SEQ ID NO: 1180)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCAGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAGCCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-2 (SEQ ID NO: 1181)
GACATCCAGATGACCCAGTCTCCATCATCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGAACCTGATTTACTGTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTCTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-3 (SEQ ID NO: 1182)
GACATCCAGATGACCCAGTCACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCTAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGCGGCAGTGAATCCGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATATTGCAACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAGGGTGGAAATCAAACGG

BMS2h-116-4 (SEQ ID NO: 1183)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCTTCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-5 (SEQ ID NO: 1184)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCGCC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATATACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGTCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-6 (SEQ ID NO: 1185)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCGTCA
CGTTTCAGTGGCAGTGGATCTGTGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGGAATCAAGCGG

BMS2h-116-7 (SEQ ID NO: 1186)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGATCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTAGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-8 (SEQ ID NO: 1187)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAGCAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-9 (SEQ ID NO: 1188)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTATGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-141 (SEQ ID NO: 1189)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATACGTTAACGTGGTACCAGCAGAAACTA
GGGAAAGCCCCTAAGCTCCTGATCTATGGTGGTTCCGAGTTGCAAAGTGGGGTCCCACCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTGTATTAGTAGTCCTTGTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-142 (SEQ ID NO: 1190)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTTTATTGGTGATTCTTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTTCTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATACTTCGCCTACTACGTTCGGCCGA
GGGACCAAGGTGAAAATCAAACGG

BMS2h-143 (SEQ ID NO: 1191)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGACTATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATTCTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTAGCTACGTACTACTGTCAACAGTATCATGGGTATCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-144 (SEQ ID NO: 1192)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGATGATTGATCAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATGGTTATCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-145 (SEQ ID NO: 1193)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGACGATTTATACTTCGTTAAGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCATTATGGTTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGGTTCATCAGGCTCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-146 (SEQ ID NO: 1194)
GACATCCGGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATTCTTTAGCGTGGTACCAGCAGAAGCCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGTATTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACTGTCTAGTAGTATGCCTCATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-147 (SEQ ID NO: 1195)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGAGATTGAGACGAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATTCGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCAGAATCCTCCGACGTTCGGCCAA
GGAACCAAGGTGGAAATCAAACGG

BMS2h-149 (SEQ ID NO: 1196)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGAGGCAGTTAGTTTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATGGGGCGACCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTTAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCAGTCGAAGGGTCCTCTTACGTTCGGCCAT
GGGACCAAGGTGGAAATCAAACGG

BMS2h-150 (SEQ ID NO: 1197)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGGGATTGGTACTGATTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATATGGGTTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATTTATTCTTTTCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-154 (SEQ ID NO: 1198)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGAGATGTTACATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTGGTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTAGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCATCATACTCGTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-155 (SEQ ID NO: 1199)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGATGGATTTAGAGTGGTACCAGCAGATACCA
GGGAAAGTCCCTAAGCTCCTGATCTATGATGCGTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAAGCTTCCTGCGACGTTTGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-156 (SEQ ID NO: 1200)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTATGGATAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAAGTTGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-157 (SEQ ID NO: 1201)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGAGCAAGTCAGAATATTGGGGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAATGCCCCTAAGCTCCTGATCTATAGTGCGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTAGTTATCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-158 (SEQ ID NO: 1202)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCCGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCGATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAATGCCCCTAAGCTCCTGATCTATAGTGCGTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGACTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCTGCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-159 (SEQ ID NO: 1203)
GACATCCAGATGATCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTAATGAGGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
AAAGATTTTGCTACGTACTACTGTCAACAGTATCATACTAATCCTACTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-160 (SEQ ID NO: 1204)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGCGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATTCTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATATGTCGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-161 (SEQ ID NO: 1205)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATAGTGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTATGCTCCTGATCTATTCTTCGTCCGATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTCTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-162 (SEQ ID NO: 1206)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTTCGGATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATTCGTCCTTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGGCAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTTTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-163 (SEQ ID NO: 1207)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGGTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATTCGTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCATCTTCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-164 (SEQ ID NO: 1208)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATACGGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCGGTGGATTCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-165 (SEQ ID NO: 1209)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTAGTACTGATTTAGAGTGGTACCAGCAGAAACTA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCCTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCGAGTCTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-166 (SEQ ID NO: 1210)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTACGACGTCTTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGCGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGTTACGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-167 (SEQ ID NO: 1211)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACCTGCCGGGCAAGTCAGAATATTCATACGAATTTAGAGTGGTATCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCGGCTAATCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGGAATCAAACGG

BMS2h-168 (SEQ ID NO: 1212)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTCATACGGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTGTGTCGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-169 (SEQ ID NO: 1213)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATAATAATTTAGAGTGGTACCAGCAGAAACCA
GGGGAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCATCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-170 (SEQ ID NO: 1214)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGGAAGCCCCTAAGCTCCTGATCTATGATCGTTCCACGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTCTTATCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-171 (SEQ ID NO: 1215)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTCTATTGAGTCTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGCGTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCGACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATCAGTGGCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-172 (SEQ ID NO: 1216)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGGCTATTGGTAATACTTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCTTAGTTCCAGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCTGAAGAAGCCTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-173 (SEQ ID NO: 1217)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAAGATTAAGAATCGGTTAGCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGAGGTTTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGAGGAGGCAGTCGCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-174 (SEQ ID NO: 1218)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTGAGGATATTGGGGAGGAGTTATTTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCGGCGTCCACGTTGCAAAGTGAGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACAT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATGAGTGGCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-175 (SEQ ID NO: 1219)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTTCTGGGGGTTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTACTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCTTTATTCTGCTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-305(SEQ ID NO: 1220)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATCAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGTTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTATGAATCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-306 (SEQ ID NO: 1221)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGAATCAGTTAAAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGGCTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTTGAGGCCTCAGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-307 (SEQ ID NO: 1222)
GACATCCAGATGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGGTGACCGTGTCACC
ATCACTTGCCGGGCGAGTCAGAAGATTTCTACGTCTTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATGATTCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGAGTATAATCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-33 (SEQ ID NO: 1223)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGACGATTGGGGAGAGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTTTGCTTCCCTGTTGCAAAGTGGGGTCCCATCG
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCATCATATGCTTCCTTCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-35 (SEQ ID NO: 1224)
GACATCCAAATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTTTATTGGTGATTCTTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTTCTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATATGGATATTCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-36 (SEQ ID NO: 1225)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATCATAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATTCTATTCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-37 (SEQ ID NO: 1226)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCAGATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTTTGCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-38 (SEQ ID NO: 1227)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGTAATAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATCATGGGTCCTGGTTGCAAAGTGGGGTCCCATCG
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTTTAATCCTACTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-39 (SEQ ID NO: 1228)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACTGTGTCACC
ATCACTTGCCGGGCAAGTCAGAATATTGATGGTCTGTTATGGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGAAGGCTTTTGAGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-405 (SEQ ID NO: 1229)
GACATCCAGATGACCCAGACTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGGTCATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGTGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTCATAATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-406 (SEQ ID NO: 1230)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGCATATTGAGAATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTGCTTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCAGCCTACGACGTTCGGCCCA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-431 (SEQ ID NO: 1231)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGGTTATTGAGGGTAGTTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATAGGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCCGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTATCAGCTTCCTTTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-432 (SEQ ID NO: 1232)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGTCCTATTAATGGTAAGTTATTTTGGTACCAGCAGAAACCA
GGCAAAGCCCCTAAGCTCCTGATCGCGTTTGCTTCCGCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGCAGGCTGTGTATCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-433 (SEQ ID NO: 1233)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATTATCAGCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-434 (SEQ ID NO: 1234)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGCATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCGGCGTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCAGCAGCAGCCTACTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-435 (SEQ ID NO: 1235)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCGCAGATTGAGGAGTCTTTATGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGCGGATGTTTCCCTGTTGCAAAGTGGAGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGGGTGTGGTGGAGCCTCGTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-436 (SEQ ID NO: 1236)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTATATTGGTCTGGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCGGCAGCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437 (SEQ ID NO: 1237)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-1 (SEQ ID NO: 1238)
GACATCCAGTTGACCCAGTCTCCAACCTCCCTGTCTGCAACTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCT
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACTGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCATCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAGCGG

BMS2h-437-2 (SEQ ID NO: 1239)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGACAGCATGTGCGTCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGGAATCAAACGG

BMS2h-437-3 (SEQ ID NO: 1240)
GACATCCAGATGACCCAGTCTCCGTCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGTAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCACCA
CGTTTCAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-4 (SEQ ID NO: 1241)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCTGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-5 (SEQ ID NO: 1242)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGATAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCCTCCTGCGACGTTCGGCAAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-438 (SEQ ID NO: 1243)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACATGCCGGGCAAGTCAGTATATTGATACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATGATGGTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCATCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCAGGTTGTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-439 (SEQ ID NO: 1244)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGTGGATTCTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGGATCGTTGGTCTCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-440 (SEQ ID NO: 1245)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCGCGGATTCAGCATATGTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGGCATTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAATCGTGTGCGTGGCCTCTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-441 (SEQ ID NO: 1246)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGGGTATTGATGGTGATTTATGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGCGGATTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGGGGCTGTTCGGCCTATGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-442 (SEQ ID NO: 1247)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGGGTATTGATACTGATTTATGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGCGGATTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGGGGCTGTTCGGCCTATGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-443 (SEQ ID NO: 1248)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTATACTATTCCGGTTGCTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGCTGATGCGTCCTTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGGTTGGCCGGGGCCTCAGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-444   (SEQ ID NO: 1249)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGCGACGGACTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATACTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTTATAATCCTTCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-445   (SEQ ID NO: 1250)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTGTGCCTATTACTGAGGGTTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCAGGCTAATTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGGAGCATGTTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-446   (SEQ ID NO: 1251)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGTATGATTCTTTATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTACTTCCGCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGGAGACGGTTCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-447   (SEQ ID NO: 1252)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTAATGGGCTTTTAATTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGATGTCCAGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTTGGCTCGGATTCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGGAATCAAACGG

BMS2h-448   (SEQ ID NO: 1253)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGAGCAAGTCAGCTGATTCGGACTTATTTAGCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGTCTTCTCAGTTGCAAAGTGGTGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAATTCTTATCCTGATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-47   (SEQ ID NO: 1254)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATTCGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTGGTTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTGCATACTCCTTCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-484   (SEQ ID NO: 1255)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGCGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATTCTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGGTTTTAATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-485   (SEQ ID NO: 1256)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCTCCTATTGAGTATGGTTTAGATTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCGGGGGGGGGTCCGCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGGAGGTTCAGCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-486   (SEQ ID NO: 1257)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCGGATTGATACTGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCACAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTGCGCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-487   (SEQ ID NO: 1258)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTGGGTGGATTGGTATGTCTTTAGAGTGGCACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCGTGGGGCTTCCTCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTAGTCAGTCTCGGTGGCCGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-488   (SEQ ID NO: 1259)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGTAATATTTCGAATGCTTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGGGGCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTACTCAGGTGTGGGATAGGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-489   (SEQ ID NO: 1260)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTATGTCGGCTTTATCTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTACTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATTTGCTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-490   (SEQ ID NO: 1261)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGAGATTGGGATTGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCTTCTTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGCTTCTAATCCTCCTACGTTCGGCCGA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-491   (SEQ ID NO: 1262)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGATGATTGGGGATTGGTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAACTCCTGATCTATCGTAGTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTTGTATTTTTGGCCTCGTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492   (SEQ ID NO: 1263)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCGATTGAGCTTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGTTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-1 (SEQ ID NO: 1264)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCCAGTCAGGCGATTGAGCATAATTTAGAGTGGTACCAGCAGAAGCCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTCCAACCT
GAAGATTTAGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTACGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-2 (SEQ ID NO: 1265)
GACATCCAGATGACACAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGGCGATAGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGTTCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCGGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCTACAGTATGATGTTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-3 (SEQ ID NO: 1266)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAACTGTAGGAGACCGTGTCACC
ATCACTTGTCGTGCAAGTCAGGCGATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGACTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-4 (SEQ ID NO: 1267)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCGATTGAGCATAACTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-5 (SEQ ID NO: 1268)
GACATCCAGATGAACCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCTCC
ATCACTTGCAGGGCAAGTCAGGCTATTGAGCATAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-6 (SEQ ID NO: 1269)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCGATTGAGTCTAATTTAGAGTGGTACCAGCAAAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGTTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-7 (SEQ ID NO: 1270)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGTGCAAGTCAGGCGATTGAGCATAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-493 (SEQ ID NO: 1271)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494 (SEQ ID NO: 1272)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-1 (SEQ ID NO: 1273)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCAGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-2 (SEQ ID NO: 1274)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGAAGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGGAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTCGGCCAT
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-3 (SEQ ID NO: 1275)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTTCTGTCAACAGTATTTTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-4 (SEQ ID NO: 1276)
GAGATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATGACTTGCCGGGCAAGTCAGAGTATTGATAAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGAGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCGACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTGGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-5 (SEQ ID NO: 1277)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCT
GAAGATATCGCTACGTACTACTGTAAACAGTATTCTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-6 (SEQ ID NO: 1278)
GACATCCAGATGACCCAGTCCCCACCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATAAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCTGGTTGCAAAGAGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACCACTGTCAACAGTATTTTCAGTATCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-495 (SEQ ID NO: 1279)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTGAGTATATTAATGCTGAGTTAGCTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGAGTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCTGCAGAATGCGATGTGGCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-496 (SEQ ID NO: 1280)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCTGGATATTAATAATGGTTTAATTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTTGGGTGCGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTTCGCAGGTGCGTTCTCGGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-497 (SEQ ID NO: 1281)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTCTGAGTGCGTTAGCTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGAGTTCCGTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGAATTATAGTCTTCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-498 (SEQ ID NO: 1282)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCTCCTATTGAGTCGTATTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCAGGTATGTGTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTTTCGGGCGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-499 (SEQ ID NO: 1283)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGTAAGTGAGTCTATTAATGCTGAGTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTCTGGGTTTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGTTTGCGATGTGGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-500 (SEQ ID NO: 1284)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTATGATGATTAGGTTTGGGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTGGGTCCTCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGAGCGGTGGCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-501 (SEQ ID NO: 1285)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGGTACTCTTTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCTTACTTCCGTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATGGTTTATCGTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-502 (SEQ ID NO: 1286)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGACTATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATGATTCTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATAAGGTTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503   (SEQ ID NO: 1287)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCATCATATTCAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503-1   (SEQ ID NO: 1288)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCATCATATTCAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCAGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503-2   (SEQ ID NO: 1289)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCATGATATTCAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCAGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-504   (SEQ ID NO: 1290)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACATGCCGGGCAAGTCAGTATATTGATACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGGGGCTGTTGTGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-508   (SEQ ID NO: 1291)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGCTTTTGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCGGCGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGTCAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAATCTTCAGCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-509   (SEQ ID NO: 1292)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAATATTGCTACGCTGTTACGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGGTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATGTGGCAGCGTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-51   (SEQ ID NO: 1293)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGTTGATGAGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCATCAGTGGTCTACTTATCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATTAAACGG

BMS2h-510 (SEQ ID NO: 1294)
GACATCCAGATGACCCAATCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTAATCGATGGTGTTTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGATTGGGATTGGCCTCGTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-511 (SEQ ID NO: 1295)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGAATATTCGTGATTGGTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGATTGGGGGTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGACGTGGGATGATCCTCTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-511-1 (SEQ ID NO: 1296)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATTTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGAATATTCGTGATTGGTTACGGTGGTACCAACAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGATTGGGGGTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGACGTGGTATGATCCTCTGACGTTCGGCCAC
GGGACCAAGGTGGAAATCAAACGG

BMS2h-512 (SEQ ID NO: 1297)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTATTGATATTCATGGTGGTTTAACTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGTGGGGGTTTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGTGTGGCGTAGGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-513 (SEQ ID NO: 1298)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGAGTTCGTTATCTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTATGCTCTTCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-514 (SEQ ID NO: 1299)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCAGATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAAGTATCTGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-52 (SEQ ID NO: 1300)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGTGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGTCTGCGTTAAGGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTGGGTTCCGATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGCAGTATTTTCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-53 (SEQ ID NO: 1301)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCGATTTATGGGGGGTTACGGTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTATGGGGAGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCATCCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATCATAAGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-536 (SEQ ID NO: 1302)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACGTGCCGGGCAAGTCAGCGTATTGGGGTGTGGTTAGATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTTTTCGAGTCCTTCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-537 (SEQ ID NO: 1303)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCCC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATGAGTTATATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAGTTCTTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTCGTTTCAGTTTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-538 (SEQ ID NO: 1304)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGTAATATTACGGGGCCGTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCCTGGTTGGTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGGTGTGGGGGGAGCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-539 (SEQ ID NO: 1305)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGTCTATAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCGTATTGCTTATGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGGGGGCGGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGCCTGGGATGCCGCCTGATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-540 (SEQ ID NO: 1306)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAAGCAGATTGTTGGTGGTTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCGTCATTCTGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGGGGGTTTGGGCTCCTGGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-541 (SEQ ID NO: 1307)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCCTGCTATTGCTGCTAAGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGCGGATTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGCTGTGGGCGGGGCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-542 (SEQ ID NO: 1308)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGTACTATTGCTGATGGGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGGCGTATTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGCTTTGGGAGGGTCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-543 (SEQ ID NO: 1309)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGGATTTATGGGTTTTTAGATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGGTGTCCTCGTTGCAAAGTGGGGTCCCATCA
CGTTTTAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTTGGCGTGGCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-544 (SEQ ID NO: 1310)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTCGGGATTGGTTAATGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTGGGGTTCCTTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCTGTATGATACTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-545 (SEQ ID NO: 1311)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAATATTAATACGGGTTTAGATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCCGCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGTCGTATTATCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-546 (SEQ ID NO: 1312)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAAGATTTTTGGTTGGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGACTTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATTCGCTTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-547 (SEQ ID NO: 1313)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCGAATATTGGGGCGGATTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGGGGGCGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTGTGGAATGGGCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-548 (SEQ ID NO: 1314)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGTCCGATTTATGATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTCTGGTGCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGTTGTGGTTGGGTCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACAG

BMS2h-549 (SEQ ID NO: 1315)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCGCGTATTTATAATGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTCGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGGTGGGGGAGGCTCCTTCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-550 (SEQ ID NO: 1316)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGTTTATTAATGAGGAGTTAGATTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCTCGTGGTCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGCCGGGGGGTGGTCCTGGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-551 (SEQ ID NO: 1317)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGGATATTCTGGATGAGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGTGGGGGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGCTGTGGCATGGGCCTCCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-552 (SEQ ID NO: 1318)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGTCCTATTTATACGGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGCGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTATGCAGGTTGGGACGGCTCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-585 (SEQ ID NO: 1319)
GACATCCGGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAATATTTCTAGGCGGTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTTCTTCCCGGTTGCAAAGTGGGGTCCCATCA
CGTTTCGGTGGCAGTGGATCTGGGACGGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGTATAGCTATCCTCATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-604 (SEQ ID NO: 1320)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGTCCGATTCCGCAGGATTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGTTGGGATTTCCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGAGTGCGCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-605 (SEQ ID NO: 1321)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAAGTCTATTGATGGGATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCCTGGTTTTTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTCGGTTGAGGCGCCTTGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-606 (SEQ ID NO: 1322)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGTATATTGCTCATCCTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCCGGGTTCGTCCGTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGTCGGTTGTGGTGCCTTGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-607 (SEQ ID NO: 1323)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGACGATTGAGGGTGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCATGGGGGGTTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGGTGGTCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-608 (SEQ ID NO: 1324)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAAGTTTATTAGGGATGAGTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGTGGTTCGTCCTTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTGTGGCGGGCGCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-609 (SEQ ID NO: 1325)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAAGCCGATTTATGGTGGTTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGGGGGGGTTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGTGTGGGGGGGTCCTGTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-610 (SEQ ID NO: 1326)
GACATCCGGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGCCGATTAGTGGTTGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGATGGGGCTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGAGTATCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-611 (SEQ ID NO: 1327)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAAGCCTATTGTGAGGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCATGGTGTGTCCACGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTTGAGGCGGCGCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-612 (SEQ ID NO: 1328)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGGATATTGGTGATTGGTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGTTTGGGCGTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGTGGGGGACTCCTCCTACGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-613 (SEQ ID NO: 1329)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAATCGTATTGAGTATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTCGGGGTCTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTTGAGGCGGCGCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-614 (SEQ ID NO: 1330)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGAATATTGGGCATTTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTTGGGGGGGTCCTCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGGTGGAGCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-615 (SEQ ID NO: 1331)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTTCGAGTATTTATAGTGATTTATATTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAAGCTCCTGATCGATGGGTGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTGCATCGTGCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-616 (SEQ ID NO: 1332)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGTTTATTACTGATCGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTGTTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGAGTTCGGAGTTGCCTTGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-617 (SEQ ID NO: 1333)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGTAAGATTGGTAGTGAGTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTAGGTCCCGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGGAGCCTCCTGCGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-618 (SEQ ID NO: 1334)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTAGGAATATTGGTAATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGGAGGGGTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTTTGGCATACTCCTCCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-619 (SEQ ID NO: 1335)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCGGAATATTTATGGTTGGTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGTGGGTGGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGATTATACGTTGCCTGGTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-730 (SEQ ID NO: 1336)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTAAGGATTGGTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTGCGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGCATTATAGTACGCCTTATACGTCCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-731 (SEQ ID NO: 1337)
GACATCCAGATGACCCAGTCTCCACCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTTGATTTCTTCTCATTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGGTCTATGATGCTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCATCGCAGTCTGCCTTTTACGTTCGGCCAA
GGGACCAAGGTAGAAATCAAACGG

BMS2h-732 (SEQ ID NO: 1338)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGTGGGGCGTTAGCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTTATCTATCAGATTTCCGTTTTGCAAAGTGGGATCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATATTCGGTCTCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-733 (SEQ ID NO: 1339)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAGTATTGGGGCGGCGTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGTCTGTCCTCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCTGTTTAGGCTTCCTTTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-734 (SEQ ID NO: 1340)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGGGGTCGTTTAGTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGTCTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGCTGAGGCTCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-735 (SEQ ID NO: 1341)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAATATTGGGTCTAGTTTAATTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTACGCTCCTGATCTATTATTCGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTCTTTGTCGAGTCCTTATACGGTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-736 (SEQ ID NO: 1342)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGAGTGAGTTAGCGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTGGACGTCCAATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATTCTGGAGACTCCTTTGACGTTTGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-737 (SEQ ID NO: 1343)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGAAGATTTGGGATGCTTTATATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCGTGGGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTTTTATCGGTGGCCTCATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-738 (SEQ ID NO: 1344)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCATATTGAGGATTCTTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTATGGTTCCGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATGTATAAGTTTCCTATTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-739 (SEQ ID NO: 1345)
GACATCCAGACGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCGGATTAATTCTTCTTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATACTTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTAGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTCGCTACGTACTACTGTCAACAGATTTGGGGTTCGCCTCCTACGTTCGGCCAG
GGGACCAAGGTGGAAATCAAACGG

BMS2h-740 (SEQ ID NO: 1346)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTCGATTCCTGTTGGTTTAAATTGGTACCAGCAGAAACCA

GGGAAAGCCCCTAGGCTCCTGATCTATTCTGGGTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGATTGGTATTATCCTAATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-785 (SEQ ID NO: 1347)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTTATGGTTGGTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTGACGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATTCATAGTTCTCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-8 (SEQ ID NO: 1348)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTTTATTGATACGTCGTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTAGCTACGTACTACTGTCAACAGTATTGGGTTCTTCCTCTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-86 (SEQ ID NO: 1349)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGGATGCTTTATTTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTATTCTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCGGCATAGTACTCCTGCTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-87 (SEQ ID NO: 1350)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATGAGTCTTTAATGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATGGGGTGTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTCGCTACGTACTACTGTCAACAGCGGTGGAAGGCTCCTTTTACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-88 (SEQ ID NO: 1351)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTTACC
ATCACTTGCCGGGCAAGTCAGGAGATTGTGGAGGATTTATATTGGTATCAGCAGAAACCA
GGGAAAGCCGCTAAGCTCCTGATCTATGGTGCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGCGTAGGCGTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-89 (SEQ ID NO: 1352)
GACATCCAGATGACCCAGTCTCCAGCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGATATTGATCCTATGTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGCTGGTGACTCCTTATACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-90 (SEQ ID NO: 1353)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGTCGATTTCGGATGCGTTATTTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTATGGTTCCGTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCGTTTTCAGGAGCCTGTGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-91 (SEQ ID NO: 1354)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCAGATTAGTGATGAGTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGTGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTGGTTGAGTTTTCCTTCGACGTTTGGCCAA
GGGACCAAGGTGGAAATCAAACGG

Example 1

Generation of Human Anti-CD40L Variable Domains BMS2h-2 through BMS2h-785

The following example describes the generation of the 2h lineage of anti-human CD40L variable domains, designated BMS2h-2 through BMS2h-785. Following recombinant expression of a repertoire of single immunoglobulin variable domains on the surface of phage, selection is performed by contacting the phage repertoire with immobilized target antigen, washing to remove unbound phage, and propagating the bound phage. This process is frequently referred to as "panning." It is applicable to the screening of single immunoglobulin variable domains, as well as other antibody fragments that can be expressed on a display library, e.g., scFv, Fab, and Fab'. Alternatively, phage may be pre-selected for the expression of properly folded member variants by panning against an immobilized generic ligand (e.g., protein A or protein L) that is only bound by folded members. This has the advantage of reducing the proportion of non-functional members, thereby increasing the proportion of members likely to bind a target antigen. Pre-selection with generic ligands is taught in WO 99/20749, for example. The screening of phage antibody libraries is generally described, for example, by Harrison et al., *Meth. Enzymol.* 267: 83-109 (1996).

Screening is commonly performed using purified antigen immobilized on a solid support, for example, plastic tubes or wells, or on a chromatography matrix, for example Sepharose^{TM} (Pharmacia). Screening or selection can also be performed on complex antigens, such as the surface of cells (Marks et al., *BioTechnology* 11: 1145 (1993); de Kruif et al., *Proc. Natl. Acad. Sci. USA* 92: 3938 (1995)). Another alternative involves selection by binding biotinylated antigen in solution, followed by capture on streptavidin-coated beads.

dAb Selection for Clone BMS2h-719 and BMS2h-7xx Series:

Three rounds of selection using decreasing concentrations of antigen (500 nM at round 1; 50 nM at round 2; 50 nM or 5 nM at round 3 depending on the library output used) were performed in parallel against biotinylated (1.2 moles biotin/mole CD40L) human CD40L monomer triple mutant (T211E, S222Y, H224K, [108-261] Construct #7) provided by Bristol-Myers Squibb. Phage from the naïve 4G and 6G Domantis dAb libraries were combined into the pools a) to g) indicated below before initiating selections:

a) 4G VH CDR3 lengths between 7 – 10 amino acids.
b) 4G VH CDR3 lengths between 11 – 15 amino acids.
c) 4G VH CDR3 lengths between 7 – 15 amino acids.
d) 4G VK
e) 6G VH CDR3 lengths between 7-9
f) 6G VH CDR3 lengths between 10-15
g) 6G VK

Each round of selection involved adding the desired concentration of biotinylated CD40L to a mixture of 200 µl of phage (from one of the naïve library pools indicated above, or subsequent selection output phage) and 1000 µl of 2% MPBS (Phosphate Buffered Saline) containing 2% (w/v) Marvel [Premier Foods, UK]) and incubating at room temperature for 1 hour by mixing end-over-end. The biotinylated antigen phage complex was then captured by adding 100 µl of resuspended Dynabeads M-280 Streptavidin [Invitrogen, UK] and incubated for 5 minutes with mixing end-over-end at room temperature. The Dynabeads were then recovered using a KingFisher magnetic separator [Thermo Fisher Scientific, UK] and washed 7 x 1 ml PBST (PBS containing 0.1% (v/v) polyoxyethylenesorbitan 20 monolaurate [Sigma-Aldrich, UK]) followed by 1 x 1 ml PBS. Bound phage retained on the washed Dynabeads were eluted by incubation with 500 µl of trypsin-PBS (50 µl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM $CaCl_2$ added to 450 µl PBS). The phage-containing solution was recovered and 250 µl used to infect 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD_{600} of 0.4) for 30 minutes at 37ºC. The *E. coli* TG1 phage infected culture was centrifuged at 11,600 g in a micro centrifuge for 1 minute and the resulting cell pellet resuspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract and 5 g NaCl in 1 litre, autoclaved for 15 minutes at 121ºC) and plated onto a 9 cm

Petri dish containing TYE media supplemented with 15 µg/ml tetracycline. The plates were incubated overnight at 37ºC then 2 ml of 2xTY supplemented with 15% glycerol was added to each plate and cells loosened with a glass spreader and mixed thoroughly. Fifty microlitres of the scraped bacteria was used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was added to 40 ml supernatant. The phage/PEG solution was mixed and left on ice for 1 h, then spun at 3,300 g for 30 min at 4ºC and the supernatant discarded. The pellet was resuspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then used for the next round of selection against the appropriate concentration of biotinylated CD40L monomer triple mutant antigen.

Phage ELISA:

Monoclonal phage ELISAs were carried out following selection rounds 2 and 3. All washes were performed using 3 washes of 250 µl PBST followed by 3 washes of 250 µl PBS. The plates were coated overnight at 4ºC with 50 µl/well of 1 µg/ml NeutrAvidin [Thermo Scientific, UK] in 0.2M carbonate-bicarbonate buffer, pH 9.4. The plates were washed and then blocked with 2% MPBS for 1 hour at room temperature. The plates were then washed and incubated with 50 µl/well of ~1.0 µg/ml biotinylated human CD40L monomer triple mutant in 2% MPBS. The plates were washed and 25 µl/well phage supernatants added to an equal volume of 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and bound phage detected with 50 µl/well anti-M13-HRP conjugate [GE Healthcare, UK] diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed using 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA]. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Specific phage were identified by comparison to wells coated with NeutrAvidin but without biotinylated CD40L monomer triple mutant.

Recovery of dAb genes from MidiPrep pDOM4 Plasmid:

The dAb V-genes from the following round 3 outputs were recovered by DNA restriction enzyme digestion of the phage vector pDOM4:

a) 4G VH CDR3 lengths between 7 – 10 amino acids (50 nM antigen concentration).

b) 4G VH CDR3 lengths between 11 – 15 amino acids (50 nM antigen concentration).

c) 4G VH CDR3 lengths between 11 – 15 amino acids (5 nM antigen concentration).

d) 4G VH CDR3 lengths between 7 – 15 amino acids (50 nM antigen concentration)..

e) 4G VK (50 nM antigen concentration).

f) 4G VK (5 nM antigen concentration).

g) 6G VH CDR3 lengths between 7-9 (50 nM antigen concentration).

h) 6G VH CDR3 lengths between 10-15 (5 nM antigen concentration).

Approximately 20 µg of MidiPrep [Qiagen, UK] DNA was digested with *Sal*I and *Not*I as follows: 20 µl DNA (~1 µg/µl) was mixed with 1.5 µl *Sal*I (20 U/µl) [NEB, UK] and 3 µl *Not*I (10 U/µl) [NEB, UK], 4 µl Buffer 3 [NEB, UK], 0.4 µl BSA (10 mg/ml) [NEB, UK] and tissue culture grade water [Sigma, UK] added to 40 µl. Samples were incubated for 5 hours at 37ºC in an air incubator following which the digested dAb genes were isolated by running the digestion mix on a 2% agarose gel [E-gel, Invitrogen, UK], the appropriate DNA bands excised and cleaned using a PCR purification kit [Qiagen, UK]. The purified V-genes were ligated into a *Sal*I and *Not*I double digested pDOM5 expression vector.

Soluble dAb ELISA:

Binding dAbs were identified as follows. Ninety-six individual colonies containing dAb V-genes cloned into the soluble dAb expression vector pDOM5 were picked from each output into 200 µl Terrific Broth containing OnEx Autoinduction media [Novagen, UK] and incubated overnight at 37° C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters [Corning Incorporated, USA] sealed with a gas permeable adhesive plastic strip. The cultures were centrifuged to pellet the cells and the supernatants assayed by antigen binding ELISA for dAbs that bound to CD40L monomer triple mutant and IZ-CD40L mutant (CD40L containing an isoleucine zipper trimerization domain, supplied by Bristol-Myers Squibb). MaxiSorp 96 well immunoplates [Nunc, USA] were coated overnight at 4ºC with 50 µl/well of 1 µg/ml NeutrAvidin in 0.2 M carbonate-bicarbonate buffer, pH 9.4. All washes were as described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 200 µl of PBS containing 1% Tween 20. The plate was then washed and incubated for 1 hour at room temperature with 50 µl/well of 1 µg/ml biotinylated human CD40L monomer triple mutant in PBST or 1 µg/ml biotinylated human IZ-CD40L mutant in

PBST (both antigens supplied by Bristol-Myers Squibb). The ELISA plate was washed and dAb-containing culture supernatant clarified by centrifugation at 1,800 g for 10 min at 4°C, then added to the ELISA plate (30 µl/well) to which was added an equal volume of PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected by adding 50 µl/well 9E10 [anti-myc IgG, Sigma-Aldrich, UK] diluted 1:2000 in PBST and incubating for 1 hour at room temperature; the ELISA plate was then washed and 50 µl/well anti-mouse Fc-HRP [Sigma-Aldrich, UK] diluted 1:2000 in PBST added and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed by adding 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA] and the colour allowed to develop. The colourimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Antigen binding dAbs were identified by comparison of the signal intensity from human CD40L monomer triple mutant and human IZ-CD40L mutant wells with control wells not containing antigen.

Expression & Purification of dAb at 50 ml Scale:

Unique dAbs were identified by DNA sequencing ELISA positive clones. The unique dAbs identified were expressed as follows in 250 ml baffled flasks, to which was added:

a) 50 ml of Terrific Broth [Sigma-Aldrich, UK].
b) 100 µg/ml carbenicillin [Sigma-Aldrich, UK].
c) 1 drop of antifoam A204 [Sigma-Aldrich, UK].
d) Novagen Overnight Express Autoinduction Kit [Novagen, UK].

A bacterial scrape from a fresh confluent 9 cm diameter agar plate or from a glycerol stock of the desired dAb clone was used to inoculate the Terrific Broth, then the flask sealed with Milliwrap PTFE membrane [Millipore, UK], and incubated for 48 hrs, 250 rpm shaking at 30°C. The bacterial overnight culture was clarified by centrifugation and the VH or VK dAb purified using Streamline Protein A [GE Healthcare, UK] or Protein L agarose [generated in-house] respectively. The resulting purified proteins were assayed by RBA to determine which clones could inhibit the binding of CD40L for CD40.

CD40L Bead Receptor Binding Assay:

Inhibitory dAbs were initially identified by screening purified dAb in a CD40L bead receptor binding assay (RBA). Sphero streptavidin polystyrene beads (0.5% w/v, 6.7µm diameter) [Saxon, Europe] were prepared and washed according to the manufacturer's instructions. The beads were then pelleted at 11,600 g for 1 minute, the supernatant discarded and the beads resuspended in 1 ml PBS by vortexing. The washing step was repeated twice more, the supernatant discarded and the beads resuspended in 1 ml (0.5 mg/ml) of biotinylated human IZ-CD40L in PBS and incubated overnight at room temperature with end-over-end rotation. Following incubation, the beads were pelleted and washed three times with 1 ml PBS as before and then resuspended in 0.5 ml PBS containing 0.1% bovine serum albumin (BSA). The antigen coated beads were then diluted 1:10 in PBS containing 0.1% BSA prior to use. The reagents for the RBA assay were added as follows to duplicate wells in a 384-well black sided clear bottomed FMAT plate [Applied Biosystems, UK]:

a) 12.5 µl dAb protein or buffer control. The dAb titration starting concentration was typically 10 µM (final concentration) which was diluted 1:3.3 (i.e., 30 µl sample added to 70 µl PBS containing 0.1% BSA) to produce an 8-point titration effect curve.

b) 12.5 µl CD40-Fc [supplied by Bristol-Myers Squibb, USA; lot CY24Feb06-1] at 0.2 µg/ml (for a final concentration of 0.05 µg/ml) diluted in PBS containing 0.1% BSA.

c) 12.5 µl Mixture of mouse anti-human Fc [Sigma-Aldrich, UK] at 2 µg/ml (for a final concentration of 0.5 µg/ml) and goat anti-mouse Alexa Fluor 647 [Invitrogen, UK] at 1 µg/ml (for a final concentration of 0.25 µg/ml) diluted in PBS containing 0.1% BSA.

d) 12.5 µl IZ-CD40L coated beads described above were added to the centre of the well so they did not disperse to the edge of the well.

Following addition of the reagents to the 384 well plate, it was incubated at room temperature for 6 hours in the dark and then read in an AB8200 FMAT system [Applied Biosystems, UK].

Example 2

dAb Selection for Clone BMS2h-572

Three rounds of selection using decreasing concentrations of antigen (300 nM at round 1; 30 nM at round 2; 3 nM at round 3) were performed in parallel against biotinylated

(1.42 moles biotin/mole trimer) human isoleucine zipper-CD40L (IZ-hCD40L) provided by Bristol-Myers Squibb. Phage from the naïve 4G and 6G Domantis dAb libraries were combined into the pools a) to h) indicated below before initiating selections:

a) 4G VH CDR3 lengths between 7 – 9 amino acids.
b) 4G VH CDR3 lengths between 10 – 12 amino acids.
c) 4G VH CDR3 lengths between 13 – 15 amino acids.
d) 4G VK
e) 6G VH CDR3 lengths between 7-9
f) 6G VH CDR3 lengths between 10-12
g) 6G VH CDR3 lengths between 13-15
h) 6G VK

Each round of selection involved adding the desired concentration of biotinylated CD40L to a mixture of phage (from one of the naïve library pools indicated above, or subsequent selection output phage) in 1000 μl of 2% MPBS (Phosphate Buffered Saline containing 2% (w/v) Marvel [Premier Foods, UK]) and incubating at room temperature for 1 hour by mixing end-over-end. The biotinylated antigen phage complex was then captured by adding 100 μl of resuspended Dynabeads M-280 Streptavidin [Invitrogen, UK] (rounds 1 and 3) or 50 μl of M-280 tosylactivated Dynabeads (Invitrogen) that had been coupled with NeutrAvidin [Thermo Fisher Scientific, UK] (round 2) and incubated for 5 minutes with mixing end-over-end at room temperature. The Dynabeads were then recovered using a KingFisher magnetic separator [Thermo Fisher Scientific, UK] and washed 7 x 1 ml PBST (PBS containing 0.1% (v/v) polyoxyethylenesorbitan 20 monolaurate [Sigma-Aldrich, UK]) followed by 1 x 1 ml PBS. Bound phage retained on the washed Dynabeads were eluted by incubation with 500 μl of trypsin-PBS (50 μl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM $CaCl_2$ added to 450 μl PBS). The phage-containing solution was recovered and 250 μl used to infect 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD_{600} of 0.4) for 30 minutes at 37ºC. The *E. coli* TG1 phage infected culture was centrifuged at 11,600 g in a micro centrifuge for 1 minute and the resulting cell pellet resuspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract and 5 g NaCl in 1 litre, autoclaved for 15 minutes at 121ºC) and plated onto a 9 cm Petri dish containing TYE media supplemented with 15 μg/ml tetracycline. The plates were incubated overnight at 37ºC then 2 ml of 2xTY supplemented with 15% glycerol was added to each plate and cells loosened with a glass spreader and mixed thoroughly. Fifty microlitres of the scraped bacteria was used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was added to 40 ml supernatant. The phage/PEG solution was mixed and left on ice for 1 h, then spun at 3,300 g for 30 min at 4ºC and the supernatant discarded. The pellet was resuspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then used for the next round of selection against the appropriate concentration of biotinylated IZ-hCD40L.

Phage ELISA:

Monoclonal phage ELISAs were carried out following selection rounds 2 and 3. All washes were performed using 3 washes of 250 µl PBST followed by 3 washes of 250 µl PBS. The plates were coated overnight at 4ºC with 50 µl/well of 1 µg/ml IZ-hCD40L in PBS. The plates were washed and then blocked with 2% MPBS for 1 hour at room temperature. The plates were washed and 25 µl/well phage supernatants added to an equal volume of 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and bound phage detected with 50 µl/well anti-M13-HRP conjugate [GE Healthcare, UK] diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed using 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA]. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Specific phage were identified by comparison to wells that were not coated with antigen but otherwise identically treated.

Recovery of dAb genes from pDOM4 plasmid:

The dAb V-genes from round 2 and 3 outputs were recovered by *Sal*I and *Not*I restriction enzyme digestion of the phage vector pDOM4 and ligated into a *Sal*I and *Not*I double digested pDOM5 expression vector.

Soluble dAb ELISA:

Binding dAbs were identified as follows. Ninety-six individual colonies containing dAb V-genes cloned into the soluble dAb expression vector pDOM5 were picked from each output into 200 µl Terrific Broth containing OnEx Autoinduction media [Novagen, UK] and incubated overnight at 37° C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters [Corning Incorporated, USA] sealed with a gas permeable adhesive plastic strip. The cultures were centrifuged to pellet the cells and the supernatants assayed by antigen binding ELISA for dAbs that bound to IZ-hCD40L. MaxiSorp 96 well immunoplates [Nunc, USA] were coated overnight at 4°C with 50 µl/well of 1 µg/ml IZ-hCD40L in PBS. All washes were as described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 200 µl of PBS containing 1% Tween 20. The ELISA plate was washed and dAb-containing culture supernatant clarified by centrifugation at 1,800 g for 10 min at 4°C, then added to the ELISA plate (30 µl/well) to which was added an equal volume of PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected by adding 50 µl/well 9E10 [anti-myc IgG, Sigma-Aldrich, UK] diluted 1:2000 in PBST and incubating for 1 hour at room temperature; the ELISA plate was then washed and 50 µl/well anti-mouse Fc-HRP [Sigma-Aldrich, UK] diluted 1:2000 in PBST added and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed by adding 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA] and the colour allowed to develop. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Antigen binding dAbs were identified by comparison of the signal intensity from IZ-hCD40L wells with control wells not containing antigen.

Example 3

Identification of Clones BMS2h-503-1, BMS2h-719-2, and BMS2h-572-6

BMS2h-503, BMS2h-719 and BMS2h-572 dAbs were subjected to error-prone affinity maturation to generate BMS2h-503, BMS2h-719 and BMS2h-572 lineages, respectively. This was performed using random mutagenesis where on average 3.6 amino acid changes were introduced per dAb. Phage libraries (average size $6x10^8$) were selected using biotinylated monomeric and trimeric human CD40L with alternating streptavidin/neutravidin bead capture of the antigen (as described). Three rounds of selections using decreasing concentrations of antigen (100 nM at round 1; 10 nM at round 2; 1 nM at round 3) were performed. Sequencing was used to monitor diversity following each selection round. Selection outputs (round 2 selected on CD40L trimer for BMS2h-572; round 3 selected on CD40L trimer for BMS2h-503 and round 3 selected on CD40L monomer for BMS2h-719) were sub-cloned into soluble expression vector pDOM13 (no C terminal tag) (as described) and screened as monoclonal bacterial micro-culture supernatants by BIAcore for improved off-rates compared to parental clones on both monomeric and trimeric CD40L. Identified improved variants were DNA sequenced and unique dAbs expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described). As a result, BMS2h-503-1 (sequence listed in TABLE 3), BMS2h-719-2 and BMS2h-572-6 dAbs (sequences listed in TABLE 1) were identified. Activities of these dAbs are listed in TABLE 5 below.

Formatting BMS2h-503-1, BMS2h-719-2 and BMS2h-572-6 as Fc fusions

BMS2h-572-6, BMS2h-503-1 and BMS2h-719-2 dAbs were cloned into pDOM38 vector containing Fc tail derived from human IgG1 to create DMS0502, DMS0500 and DMS0501, respectively. BMS2h-572-6, BMS2h-503-1 and BMS2h-719-2 dAbs were also cloned into pDOM38 vector containing Fc tail derived from human IgG4 to create DMS0505, DMS0506 and DMS0504, respectively. The constructs were transiently expressed in HEK293 cells and the proteins were purified using Protein A. Purified Fc fusions were analysed by Biacore for binding to monomeric and trimeric CD40L as well as in various cell assays (as described).

Identification of clones BMS2h-572-608, BMS2h-572-614 and BMS2h-572-619

BMS2h-572-6 dAb was subjected to affinity maturation using doped oligo approach. Four doped libraries were constructed for this dAb:

Library 1 – 5 residues in CDR1 diversified

Library 2 – 6 residues in CDR2 diversified

Library 3 – 13 residues in CDR2 diversified

Library 4 – 7 residues in CDR3 diversified

In each library, diversification was performed using nnS codons where n retained a large fraction of the parent base (85%) and split the rest between the equimolar amounts of the remaining three bases (5% each) and S stood for G or C. Phage libraries (average size $8x10^8$) were selected using biotinylated monomeric and trimeric human CD40L with alternating streptavidin/neutravidin bead capture of the antigen (as described). Libraries 2 and 3 were pulled together during the selection process. Three rounds of selections using decreasing concentrations of antigen (50 nM at round 1; 5 nM at round 2; 1 nM at round 3 with 200 fold excess of competitor – non biotinylated CD40L trimer) were performed.

Sequencing was used to monitor diversity following each selection round. Selection outputs (rounds 2 and 3) were sub-cloned into soluble expression vector pDOM13 (no C terminal tag) (as described) and screened as monoclonal bacterial micro-culture supernatants by BIAcore for improved off-rates compared to parental clones on both monomeric and trimeric CD40L. Identified improved variants were DNA sequenced and unique dAbs expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described). As a result, BMS2h-572-608, BMS2h-572-614 and BMS2h-572-619 dAbs were identified.

Construction of clone BMS2h-572-633

Sequence analysis revealed that all of the amino acid differences between BMS2h-572-608 and the parental dAb BMS2h-572-6 were located in CDR1 and the differences between BMS2h-572-614 and parental dAb BMS2h-572-6 were located in CDR3. Both matured dAbs shared CDR2 with the parental dAb BMS2h-572-6. This created an opportunity to construct a combination mutant which had CDR1 of BMS2h-572-608 and CDR3 of BMS2h-572-614. Firstly, CDR1 region of BMS2h-572-608 was PCR amplified. Secondly, CDR2+CDR3 fragment of BMS2h-572-614 was PCR amplified. This was followed by SOE PCR assembly of the two fragments to create a combination mutant BMS2h-572-633. The assembled dAb PCR product was cloned into soluble expression vector pDOM13 (no C terminal tag), sequence verified, expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described).

Formatting BMS2h-572-633 as Fc fusion

BMS2h-572-633 dAb was cloned into pDOM38 vector containing Fc tail derived from human IgG1 to create DMS0507. The construct was transiently expressed in HEK293 cells and the protein was purified using Protein A. Purified Fc fusion was analysed by Biacore for binding to monomeric and trimeric CD40L as well as in various cell assays (as described).

Example 4

CD40L Activity Cell Assays

Anti-human CD40L dAbs were assayed functionally for their ability to antagonize CD40L activities. The CD40L activities tested were B cell proliferation and cytokine production by hCD40L-driven activation of primary monocytes-derived dendritic cells

(DCs). Unless otherwise noted, all assays were performed in RPMI media supplemented with 10% fetal calf serum (FCS). The results of various assays, described in detail below, are shown in TABLE 5 and TABLE 6.

Soluble IZ-hCD40L-driven primary human B cell proliferation:

1x10^5 tonsillar human B cells were incubated with 0.6 µg/ml of IZ-hCD40L along with varying titration of dAb or mAb in a final volume of 200µl/well in a 96-well round bottom plate. The plates were incubated at 37ºC for 72 hours following which thymidine (^{3}H; 0.5µci/well) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

CHO-hCD40L-driven primary human B cell proliferation:

CHO cells were transfected with human CD40L to generate a stable cell line expressing high levels of CD40L on the cell surface. CHO-CD40L cells were irradiated at 10,000 Rads before incubation with human B cells. 1x10^5 tonsillar human B cells were incubated with 1x10^3 CHO-CD40L cells (1:100 ratio of CHO-CD40L: human B cells) along with varying titration of dAb or mAb in a final volume of 200µl/well in a 96-well round bottom plate. The plates were incubated at 37ºC for 72 hours following which thymidine (^{3}H; 0.5µci/well) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

Primary T cell-driven human B cell proliferation:

T cells were isolated from human peripheral blood mononuclear cells (PBMCs) and enriched using via sheep red blood cell (SRBC) affinity. Enriched human T cells were cultured with PM-LCLs (EBV-transformed B cell line; irradiated at 10,000 Rads) at a 5:1 ratio (T:LCL) for 6 days at 37ºC to generate a population of allogeneic T cells. At day 6, the expanded T cells were isolated and irradiated at 3000 Rads, and then cultured (5x10^4 T cells/well) with primary human tonsillar B cells (1x10^5 B cells/well) at a 1:2 ratio in 96-well flat bottom plated coated with anti-CD3 mAb (OKT3). Varying titrations of dAbs/mAbs were added to each well; the final volume in each well was 200 µl. Test plates were incubated at 37ºC for 3 days. Human B cell proliferation was determined via the addition of thymidine (^{3}H; 0.5µci/well) to the cultures for the last 18 hours. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS). In some instances, the supernatant was harvested and measured for the presence of IL-6.

CHO-hCD40L-driven activation of primary human monocytes-derived dendritic cells (DCs):

Human PBMCs were enriched for monocytes by depleting T cells via SRBC resetting. The monocyte-enriched PBMCs were cultured with 10 ng/ml GM-CSF and 5 ng/ml IL-4 in 6-well plates for six days at 37ºC. The cultured plates were replenished with fresh media (with GM-CSF and IL-4) on days 2 and 5. The immature DCs were used in cell assays on day 6. $8x10^4$ immature DCs were cultured with $4x10^3$ CHO-hCD40L cells (irradiated at 10,000 Rads) along with varying titrations of dAbs/mAbs in a 96-well flat bottom plate. After 24 hours, supernatants were harvested and tested for the presence of various cytokines (IL-12, TNF, IL-23). DC activation was determined by the levels of cytokine production. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

TABLE 5

Potency of Monomeric dAb Molecules in Various Primary Cell Assays

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
2h116-13	130.0 ± 40.0	1300.0, 700.0		888.0, >2000.0, 1000.0
2h116-1312	23.0 ± 3.0	530.0 ± 300.0	234 ± 46	112.0 ± 47.0
2h116-1313	29.0 ± 4.0	211.0, 334.0	258 ± 79	136.0 ± 51.0
2h116-1314	41.0 ± 10.0	1300.0, 4400.0	1687 ± 1150	664.0 ± 353.0
2h116-1319	180.0 ± 57.0	>7000.0		
2h116-1320	20.0 ± 7.0	138.0 ± 60.0	191 ± 72	32.0 ± 10.0
2h437	5700.0 ± 1800			
2h437-4	203.0 ± 90.0	>7000.0		1329.0 ± 412.0
2h492	>7000.0			
2h492-3	1100.0 ± 400.0	>7000.0		
2h492-4	1700.0 ± 900.0	>7000.0		
2h492-5	2300.0 ± 700.0			
2h492-6	6300.0 ± 1400.0			
2h492-7	1900.0 ± 600.0			
2h494	6100.0 ± 1200.0			
2h494-2	4800.0 ± 2300.0			
2h494-3	>7000.0			
2h494-4	590.0 ± 250.0	>7000.0		
2h494-6	2000.0 ± 2100.0	>7000.0		
2h503	4200.0 ± 316.0	>7000.0		
2h503-1	24.0 ± 2.0	2300.0 ± 700.0		756.0 ± 333.0

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
2h503-104	16.0, 19.0			
2h503-2	44.0 ± 6.0	3000.0 ± 1000.0		1562.0 ± 96.0
2h572	>7000.0			
2h572-6	208.0 ± 73.0	>7000.0	>7000.0	>2000.0, 608.0 ± 260.0
2h572-604	254.0, 354.0	>700.0		387.0
2h572-608	96.0 ± 19.0		>7000.0	152.0 ± 61.0
2h572-610	109.0 ± 34.0		>7000.0	207.0± 87.0
2h572-614	93.0 ± 53.0		>7000.0	135.0± 54.0
2h572-616	204.0, 340.0		>7000.0	608.0 ± 136.0
2h572-617	157.0, 189.0		>7000.0	338.0 ± 101.0
2h572-619	90.0 ± 62.0	421.0, 1496.0	>7000.0	188.0± 41.0
2h572-622	301.0, 293.0		>7000.0	281.0± 127.0
2h572-623	181.0, 261.0		>7000.0	280.0 ± 73.0
2h572-630	103.0 ± 71.0			246.0± 240.0
2h572-631	108.0 ± 77.0			230.0 ± 200.0
2h572-632	117.0 ± 91.0			241.0 ± 190.0
2h572-633	20.0 ± 15.0			53.0 ± 60.0
2h572-634	31.0 ± 18.0			77.0 ± 67.0
2h572-635	29.0 ± 19.0			52.0 ± 26.0
2h572-9	324.0, 243.0			>2000.0
2h572-11	140.0 ± 33.0	>7000.0		671.0 ± 165.0
2h572-12	79.0, 76.0			225.0, >2000.0
2h572-14	134.0 ± 12.0	>7000.0		882.0 ± 310.0

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
2h572-15	168.0 ± 67.0	>7000.0		876.0 ± 391.0
2h572-22	357.0, 305.05			
2h702	>7000.0			
2h703	>7000.0			
2h706	>7000.0			
2h707	>7000.0			
2h710	>7000.0			
2h712	>7000.0			
2h717	>7000.0			
2h719	600.0 ± 640.0			134.0, 646.0
2h719-2	82.0 ± 39.0	>7000.0		196.0 ± 150.0
2h719-202	29.0 ± 12.0			79.0 ± 29.0
2h719-203	81.0, 96.0			
2h719-213	62.0, 98.0			
2h719-214	66.0, 89.0			
2h719-215	92.0, 91.0			
2h719-218	57.0, 60.0			
2h719-225	253.0, 198.0			176.0 ± 84.0
2h719-226	164.0, 247.0			812.0 ± 53.0
2h719-12	358.0 ± 159.0			266.0 ± 66.0
2h719-13	50.0 ± 8.0	659.0, 683.0, 4450.0, 1750.0		219.0 ± 88.0
2h719-17	132.0 ± 50.0	236.0, 268.0		113.0 ± 49.0
2h719-19	138.0 ± 31.0	202.0, >7000.0, >7000.0, 3800.0,		184.0 ± 99.0

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
		5400.0		
2h722	>7000.0			
2h723	>7000.0			
2h725	6400.0 ± 1200.0			
2h725-2	>7000.0			
2h725-9	>7000.0			
2h725-19	>7000.0			
2h726	>7000.0			
2h730	>7000.0			
2h731	5800.0 ± 2500.0			
2h744	>7000.0			
2h745	6400.0, 3500.0, >7000.0			
2h745-1	>7000.0			
2h745-2	>7000.0			
2h745-9	>7000.0			
2h745-13	>7000.0			
2h745-14	>7000.0			
2h746	>7000.0			
2h747	>7000.0			
2h752	>7000.0			
2h754	6600.0 ± 900.0			
2h757	6400.0 ± 800.0			
2h758	5900.0 ± 1500.0			

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
2h758-1	>7000.0			
2h758-2	>7000.0			
2h758-3	>7000.0			
2h758-4	>7000.0			
2h758-5	>7000.0			
2h765	>7000.0			
2h766	>7000.0			
2h774	>7000.0			
2h775	>7000.0			
2h780	>7000.0			
2h781	>7000.0			
2h782	>7000.0			
2h783	>2000.0			
2h784	>4700.0			
2h785	3700.0, >7000.0			

TABLE 6

Potency of Fc[*]-formatted Molecules in Various Primary Cell Assays

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-23 EC50 (nM)	CHO-hCD40L-driven DC Activation TNF EC50 (nM)
2h116-1320-Fc	13.0 ± 2.0	>130.0	244.0 ± 112.0		14.0 ± 11.0			
2h503-1 Fc	4.0 ± 0.5	60.0 ± 20.0	45 ± 6		2.8 ± 2.0			
2h503-1 IgG1	4.5 ± 1.0	67.0 ± 40.0	39.5 ± 12.04		1.4 ± 0.7			
2h503-1 IgG4	2.5 ± 1.0	69.0 ± 50.0	48.3 ± 8.8		18.1 ± 6.4			
2h572-6 Fc	0.6 ± 0.4	3.0 ± 1.0	1.9 ± 0.7		0.22 ± 0.18			
2h572-6 IgG1	1.0 ± 0.4	10.0 ± 5.0	3.1 ± 1.4	2.9 ± 1.7	0.58 ± 0.36			
2h572-6 IgG4	0.9 ± 0.2	11.0 ± 5.0	3.2 ± 1.5	1.3 ± 0.5	1.1 ± 0.5			
2h572-6-CT Long Fc	1.0 ± 0.5	6.0 ± 6.0	13.6 ± 9.2	8.1 ± 3.1	3.0 ± 1.9			

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[*] FIG. 3 provides sequences of various Fc domains. FIG. 4 shows examples of various Fc-formatted dAbs.

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-23 EC50 (nM)	CHO-hCD40L-driven DC Activation TNF EC50 (nM)
2h572-633 Fc	3.5 ± 0.6	3.0 ± 3.0	0.15 ± 0.02	0.11 ± 0.02	0.34 ± 0.17			
2h572-634 Fc	3.0 ± 0.0	3.5 ± 3.0	0.23 ± 0.08	0.19 ± 0.03	0.42 ± 0.05			
2h572-635 Fc	2.0 ± 0.8	2.5 ± 1.0	0.16 ± 0.09	0.11 ± 0.02	0.445 ± 0.14			
2h572-619-Ctshort Fc	1.5 ± 0.6	2.0	0.40 ± 0.1	0.3 ± 0.07	1.8 ± 1.3			
2h572-619-Ctlong Fc	1.6 ± 0.5	2.0 ± 1.0	0.72 ± 0.45	0.43 ± 0.12	1.4 ± 0.6	1.5 ± 0.36	1.5 ± 0.46	2.0 ± 0.7
2h572-619-N297Qshort Fc	0.9 ± 0	1.0 ± 0.6	0.226, 0.216	0.1, 0.1	1.2 ± 0.6			
2h572-619-N297Qlong Fc	0.98 ± 0.05	2.0 ± 0.0	0.480, 0.474	0.22, 0.11	1.1 ± 0.23			
2h572-608-N297Qshort Fc	1.0 ± 0.05	2.0 ± 0.0			0.93 ± 0.4			

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-23 EC50 (nM)	CHO-hCD40L-driven DC Activation TNF EC50 (nM)
2h572-608-CT Long Fc	2.0 ± 1.0	2.0 ± 1.0	0.468 ± 0.156	0.38 ± 0.06	1.6 ± 0.74			
2h572-614-CT Long Fc	2.0 ± 1.0	2.0 ± 0.5	0.283 ± 0.038	0.25 ± 0.02	1.4 ± 0.68			
2h572-633-CT Long Fc	3.0 ± 0.7	1.0 ± 1.0	0.174 ± 0.077	0.13 ± 0.07	1.9 ± 1.3	1.3 ± 0.3	1.2 ± 0.3	1.7 ± 0.43
2h572-633-CT-Fc SP5	5.0 ± 0.5	1.0 ± 0.5	0.161 ± 0.053	0.13 ± 0.04	2.3 ± 1.5	1.5 ± 0.7		2.9 ± 1.3
2h572-634-CT Long Fc	2.0 ± 1.0	1.0 ± 0.6	0.162 ± 0.029	0.13 ± 0.02	1.5 ± 0.91			
2h572-635-CT Long Fc	3.0 ± 1.0	2.0 ± 0.6	0.149 ± 0.014	0.13 ± 0.01	1.6 ± 0.93			
2h719-2 Fc	1.0 ± 0	0.7 ± 0.4	6 ± 1.4		0.13 ± 0.08			
2h719-2 IgG1	1.0 ± 0.5	6.0 ± 0.3	13.8 ± 10.6	2.2 ± 1.3	0.35 ± 0.23			
2h719-2 IgG4	1.5 ± 0.6	16.0 ± 13.0	15.9 ± 10.9	2.1 ± 0.7	1.1 ± 0.48			
2h719-202-N297Qshort	1.8 ± 0.5	1.7 ± 0.7			0.66 ± 0.26			

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-23 EC50 (nM)	CHO-hCD40L-driven DC Activation TNF EC50 (nM)
Fc								
2h719-202-CT Long Fc	3.0 ± 1.0	2.5 ± 0.6	1.7 ± 0.7	1.3 ± 0.3	3.1 ± 2.0			

Example 5

Binding Kinetics and CD40L Affinity of Various Antibodies

BMS-986004 is a dimeric fusion protein, composed of a modified Fc fragment of IgG1 linked to the C-terminus of the dAb BMS2h-572-633. Surface plasmon resonance (SPR) was used to characterize the kinetics and affinity of BMS-986004 or the monovalent component domain antibody BMS2h-572-633 binding to CD40L. The BMS-986004 values were compared to those for the benchmark antibodies 5c8-IgG1 and 5c8-CT and the monovalent component 5c8 FAB fragment. The SPR experiments utilized a hCD40L construct containing an N-terminal isoleucine zipper motif (IZ-hCD40L) which facilitates the specific assembly of the CD40L molecule into the native trimeric form. A biotinylated version of IZ-hCD40L (biot-IZ-hCD40L) with equivalent binding activity was also utilized for some SPR experiments.

The monovalent BMS2h-572-633 domain antibody binds biot-IZ-hCD40L with a Kd of 7.8 nM, compared to an affinity of 5.4 nM for the monovalent 5c8 FAB fragment, TABLE 7. Because BMS-986004 is bivalent, and the IZ-hCD40L target is trivalent, the SPR binding data are influenced by avidity regardless of whether CD40L target is on the chip surface or in solution. To estimate the avidity-influenced binding affinity, the SPR data for BMS-986004 binding to a biot-IZ-hCD40L surface was fitted to a 1:1 Langmuir model, suggesting a dissociation constant of less than 1 nM, TABLE 7. Similar results were obtained for 5c8-IgG1 and 5c8-CT.

TABLE 7

IZ-hCD40L kinetic and affinity values as determined using SPR (Biacore)

Anti-CD40L Ab	**Temperature (^{o}C)**	**Model**	**ka (M-1s-1)**	**kd (s-1)**	**Kd (nM)**
BMS-986004	25	1:1 Langmuir	2.3 E+06*	2.6 E-04*	0.11*
2h572-633	25	1:1 Langmuir	1.0 E+06	8.1 E-03	7.8
5c8-IgG1	25	1:1 Langmuir	5.4 E+05*	2.3 E-04*	0.42*
5c8-CT	25	1:1 Langmuir	5.8 E+05*	1.3 E-04*	0.22*
5c8 FAB fragment	25	1:1 Langmuir	1.4 E+05	7.6 E-04	5.4

* Value is influenced by avidity due to analyte bivalency.

FIG. 5 shows SPR sensorgram data for the binding of 12.5-0.39nM BMS-986004 (2:1 dilution series) to biot-IZ-hCD40L captured on a streptavidin SPR sensor chip at 25 °C. Colored lines show the double-referenced sensorgram data, and black lines show the 1:1 Langmuir fit to the data, with an avidity-influenced apparent Kd value of 0.11 nM.

The affinity and thermodynamics of BMS-986004 binding to CD40L were also characterized in solution using isothermal titration calorimetry (ITC) at temperatures ranging from 15–37°C. These data suggested the presence of multiple thermodynamically distinct binding modes (FIG. 6) with Kd values for the different modes beyond the high-affinity limit of detection (Kd <2 nM) (TABLE 8), consistent with the SPR data. The affinity of the monovalent 5c8 FAB fragment for IZ-hCD40L as determined by ITC (3.5 nM) was also consistent with the value determined by SPR.

TABLE 8

IZ-hCD40L affinity as determined using ITC

Molecule in the ITC syringe	Molecule in the ITC cell	Kd (nM)
BMS-986004	IZ-hCD40L	< 2
5c8-CT	IZ-hCD40L	< 2
IZ-hCD40L	BMS-986004	< 2
IZ-hCD40L	5c8-CT	< 2
IZ-hCD40L	5c8 FAB fragment	3.5

Example 6

Fc receptor Affinity of Various Antibodies

The Fc-domain of BMS-986004 (termed “CT”) was engineered from a wild type IgG1 Fc domain to retain the ability to bind FcRn, but to disrupt the binding to Fcγ receptors. To confirm that the engineered molecule has the desired Fc receptor binding profile, the binding affinities of BMS-986004 for human FcRn, and the human Fcγ receptors CD64 (FcγRI), CD32a (FcγRIIa), CD32b/c (FcγRIIb/c), CD16a (FcγRIIIa), CD16b (FcγRIIIb) were measured using SPR, in comparison to 5c8-IgG1 and 5c8-CT. For these experiments, BMS-986004 was captured via the domain antibody domains on a biot-IZ-hCD40L sensor surface, and the soluble Fc receptor proteins were tested for binding to the exposed Fc domain. Likewise, 5c8-IgG1 and 5c8-CT were captured on a biot-IZ-hCD40L surface via the FAB domains, with soluble FcR binding.

BMS-986004 bound FcRn with Kd of 670 nM at pH 6.0 which is the relevant pH for binding within the endosome, TABLE 9. However, binding was significantly reduced (Kd >5000 nM) at neutral pH suggesting efficient release of from FcRn under these conditions. BMS-986004 bound CD64 with a Kd of 0.6 nM, and had a statistically weak affinity for CD32a, CD32b/c, CD16a and CD16b (Kd >3000 nM). Both 5c8-IgG1 and 5c8-CT had a similar FcRn affinity as BMS-986004. 5c8-CT, which has the identical "CT" Fc region as BMS-986004, also had a similar FcγR binding properties as BMS-986004, whereas 5c8-IgG1, which has a wild type IgG1 Fc domain, bound more strongly to FcγRs, TABLE 9.

TABLE 9

Fc receptor affinity as determined using SPR (Biacore).

Sample	pH	BMS-986004 Kd (nM)	5c8-IgG1 Kd (nM)	5c8-CT Kd (nM)
hFcRn	6	670	590	720
hFcRn	7.1	>5000	>5000	>5000
CD64	7.1	0.6	<0.05	0.9 ± 0.4
CD32a	7.1	>3000	~10^{-7} M*	>3000
CD32b/c	7.1	>3000	>3000	>3000
CD16a	7.1	>3000	240±40	>3000
CD16b	7.1	>3000	>3000	>3000

* CD32a binding to 5c8-IgG1 was biphasic. Kd was estimated as ~10^{-7} M based on steady state fit to dominant binding even. This Kd is in range of literature reported KD for CD32a binding to IgG1.

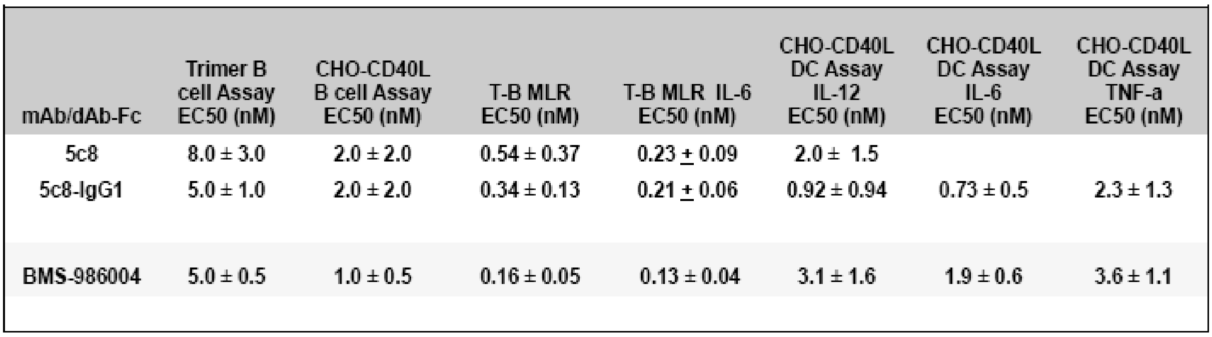
Example 7

In-vitro Cell-based Assays

The potency of BMS-986004 was evaluated in various primary immune cell assays to ensure robust potency across different cell types. The primary human B cell proliferation assays were conducted two ways, as described in detail above in Example 4: (1) recombinant CD40L trimer was used to drive B cell proliferation; and (2) CHO cells expressing CD40L on the membrane (CHO-CD40L) were utilized to induce B cell proliferation. The utility of CHO-CD40L cells was particularly important to ensure that signals from membrane-bound CD40L were inhibited equally well when compared to the soluble CD40L trimer. The CHO-CD40L cells were also used to drive the activation of primary human DCs differentiated from culturing PBMC-derived monocytes in presence of GM-CSF and IL-4. Similarly, the T-B MLR assay measured B cell activation driven by CD40L present on activated T cells. In all of the above described primary assays, BMS-986004 was equipotent to the benchmark 5c8 mAb: potencies ranged from was single-digit nM to sub-nM, depending on the assay (TABLE 10).

TABLE 10

Potency of BMS-986004 in Various Primary Cell Assays



mAb/dAb-Fc	Trimer B cell Assay EC50 (nM)	CHO-CD40L B cell Assay EC50 (nM)	T-B MLR EC50 (nM)	T-B MLR IL-6 EC50 (nM)	CHO-CD40L DC Assay IL-12 EC50 (nM)	CHO-CD40L DC Assay IL-6 EC50 (nM)	CHO-CD40L DC Assay TNF-a EC50 (nM)
5c8	8.0 ± 3.0	2.0 ± 2.0	0.54 ± 0.37	0.23 ± 0.09	2.0 ± 1.5		
5c8-IgG1	5.0 ± 1.0	2.0 ± 2.0	0.34 ± 0.13	0.21 ± 0.06	0.92 ± 0.94	0.73 ± 0.5	2.3 ± 1.3
BMS-986004	5.0 ± 0.5	1.0 ± 0.5	0.16 ± 0.05	0.13 ± 0.04	3.1 ± 1.6	1.9 ± 0.6	3.6 ± 1.1

Example 8

Assessment of Whole Blood Receptor Occupancy (RO)

A receptor occupancy method was developed to measure CD40L target engagement by BMS-986003 in cynomolgus whole blood samples and, subsequently, in BMS-986004 in human whole blood samples. BMS-986003 is a dAb which shares the same amino acid sequence as BMS-986004, except for a non-native glycine residue at its amino-terminus.

Occupancy is measured on CD4+ T cells by flow cytometry using an anti-CD40L mAb that competes for binding to CD40L with BMS-986003 / BMS-986004, and is cross-reactive with human and cynomolgus CD40L. In the presence of bound dAb, the anti-CD40L detection mAb is blocked from binding to CD40L in a concentration-dependent manner, providing a measure of target occupancy. Given that basal CD40L is expressed at low levels on resting T cells in peripheral blood, RO was assessed in both unstimulated blood samples and in samples where phytohemagglutinin (PHA) was used to induce up-regulation of CD40L on the T cell surface. Binding potency curves were generated following *ex vivo* whole blood treatment with BMS-986003 and BMS-986004. The average EC_{50} and EC_{90} values obtained are shown in TABLE 11.

TABLE 11

Binding Potency of BMS-986003 and BMS-986004 on CD4+ T-cells in *ex vivo* Whole Blood Receptor Occupancy Assay

BMS-986003	***n***	**Average EC_{50}, nM**	**Average EC_{90}, nM**
Human (basal)	1	0.9	3
Human (PHA-induced)	6	0.8	9
Cyno (basal)	3	0.6	3
Cyno (PHA-induced)	3	0.4	2
BMS-986004			
Human (basal)	3	0.4	3
Human (PHA-induced)	3	0.7	5

The target binding potency in whole blood for BMS-986003 and BMS-986004 closely correlates between human and cynomolgus monkey. The EC_{50} values for BMS-986003 and BMS-986004 are also similar when bound to basal and PHA-induced CD40L. Additionally, these values are comparable to those obtained in human *in vitro* cell based assays (see TABLE 10). Based on the measured EC_{90} values, full target saturation in peripheral blood should be achieved at concentrations $\leq$ 10nM.

To support the preclinical PK/PD profile of BMS-986003 and BMS-986004, RO was assessed in both the cynomolgus KLH study (immunization with keyhole limpet hemocyanin) with BMS-986003 and the IV bridging study with BMS-986004. Further details of these findings can be found in Examples below.

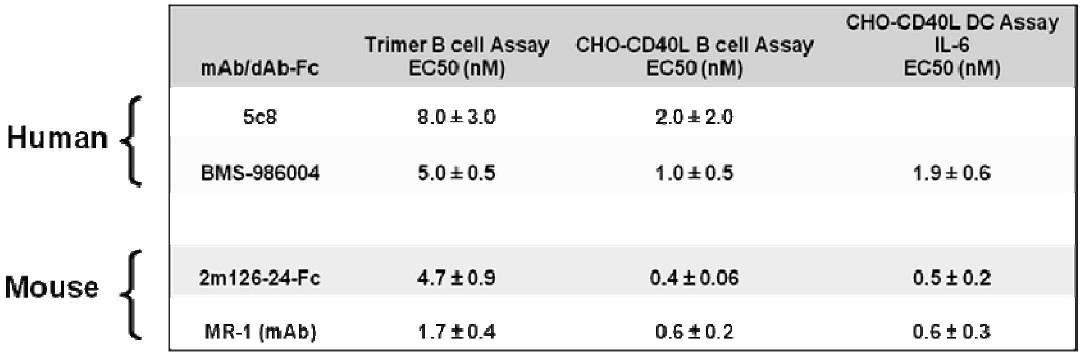
Example 9

In vivo Pharmacology

To show efficacy of a CD40L dAb in mouse disease models, a mouse CD40L dAb 2m126-24 was formatted with mouse IgG1 Fc with D265**A** point mutation to further lower the Fc effector function. This mouse surrogate dAb 2m126-24-Fc shows potency comparable to BMS-986004 and MR-1, a hamster anti-mouse CD40L antibody (TABLE 12).

TABLE 12

***In vitro* Potency Comparison**



	mAb/dAb-Fc	Trimer B cell Assay EC50 (nM)	CHO-CD40L B cell Assay EC50 (nM)	CHO-CD40L DC Assay IL-6 EC50 (nM)
Human	5c8	8.0 ± 3.0	2.0 ± 2.0	
	BMS-986004	5.0 ± 0.5	1.0 ± 0.5	1.9 ± 0.6
Mouse	2m126-24-Fc	4.7 ± 0.9	0.4 ± 0.06	0.5 ± 0.2
	MR-1 (mAb)	1.7 ± 0.4	0.6 ± 0.2	0.6 ± 0.3

Inhibition of KLH Induced Antibody Response by the Mouse CD40L dAb

Female BALB/c mice were injected intraperitoneally (i.p.) with 250 µg KLH on day 0. Mice were dosed subcutaneously (s.c.) with MR-1 or BMS-2m-126-24-Fc at indicated doses on day -1 and day 6. Blood was collected and the serum was analyzed for anti-KLH IgM on day 7 and IgG on day 14 by ELISA. Serum from BALB/c mice collected on day 14 after immunization with KLH was pooled and used as a positive comparator, and the data is expressed as a ratio of the titre of the test serum to the titre of the pooled BALB/c serum. As shown in FIG. 7, BMS-2m-126-24-Fc demonstrated a dose dependent suppression of IgG titers with maximal effect shown at 3 mg/kg, with ED50 calculated to be 0.26 mg/kg. Both the CD40L dAb and the antibody were tested at 1 mg/kg, showing 70% vs. 30% reduction in IgG response, respectively. Similar exposure of the dAb and the antibody were observed at 1 mg/kg, suggesting that the dAb is slightly more potent than the antibody at suppressing KLH-induced IgG response. In conclusion, the CD40L dAb has demonstrated at least the same level of efficacy as the anti-CD40L antibody at inhibiting a T cell dependent antibody response.

Inhibition of TNBS-induced Colitis by the Mouse CD40L dAb

Male SJL/J mice were intrarectally administered with 2.5 mg Trinitrobenzene sulfonic acid (TNBS) in 50% EtOH via a catheter inserted 4 cm distal to the anus. Mice were dosed once s.c. with MR-1 or BMS-2m-126-24-Fc at indicated doses 4 hours prior to TNBS injection. FIG. 8 presents the changes in the mean body weight and the percent survival of groups of mice treated with PBS/IgG or varying dose levels of MR-1 or the dAb. Abatacept was used as a positive control (20 mg/kg, i.p. every other day). A typical profile of TNBS-induced colitis was shown in the IgG control group: loss of body weight, peaking at day 3-4; colitis-related death occurring at day 3 and beyond; and the survived mice showing signs of recovery after day 4. Treatment with the CD40L dAb or the antibody (both tested at 2, 8 and 20 mg/kg) caused a dose-dependent inhibition of the body-weight loss and the increase in survival rate; both compounds at 8 mg/kg yielded a degree of efficacy that is comparable to that of Abatacept at 20 mg/kg. In conclusion, the mouse CD40L dAb BMS-2m-126-24-Fc has demonstrated comparable efficacy to the anti-CD40L antibody MR-1 in an acute TNBS-induced colitis model.

Synergistic Effect between CTLA4 Ig and the Mouse CD40L dAb in a Mouse “Heart-to-Ear” Transplant Model

Heart grafts from neonatal (48-72 hrs) C57Bl/6 mice were implanted into a subcutaneous pocket created in the ear pinnae of BALB/c mice. Mice were treated with CTLA4-Ig (i.p. 2x/wk), BMS-2m126-24-Fc (s.c. 1x /wk), or combination of both at indicated doses, with first dosing initiated the day prior to transplantation. Time to rejection was defined by the absence of cardiac contractility for three consecutive days as assessed daily by the electrocardiogram (ECG) device of allograft. As expected, without any treatment, C57BL/6 mice that received the neonatal BALB/c heart rejected the graft shortly thereafter, with median survival time (MST) of

12 days. The monotherapy with 3, 20 mg/kg of the dAb or 25 mg/kg of CTLA4-Ig had no or little impact on prolonging the survival of the allograft (MST: 12, 15 and 13 days respectively). However, in the groups treated with combination of 20 mg/kg of the dAb and 25 mg/kg of CTLA4-Ig, the graft survival was significantly prolonged showing MST of 35 days (FIG. 9). This data has provided rationale for combining CD40L dAb with belatacept in human renal transplant patients. Future transplant studies in non-human primates will further define the dose level and assess the potential effect on tolerance induction with CD40L dAb BMS-986004.

Example 10

In vivo Nonclinical Pharmacokinetics (PK) and Pharmcodynamics (PD)

Various *in vivo* studies were conducted to characterize the PK and PD of BMS-986004, BMS-986003, and a mouse CD40L dAb-Fc surrogate BMS-2m-126-24-CT, in the nonclinical setting. The key findings are summarized below.

ELISA to measure BMS-986004 dAb

Enzyme-linked immunosorbency assay (ELISA)-based bioanalytical methods were developed to support the PK studies, acute and chronic efficacy studies in mice, and exploratory PK/PD studies employing cynomolgus monkeys. In all cases, whole blood was obtained and plasma prepared in the presence of EDTA, the samples were then subjected to ELISA analysis.

Plasma concentrations of BMS-986004 were measured with an ELISA assay that utilized human CD40L antigen to capture the analyte from test samples. Test samples were thawed at 4°C, mixed well and diluted 1:100 in assay diluent composed of 1× PBS, 0.05% Tween-20, and 1% BSA (PTB). Subsequent dilutions of the sample were made using 1% normal monkey plasma/PTB as diluent. This allowed the test analyte to be assayed at several dilutions (10^2 – 10^5) while keeping the sample matrix at 1%.

Recombinant trimeric human CD40L was obtained from Protein Structure and Science (PSS), LVL and was bound to 96 well plates at a final concentration of 2 μg/mL. Test samples, quality control (QC) samples and the standards were detected with affinity-purified rabbit anti-heavy chain (Vh) domain framework polyclonal antibody (Covance Research Products, Denver, PA) diluted to a concentration of 0.25 μg/ml in PTB, followed by horseradish peroxidase-labeled donkey anti-rabbit polyclonal secondary antibody (Jackson Immunoresearch, West Grove, PA) with substrate (TMB - tetramethylbenzidine) added, and the enzymatic reaction stopped with 1 M phosphoric acid. Absorbance was measured at a wavelength of 450 nm. The analysis of BMS-986004 in test samples was conducted using a standard curve. Standard curve calibrators prepared on the day of each run in 1% monkey plasma were used to define the dynamic range of the bioanalytical method. The range of resulting standard curve in 100% plasma was 10 - 1200 ng/mL. The reference standard for BMS-986004 was obtained from Biologics Process and Product Development (BPPD), HPW. The reference standard material was representative of the manufacturing batch and was used in the study protocol. Standard curves and QCs were evaluated using criteria for accuracy and precision of ≤ 20% which was considered to be acceptable for assay performance. Test samples were quantified using a 4-parameter logistic fit regression model weighted by reciprocal concentration (1/x) derived from the calibrators.

Performance of the QC samples, measured by the deviation of the calculated concentration from its nominal value indicated the reference material was stable in neat monkey plasma at concentrations of 30 - 1000 ng/ml when stored at -70° C for over 2 months.

ELISA to measure a mouse surrogate dAb

Mouse CD40L-specific dAb BMS-2m-126-24-CT was measured in mouse plasma samples to provide exposure data in support of several acute and chronic efficacy studies as well as PK assessment.

While the assay format for mouse dAbs was quite similar to that for human dAbs in monkey samples, there were a few differences. The mouse plasma matrix was diluted to 1:10 (10%) in assay diluent, and all subsequent dilutions of test samples were made using 10% mouse matrix. Likewise, all standards and QCs were also incubated on ELISA plates in 10% mouse plasma. The concentration of BMS-2m-126-24-CT in test samples from mice was measured using mouse CD40L to capture the analyte. As the mouse dAb has Vk framework, all test samples, QCs, and the standards were detected with affinity purified rabbit anti-kappa (Vk) domain polyclonal antibody (Covance Research Products, Denver, PA) diluted to a concentration of 0.5 μg/mL in PTB. The rest of the assay and analysis procedure was similar to the procedure for the analysis of human CD40L dAbs. Acceptance criteria for back-calculated concentrations of standards and QCs were also similar to those for human CD40L dAbs. The quantitative range of BMS-2m-126-24-CT as determined from the standard curve was 12.5 to 600 ng/mL in neat sample matrix.

Nonclinical Pharmacokinetics

TABLE 13 summarizes the PK parameters for BMS-986004, BMS-986003, and BMS-2m-126-24-CT in nonclinical animal species.

TABLE 13

Single-dose PK Parameters (mean ± SD) from Two Nonclinical Animal Species

Species	dAb	Route	Dose (mg/kg)	Cmax (µM)	Tmax (h)	AUC0-inf (µM.h)	T1/2 (h)	CLTp (mL/h/kg)	Vss (L/kg)	F (%)
Mouse	BMS-2m-126-24-CT	IV	1 (N=3)	-	-	6.9	101	1.85	0.26	-
		SC	1 (N=3)	0.063	24	10	100	-	-	100
			10 (N=3)	0.68	24	114	120	-	-	100
Monkey	BMS-986003	IV	2 (N=2)	-	-	40	106	0.67	0.067	-
		SC	0.2 (N=4)	0.019 ±0.004	60 ±72	4.0± 2.7	85± 29	-	-	88
			2 (N=4)	0.22 ± 0.075	33 ± 43	29.7 ± 4.9	68 ± 11	-	-	74
			20 (N=4)	1.48 ±0.34	11 ±9	175 ±27	105 ±18	-	-	44
	BMS-986004	IV	11 (N=4)	-	-	241 ± 18	124 ± 12	0.59 ± 0.04	0.098 ± 0.01	-
	5c8-IgG1	IV	20 (N=4)	-	-	1800 ± 74	400	0.074	0.042	

BMS-986004 and BMS-986003 exhibited comparable PK profiles in monkeys (FIG. 11A and FIG. 11B). After IV administration, the plasma concentrations of BMS-986004 and BMS -986003 exhibited a bi-exponential decline up to 504 and 408 h, respectively. Accelerated clearance was observed afterward in 50% of monkeys enrolled in both studies. Immunogenicity testing of the plasma samples collected at 38 d after BMS-986004 treatment suggested that all monkeys developed anti-drug antibody (ADA); and that the monkeys with higher ADA levels showed faster clearance. Although no immunogenicity test was conducted for the IV PK study with BMS-986003, a similar level of immunogenicity was observed in monkeys after subcutaneous dosing with BMS-986003 in the PK/PD study, suggesting both proteins were immunogenic in monkeys. The terminal half-life (T1/2) of 124 and 106 h for BMS-986004 and BMS-986003 was, therefore, determined using the exposures collected up to two weeks (336 h) only. The steady-state volume of distribution (Vss) of BMS-986004 and BMS-986003 was 0.098 and 0.074 L/kg, respectively. The values are greater than the plasma volume (0.06 L/kg) but less than the volume of extracellular fluid (0.2 L/kg), suggesting that the proteins largely reside in the extracellular space. The total body plasma clearance (CLTp) of BMS-986004 and BMS-986003 was 0.59 and 0.65 mL/h/kg, respectively.

The PK parameters of BMS-986004 in monkeys were compared to those of abatacept, a similar size protein (78.5 vs 78-kDa BMS-986004, based on amino acid sequence), with the same modified human IgG1 Fc format. As expected, the parameters of BMS-986004 were nearly identical with those of abatacept (CLTp of 0.6 mL/h/kg, Vss of 0.087 L/kg, T1/2 of 5 d), suggesting the humans PK of BMS-986004 and abatacept is likely to be similar.

The absorption of BMS-986003 after subcutaneous (SC) administration was evaluated in the monkey PK/PD study. The monkeys were administered with BMS-986003 as single subcutaneous doses of 0 (vehicle control), 0.2, 2 and 20 mg/kg, at 24 h prior to the immunization with keyhole limpet hemocyanin (KLH), a T cell-dependent antigen. After dosing, BMS-986003 was slowly absorbed, with a Tmax ranging from 6-96 h (FIG. 12). The exposure of BMS-986003 appeared to be less than dose-proportional across all dose levels. With a dose ratio of 1:10:100, the average Cmax and AUC0-inf ratios were 1:12:80 and 1:7:44, respectively. With the exposure following the IV dose (2 mg/kg) as reference, and assuming linear PK after IV dosing, the SC bioavailability of BMS-986003 was 88%, 74%, and 44% at 0.2, 2, and 20 mg/kg, respectively. The terminal T1/2 was confounded by the immunogenicity observed with most of the monkeys at 2 to 5 weeks after dosing. Therefore, the T1/2 was estimated to be 85, 66, and 105 h at 0.2, 2 and 20 mg/kg, respectively.

The PK of 5c8-IgG1, an anti-human CD40L monoclonal antibody used as a positive control in the PK/PD study, was evaluated after IV administration at 20 mg/kg (FIG. 12). 5c8-IgG1 exhibited 10-fold higher plasma exposures and 4-fold longer T1/2 when compared to BMS-986003 given SC at the same dose (TABLE 13).

The PK of the mouse surrogate dAb-Fc fusion protein, BMS-2m-126-24-CT, was evaluated in mice following single IV and SC administration (TABLE 13). After a single IV (1 mg/kg), the plasma concentrations followed a mono-exponential decline with a terminal T1/2 of 101 h (FIG. 13). The CLTp was 1.85mL/h/kg; and the Vss was at 0.26L/kg, indicating extracellular distribution. After single SC doses of 1 and 10 mg/kg, BMS-2m-126-24-CT was slowly absorbed with a Tmax of 24 h. The systemic exposures increased in a dose-proportional manner. With a dose ratio of 1:10, the Cmax and AUC0-inf increased in the proportion of 1:11. The terminal T1/2 was 100 and 120 h at 1 and 10 mg/kg, respectively. The ratio of the dose-adjusted exposure (AUC0-inf) after SC and IV administration was greater than 1, suggesting complete absorption after SC administration.

Pharmacokinetic / Pharmacodynamic Modeling

The PD of BMS-986003 was measured as the suppression of anti-KLH antibody response in the PK/PD study. BMS-986003 suppressed 70% the antibody response to KLH (% response suppressed = $(1-\frac{AUEC_{0-1008h\ \mathrm{IgG\ titers}}\mathrm{treatedgroup}}{AUEC_{0-1008h\ \mathrm{IgG\ titers}}\mathrm{vehicle\ group}})*100$) at the highest dose of 20 mg/kg. Marginal (15%) and no suppression of the antibody response occurred at 2 and 0.2 mg/kg. In comparison, 5c8-IgG1 exhibited 10-fold higher plasma exposures and 4-fold longer T1/2 than BMS-986003 at the same dose level (20 mg/kg). As a result, 5c8-IgG1 suppressed 97% anti-KLH antibody response. In order to compare the in vivo potency between BMS-986003 and 5c8-IgG1, PK/PD modeling was performed using SAAM II (version 1.2.1, Seattle, WA). The plasma concentrations of BMS-986003 following SC administration were described using a first-order absorption kinetics coupled with a 2-compartment model, where the elimination occurred in both central and peripheral compartments. Because of complications from immunogenicity and possible nonlinear absorption, the PK data were fitted individually at each dose.

For 5c8-IgG1, a two-compartment model with central elimination was used. The anti-KLH antibody response, expressed as the average value of IgG titers, was modeled using a 6-

compartment signal transduction model. The kinetics of KLH in the body was assumed to be a 1-compartment model. The inhibition of the IgG production by BMS-986003 and 5c8-IgG1 was described using an Imax model, with a maximum inhibition equal to 100%. As shown in FIG. 14, the model-fitted curves were able to describe both the PK and PD profile. The plasma IC50 of BMS-986003 and 5c8-IgG1 for the suppression of KLH-induced IgG production was estimated to be 74 ± 14 and 60 ± 18 nM, respectively. These results demonstrated that the potency of these two molecules was comparable *in vivo*.

The CD40L receptor occupancy (RO) of BMS-986004 was measured in the IV PK study. Following IV administration of 11 mg/kg, the RO of BMS-986004 on the peripheral-blood mononuclear cells (PBMC) was time- and concentration-dependent. PK/PD modeling was performed to estimated an RO EC50. The plasma concentrations were modeled using a modified two-compartment model with an additional ADA-mediated first order elimination constant introduced at 504 h after dosing; and the RO was modeled using an Emax model ($RO\% = \frac{E\max * Cp^{\gamma}}{EC50^{\gamma} + Cp^{\gamma}}$). As shown in FIG. 15, the fitted curves were able to describe both exposure and RO, with an estimated RO EC50 of 3.4 ± 0.3 nM and the γ (hill factor) of 3.1 ± 0.1. In comparison, the RO EC50 was ~22-fold lower than the anti-KLH antibody response IC50 of 74 ± 14 nM, suggesting that >95% RO is required in order to achieve appreciable (>50%) anti-KLH antibody suppression.

Example 11

Nonclinical Toxicology Single-dose PK/PD Study

The objectives of this study were to 1) determine the tolerability of BMS-986003, including its potential immunogenicity, when given subcutaneously as a single dose to monkeys; 2) evaluate its PD (e.g., inhibition of the antibody response to T-cell-dependent antigen) and PK profiles; 3) evaluate the receptor occupancy of BMS-986003 and peripheral T-cell counts following subcutaneous dosing; and 4) aid dose selection for renal transplant studies and first-in-human dosing.

BMS-986003 was administered s.c. in the posterior thorax as single doses of 0 (vehicle control), 0.2, 2, or 20 mg/kg to groups of 2 cynomolgus monkeys per sex. An additional two monkeys/sex received a single intravenous dose of 20 mg/kg 5c8-IgG1, a monoclonal antibody to human CD40L that was used as a positive control in this study. All doses were administered at 2 mL/kg in the vehicle (PBS; pH 7.2). To assess the effects on the T-cell dependent antibody response, animals were immunized at approximately 24 hours after dosing with test article or immediately after dosing the positive control with 10 mg of KLH by intramuscular injection (posterior quadriceps or caudal thigh). Criteria for evaluation included survival, PK, immunogenicity, PD (inhibition of the antibody response to the T-cell-dependent antigen, KLH), clinical signs, body weights, food consumption, peripheral-blood immunophenotyping, receptor occupancy, and clinical-pathology evaluations (hematology, serum chemistry, and coagulation). Animals were returned to stock following a 6-week post-dose observation period.

At doses ≤ 20 mg/kg, BMS-986003 was slowly absorbed (Tmax = 6-96 h) and Cmax and AUCtot values increased in a less than dose-proportional manner across all dose groups and there were no apparent gender differences. The T1/2 values estimated ranged from 69-104 h across all doses. BMS-986003 was substantially immunogenic; all monkeys developed a positive anti-drug antibody (ADA) response during the 6-week post-dose period. At 0.2 and 2 mg/kg, the mean group total ADA response peaked at Day 22 at mean group end point titers (EPT) of 4203 and 6469, respectively. At 20 mg/kg, the ADA response, while positive, was somewhat delayed and partially suppressed, consistent with target pharmacology, peaking at Day 36 at a mean group EPT of 1828. Further characterization of the antibodies demonstrated the majority of binding to the dAb (non-Fc) portion of the molecule and these antibodies were shown to block the binding of BMS-986003 to CD40L in 2 different immunoassay formats suggesting that the ADA were neutralizing. In addition, the formation of ADA appeared to accelerate the elimination of BMS-986003 in several monkeys.

Mean PK parameters for BMS-986003 are presented in TABLE 14.

TABLE 14

Pharmacokinetic Summary

Mean Parameter	**BMS-986003**			**5C8-IgG1**
	SC			**IV**
	0.2 mg/kg (N = 4)	**2 mg/kg (N = 4)**	**20 mg/kg (N = 4)**	**20 mg/kg (N = 4)**
Gender	**Male/Female**	**Male/Female**	**Male/Female**	**Male/Female**
AUC(0-inf) µg·h/mL	219/407	2165/2477	14195/13114	267750/272250
CLTp mL/h/kg	Not applicable	Not applicable	Not applicable	ND/0.074
T1/2 h	69/101	68/69	107/104	ND/400
Cmax µg/mL	69/101	45/49	88/91	Not applicable
Tmax h	24/96	51/15	6/15	Not applicable

Molecular weight used for conversion was 78104 Da for BMS-986003, 150000 Da for 5c8-IgG1 mAb.
ND = not determined,; AUCextra for males was above 20%, therefore the T1/2 was not reported.

There were no BMS-986003- or 5c8-IgG1-related clinical observations or effects on body weights or clinical pathology parameters except 1 male treated with 5c8-IgG1 had decreased red blood cells (0.74 × control), hemoglobin (0.73× predose), and hematocrit (0.75× predose) on Day 8, and 3 of 4 monkeys receiving 5c8-IgG1 had decreased lymphocytes (0.53× to 0.65× predose) on Day 8, suggestive of lymphocyte depletion.

CD40L receptor occupancy was generally time- and dose-dependent and more sustained following administration of 20 mg/kg BMS-986003, consistent with higher and more sustained exposures at this dose and PD activity. For BMS-986003, mean peak receptor occupancy on peripheral-blood mononuclear cells (PBMC) was achieved at 24 hrs (97%), 6 hrs (99%) or 48 hrs (99%) post-dose, decreasing to <90% occupancy at 240, 360, or 696 hrs and to <50% occupancy at 360, 696, or 1032 hrs, at 0.2, 2, or 20 mg/kg, respectively. In comparison, for 5c8-IgG1 at 20 mg/kg, mean peak receptor occupancy on PBMC was achieved at 48 hours (≥ 100%), and was sustained at ≥ 97% for the entire study (1032 hr or through Day 44).

BMS-986003 suppressed the antibody response to KLH only at the high dose of 20 mg/kg. On Days 8-30 at 20 mg/kg, there was a 69 to 83% suppression of the geometric group mean antibody response to KLH, relative to the control group, with a peak suppression of 83% occurring on Day 16. No suppression of the antibody response occurred at 0.2 or 2 mg/kg BMS-986003. These data demonstrate that BMS-986003 at a sustained receptor occupancy of >90% for at least 1 month and at sustained plasma concentrations above ~10 μg/mL through Day 11 is able to inhibit a T-cell dependent antibody response in cynomolgus monkeys. For the positive control antibody, 5c8-IgG1, suppression of 74-97% of the geometric group mean antibody response to KLH occurred on Days 8-30, with peak suppression of 97% by Day 16 which was generally sustained through Day 30.

No biologically relevant BMS-986003 related changes in absolute numbers of B cells (CD45+, CD20+, CD3-), total T (CD45+, CD3+) cells, helper T (CD45+, CD3+, CD4+, CD8-) cells, cytotoxic T (CD45+, CD3+, CD4-, CD8+) cells, or natural killer (CD45+, CD3-, CD16+) cells occurred during the study, which confirmed lack of any Fc effector function. However, on Day 8, 3 of 4 monkeys treated with 20 mg/kg 5c8-IgG1 had decreased T-lymphocytes (0.53×-0.66× predose), both helper T-cell (0.64× to 0.77× predose) and cytotoxic (0.40× to 0.61× predose) T-cell populations, suggestive of depletion.

In conclusion, BMS-986003 administered as single SC doses of 0.2, 2, or 20 mg/kg (AUC ≤ 14195 μg*hr/mL) was well tolerated in cynomolgus monkeys with no adverse drug-related effects. The positive control, 5c8-IgG1, at a dose of 20 mg/kg, resulted in complete, sustained inhibition of the antibody response to KLH and sustained receptor occupancy of nearly 100% through 30 days post-dose. Mild depletion of T-cells was also noted by Day 8 in monkeys receiving 5c8-IgG1 (0.40x to 0.77x predose), which was not observed with BMS-986003. BMS-986003 was able to suppress an antibody response to KLH at 20 mg/kg (peak suppression of 83%) following KLH immunization on Day 1 and had sustained receptor occupancy of ≥ 90% through Day 22 and ≥ 50% through Day 29. Similar dampening of the immunogenicity to BMS-986003 occurred at 20 mg/kg. However, lower BMS-986003 doses of 0.2 and 2 mg/kg did not suppress the antibody response to KLH or the anti-drug antibody response. The lack of pharmacology at the lower doses also correlated with decreasing receptor occupancy (i.e., <90% by Day 11 [0.2 mg/kg] or 16 [2 mg/kg]; <50% by Day 16 [0.2 mg/kg] or 30 [2 mg/kg]) and accelerated clearance, presumably due to the formation of ADA. The inhibition of TDAR is consistent with the mechanism of action of this compound and was not considered adverse.

Example 12

Evaluation of the Risk for TE / Thrombosis

It has been hypothesized that the TE associated with administration of the anti-CD40L monoclonal antibodies is mediated by anti-CD40L mAb-CD40L immune complex (IC)-mediated cross linking of platelets, facilitated by IC binding to FcgRIIa, an IgG Fc receptor, causing activation and aggregation (FIG. 10). Blocking the interaction of Fc moiety of IgG with FcgRIIa is, therefore, expected to mitigate platelet cross linking and thrombosis. The following methods and approaches were designed to evaluate the risk of TE and/or thrombosis.

<u>*In vitro* platelet activation assays</u>

Several in vitro assays were conducted to test the hypothesis that platelets are activated by CD40L mab/sCD40L IC in a FcgRIIa-dependent manner. The positive control 5c8-IgG1 was used to validate the assays prior to testing BMS-986003 and BMS-986004. Blood from human donors or mice expressing hFcgRIIa receptor on platelets were used for these studies. Platelet activation was detected by flow cytometry using antibodies against the well-validated platelet activation markers P-selectin (CD62P) and PAC-1 (activated GPIIb/IIIa). Briefly, blood was diluted 1:25 in modified Tyrodes-HEPES containing 1mM CaCl2 to which detection antibodies and test reagents was added, incubated, and analyzed for platelet activation. Initial experiments determined that sCD40L or 5c8IgG1 alone did not activate platelets, but different immune complex ratios of 1:1 to 1:8 of 5c8:sCD40L significantly activated platelets. Subsequent experiments used 5c8-IgG1 or 5c8-mIgG2a IC, mostly at a 1:3 molar ratio of 5c8:sCD40L.

Platelet activation by 5c8/sCD40L IC can be blocked by anti-FcgRIIa antibody

Studies were conducted with the FcgRIIa blocking antibody IV.3 to test whether activation of platelets by 5c8/sCD40L IC was indeed FcgRIIA-mediated. Blood from human donors was pre-incubated with 0.5µg/µl of the FcgRIIa blocking antibody IV.3 prior to dilution and incubation with detection antibodies as described above. Adenosine diphosphate (ADP), a platelet activator via a different mechanism, was used as a positive control. As illustrated in FIG. 16, platelet activation by 5c8/sCD40 IC was completely blocked by IV.3, while activation by ADP was not inhibited by the blocking antibody, indicating that activation by the IC is FcgRIIa-mediated.

Selection of inert Fc tails

A requirement for potential candidate molecules was absence of binding to FcgRIIa to prevent potential platelet activation. Several 5c8 constructs containing different mutations derived from IgG1 (e.g 5c8-CT and N297Q) or IgG4 (e.g., 5c8-S228P) were expressed and screened for Fc tails that did not activate platelets using different molar ratios of sCD40L to mAbs. Wild-type and most mutated constructs activated platelets except for 5c8-CT and 5c8-N297Q (FIG. 17). Absence of Fc (5c8-Fab2) also did not activate platelets further confirming that IC-platelet activation is Fc-mediated. The CT tail was chosen to format the dAb candidates BMS-986003 and BMS-986004.

Effect of FcgRIIa polymorphism on platelet activation

The gene for FcgRIIa is variable at codon 131, resulting in His-Arg (C**<u>A</u>**T/C**<u>G</u>**T) polymorphism. The genotype distribution in approximately 100 individuals with about equal distribution of Caucasians and African Americans was A/A (His homozygous; 14%), A/G (His/Arg heterozygous; 60%), and G/G (Arginine homozygous; 26%) for Caucasian Americans and A/A (30%), A/G (51%), and G/G (19%) for African-Americans. Reilly et al., *Clin. Diagn. Lab. Immunol.* 1: 640-644 (1994). Fc-dependent platelet aggregation was noted in samples from R131 individuals when treated with anti-CD9 in mIgG2 or mIgG1 Fc format, while platelets from H131 individuals aggregated only with anti-CD9 as mIgG2 format; this suggests that Fc-dependent aggregation with an IgG1 mAb could potentially segregate a patient population into low and high responders, which has previously been reported with this polymorphism. Tomiyama et al., *Blood* 80: 2261-2268 (1992). To address any potential differences in platelet activation with the IgG1 and CT Fc tail, 19 donors were genotyped for hFcgRIIa polymorphism and samples tested for platelet activation. The donor pool polymorphism (RR; 42%, HH; 21%, HR; 37%) was sufficient to evaluate any potential differences in platelet activation to the IgG1 format. Representative of literature reports, platelet activation with 5c8-IgG1/sCD40L IC was similar across all genotyped individuals. No activation was found with 5c8-CT/sCD40L IC (FIG. 18), suggesting no or minimal risk of increased TE in a patient population with an antibody formatted with the CT tail.

BMS-986004: Platelet activation in human blood donors

The experiments described above using 5c8, supported selection of the CT-tail as the best format for BMS-986004 (also called BMS2h-572-633-CT-L2). Blood obtained from 6 donors was treated with 5c8-IgG1, 5c8-CT, $F(ab)_2$, and BMS-986004. Platelets were activated by 5c8-IgG1 but not by any of the other constructs, including BMS-986004 (FIG. 19), suggesting that this dAb has no or low risk for causing platelet activation and TE in clinical studies.

BMS-986003: Platelet activation in blood from mice expressing hFcgRIIa

To further confirm that activation of platelets by anti-CD40L antibodies was mediated by FcgRIIa receptor, blood from transgenic mice expressing the human receptor (R131 genotype) was treated with 5c8-IgG1, 5c8-IgG2a, dAb-IgG1, 5c8-CT, and BMS-986003 (also called BMS-2h572-633-CT). Platelets were specifically activated by 5c8-IgG1, 5c8-IgG2a, and dAb-IgG1/sCD40L IC in blood from mice expressing hFcgRIIa, but not wild-type littermates. 5c8-CT and BMS-986003 did not activate platelets, further confirming a low risk for TE with the presently disclosed antibodies (FIG. 20).

Example 13

Epitope Binding Experiments

FIG. 25 shows SPR sensorgram data for experiments designed to test whether or not monovalent dAb molecules BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and the monovalent anti-CD40L 5c8 Fab fragment compete with each other for binding to CD40L. Experiments were performed using biotinylated CD40L (biot-IZ-hCD40L) that was captured on a streptavidin sensor chip surface. The tests involved the sequential injection of a specified molecule (phase “a”), immediately followed by injection of the same molecule in the presence of a second specified molecule (phase “b”), followed by dissociation (phase “c”). Competition for binding is identified as a reduction (blocking) of the binding signal for the second molecule in the presence of the first, with the level of blocking being governed by the association and dissociation kinetics of each molecule. For each pair of molecules tested, the binding of the second molecule was shown to be reduced when the first molecule was present. These result suggest that BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and 5c8 Fab compete with each other for binding to biot-IZ-hCD40L.

FIG. 26 shows SPR sensorgram data for binding of the indicated dAb-CT-long and the 5c8-CT-long molecules to either human CD40L monomer (triple CD40L mutant (T211E, S222Y, H224K, [108-261])) or to CD40L trimer (IZ-hCD40L). The dAb-CT-long and the 5c8-CT-long molecules were captured via their “CT-long” Fc-domain on an immobilized anti-human IgG Fc (Biacore, GE Healthcare) antibody sensor chip surface. The data in the top 3 panels show that human CD40L monomer binds specifically to BMS2h-719-202-CT-long and 5c8-CT-long, but does not bind to any of the indicated dAb-CT-long molecules that contain dAbs from the BMS2h-572-6 lineage.. In contrast, the bottom 3 panels show that CD40L trimer (IZ-hCD40L) binds strongly to all the tested dAb-CT-long molecules from the BMS2h-572-6 lineage, as well as to BMS2h-719-202-CT-long and 5c8-CT-long. These results suggest that the molecules from the BMS2h-572-6xx-CT-long lineage are specific for an epitope that is only present on the CD40L trimer and not present on monomeric human CD40L, whereas BMS2h-719-202-CT-long and 5c8-CT-long bind to an epitope that is present on both the CD40L monomer and trimer.

Although the present embodiments have been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of these embodiments, and would be readily known to the skilled artisan.

What is claimed is:

1. An isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain is at least 95% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

2. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain is at least 96% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

3. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain is at least 97% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

4. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain is at least 98% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

5. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain is at least 99% identical to the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

6. The antibody polypeptide of claim 1, wherein the first variable domain comprises the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

7. The antibody polypeptide of claim 1, wherein the first variable domain is set forth in SEQ ID NO: 274.

8. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain comprises:

(a) a CDR1 region having a sequence Trp-X_1-Leu-Met-Gly (SEQ ID NO: 2), wherein X_1 is Glu or Gln;

(b) a CDR2 region having a sequence Gly-Ile-Glu-Gly-Pro-Gly-Asp-Val-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (SEQ ID NO: 3); and

(c) a CDR3 region having a sequence Lys-X_2-Y_2- Z_2-Ser-Asp-Tyr (SEQ ID NO: 4), wherein X_2 is Asp or Glu, Y_2 is Ala or Ser, and Z_2 is Lys, Asn, or Arg.

9. The antibody polypeptide of claim 1, wherein the first variable domain comprises the amino acid sequence of: BMS2h-572-11 (SEQ ID NO: 226), BMS2h-572-12 (SEQ ID NO: 227), BMS2h-572-14 (SEQ ID NO: 229), BMS2h-572-6 (SEQ ID NO: 243), BMS2h-572-601 (SEQ ID NO: 244), BMS2h-572-602 (SEQ ID NO: 245), BMS2h-572-603 (SEQ ID NO: 246), BMS2h-572-604 (SEQ ID NO: 247), BMS2h-572-606 (SEQ ID NO: 249), BMS2h-572-607 (SEQ ID NO: 250), BMS2h-572-608 (SEQ ID NO: 251), BMS2h-572-609 (SEQ ID NO: 252), BMS2h-572-610 (SEQ ID NO: 253), BMS2h-572-611 (SEQ ID NO: 254), BMS2h-572-612 (SEQ ID NO: 255), BMS2h-572-613 (SEQ ID NO: 256), BMS2h-572-614 (SEQ ID NO: 257), BMS2h-572-615 (SEQ ID NO: 258), BMS2h-572-616 (SEQ ID NO: 259), BMS2h-572-617 (SEQ ID NO: 260), BMS2h-572-618 (SEQ ID NO: 261), BMS2h-572-619 (SEQ ID NO: 262), BMS2h-572-620 (SEQ ID NO: 263), BMS2h-572-622 (SEQ ID NO: 265), BMS2h-572-623 (SEQ ID NO: 266), BMS2h-572-624 (SEQ ID NO: 267), BMS2h-572-625 (SEQ ID NO: 268), BMS2h-572-626 (SEQ ID NO: 269), BMS2h-572-627 (SEQ ID NO: 270), BMS2h-572-630 (SEQ ID NO: 271), BMS2h-572-631 (SEQ ID NO: 272), BMS2h-572-632 (SEQ ID NO: 273), BMS2h-572-634 (SEQ ID NO: 275), BMS2h-572-635 (SEQ ID NO: 276), or BMS2h-572-9 (SEQ ID NO: 279).

10. The antibody polypeptide of any of claims 1-9, wherein the antibody polypeptide is a domain antibody (dAb).

11. The antibody polypeptide of any of claims 1-9, wherein the antibody polypeptide is a fusion polypeptide comprising the first variable domain and an Fc domain.

12. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises an IgG4 Fc domain.

13. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises an IgG1 Fc domain.

14. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises a CT-Long domain (amino acids 139 to 370 of SEQ ID NO: 1362).

15. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises a CT-short domain (amino acids 138 to 362 of SEQ ID NO: 1363).

16. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises a N297Q Long Fc domain (amino acids 139 to 370 of SEQ ID NO: 1364).

17. The antibody polypeptide of claim 11, wherein the fusion polypeptide comprises a N297Q Short Fc domain (amino acids 138 to 362 of SEQ ID NO: 1365).

18. The antibody polypeptide of claim 11, wherein the antibody polypeptide comprises the amino acid sequence of SEQ ID NO: 1355.

19. The antibody polypeptide of claim 11, wherein the amino acid sequence of the antibody polypeptide is set forth in SEQ ID NO: 1355.

20. The antibody polypeptide of any of claims 1-9, wherein the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, wherein the second antigen is an antigen other than human CD40L.

21. The antibody polypeptide of claim 20, wherein the second antigen is a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule.

22. The antibody polypeptide of claim 20, wherein the second antigen is serum albumin (SA).

23. A nucleic acid encoding the antibody polypeptide of any one of claims 1-22.

24. A vector comprising the nucleic acid of claim 23.

25. An isolated host cell comprising the vector of claim 24.

26. A pharmaceutical composition comprising a therapeutically-effective amount of the antibody polypeptide of claim 1 and a pharmaceutically acceptable carrier.

27. The pharmaceutical composition of claim 26, further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

28. The pharmaceutical composition of claim 26 or 27, wherein the first variable domain of the antibody polypeptide comprises the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

29. The pharmaceutical composition of claim 26 or 27, wherein the antibody polypeptide comprises the amino acid sequence of SEQ ID NO: 1355.

30. Use of an isolated antibody polypeptide according to any one of claims 1-22 for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease.

31. The use of claim 30, in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

32. The use of claim 30, wherein the immune disease is an autoimmune disease or a graft-related disease.

33. The use of claim 30, wherein the immune disease is a graft-related disease.

34. The use of claim 33, wherein the graft-related disease comprises solid organ, tissue and/or cell transplant rejection.

35. The use of claim 33, wherein the graft-related disease is graft versus host disease (GVHD).

36. The use of claim 33, wherein the graft-related disease is an acute transplant rejection.

37. The use of claim 33, wherein the graft-related disease is a chronic transplant rejection.

38. The use of claim 31, wherein the immunosuppressive/immunomodulatory and/or anti-inflammatory agent is a CTLA4 mutant molecule.

39. The use of claim 38, wherein the CTLA4 mutant molecule is L104EA29Y-Ig (belatacept).

40. The use of claim 30, wherein the immune disease is selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy,

bronchial asthma, eczema, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, epilepsy, Arthus's phenomenon, anaphylaxis, and drug addiction.

41. The use of claim 30, wherein the immune disease is idiopathic thrombocytopenic purpura.

42. The use of claim 30, wherein the immune disease is systemic lupus erythematosus.

43. The use of claim 30, wherein the first variable domain of the antibody polypeptide comprises the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

44. The use of claim 30, wherein the antibody polypeptide comprises the amino acid sequence of SEQ ID NO: 1355.

45. An antibody polypeptide as claimed in any one of claims 1 to 22, substantially as herein described with reference to any example thereof.

46. A nucleic acid as claimed in claim 23, substantially as herein described with reference to any example thereof.

47. An isolated host cell as claimed in claim 25, substantially as herein described with reference to any example thereof.

48. A pharmaceutical composition as claimed in claim 26, substantially as herein described with reference to any example thereof.

49. A use as claimed in any one of claims 30 to 44, substantially as herein described with reference to any example thereof.

FIG. 1A

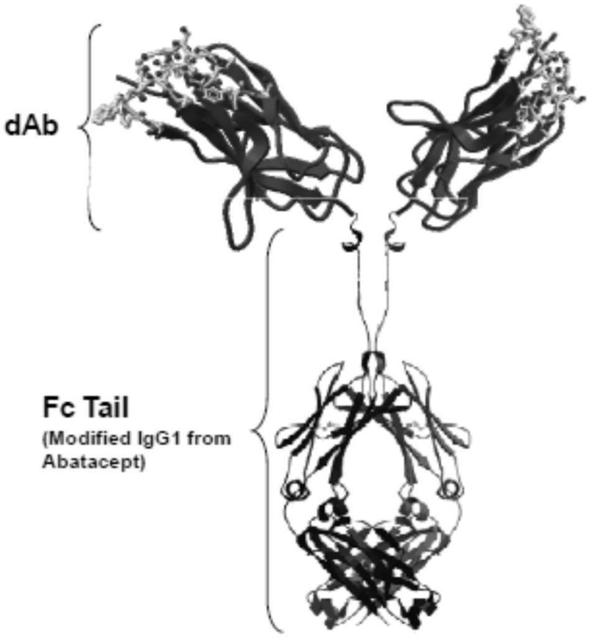
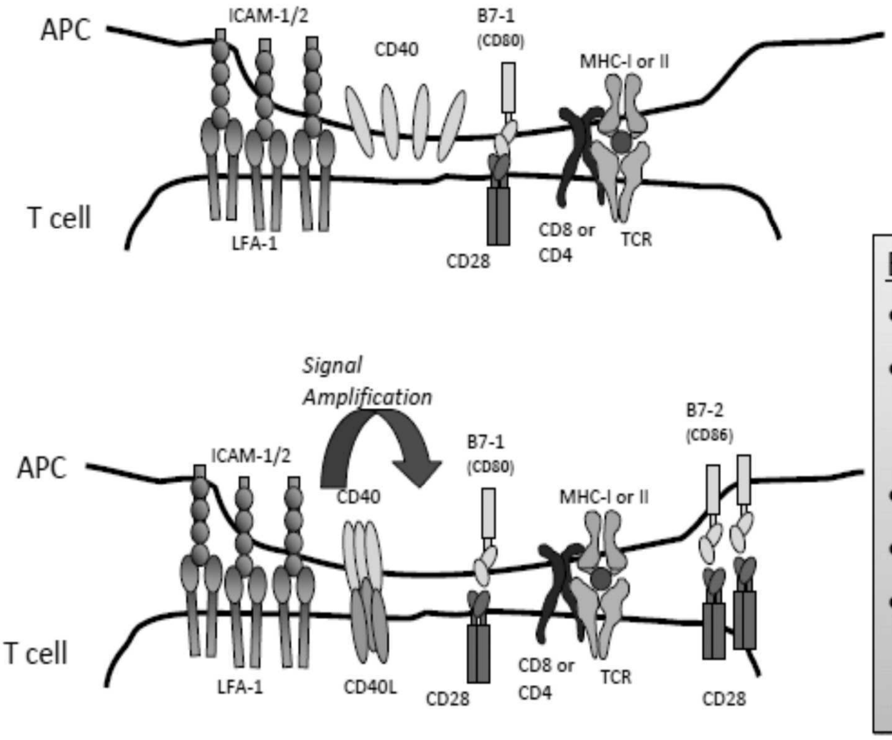


FIG. 1B

EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY
CVKVGKDAKSDYRGQGTLVTVSSASTEPKSSDKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(MW=77,984 daltons)

dAb
Linker
Modified IgG1 Fc from Abatacept (Cys→Ser; Pro→Ser)

FIG. 2



Effects:

- *Increases Co-stim*
- *Enhanced Ag presentation/ MHC molecules*
- *Cytokine production*
- *CD4 help to CD8*
- *Ab class switch and affinity maturation*

FIG. 3

Fc

Domain antibody-AS-THT**C**PP**C**P…

CT-long

Domain antibody-AST-EPKSSDKTHT**S**PP**S**P …

CT-short

Domain antibody-AS-THT**S**PP**S**P…

N297Qlong Fc

Domain antibody-AST-EPKSSDKTHT**S**PP**S**P…

N297Qshort Fc

Domain antibody-AS-THT**S**PP**S**P…

Osteonectin signal peptide sequence:

MRAWIFFLLCLAGRALA ^ EVQLLES…(start of Domain antibody)

FIG. 4

BMS2h-572-633-CT-L2

MRAWIFFLLCLAGRALA^EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSSASTEPKS**S**DKTHT**S**PP**S**PAPELLGG**S**SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY**N**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

BMS2h-572-633-CT-S1

MRAWIFFLLCLAGRALA^EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSSASTHT**S**PP**S**PAPELLGG**S**SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY**N**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

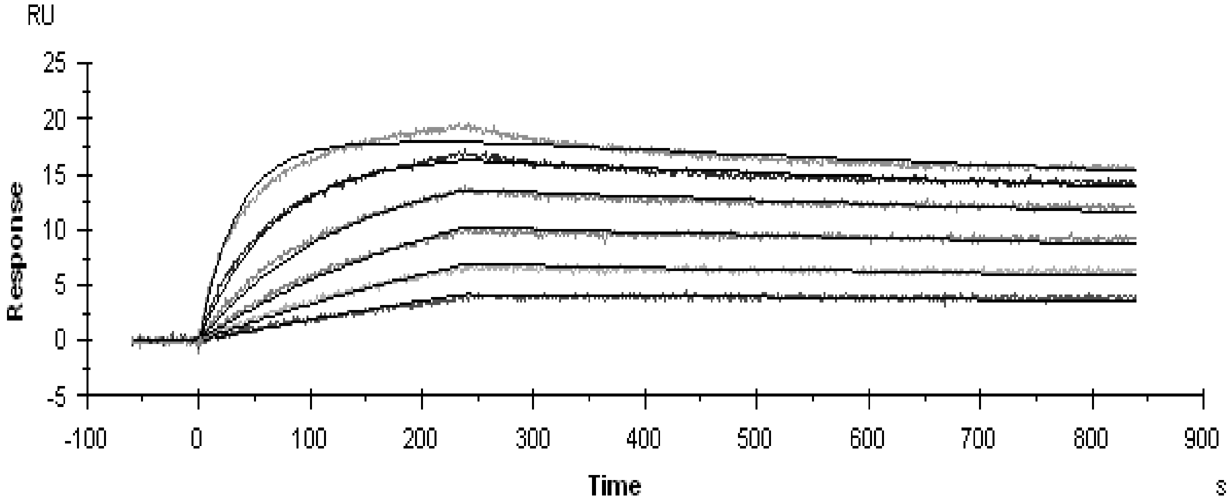
BMS2h-572-633-N297Q long Fc

MRAWIFFLLCLAGRALA^EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSSASTEPKSSDKTHT**C**PP**C**PAPELLGG**P**SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY**Q**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

BMS2h-572-633-N297Q short Fc

MRAWIFFLLCLAGRALA^EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSSASTHT**C**PP**C**PAPELLGG**P**SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY**Q**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIG. 5



RU
25
20
15
10
5
0
-5
Response
-100
0
100
200
300
400
500
600
700
800
900
Time
s

FIG. 6

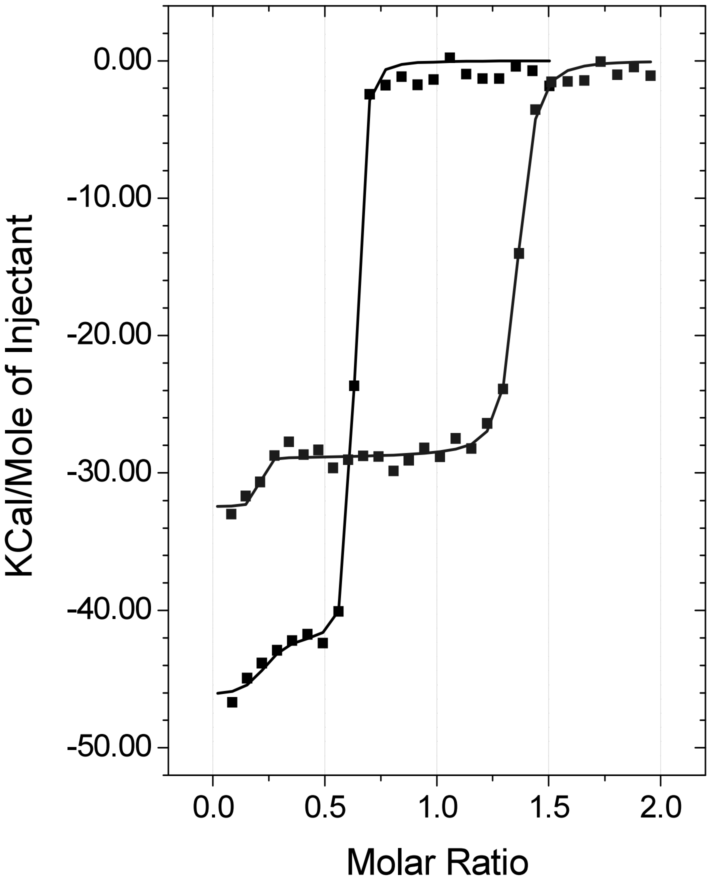

0.00
-10.00
-20.00
-30.00
-40.00
-50.00
KCal/Mole of Injectant
0.0
0.5
1.0
1.5
2.0
Molar Ratio

FIG. 7

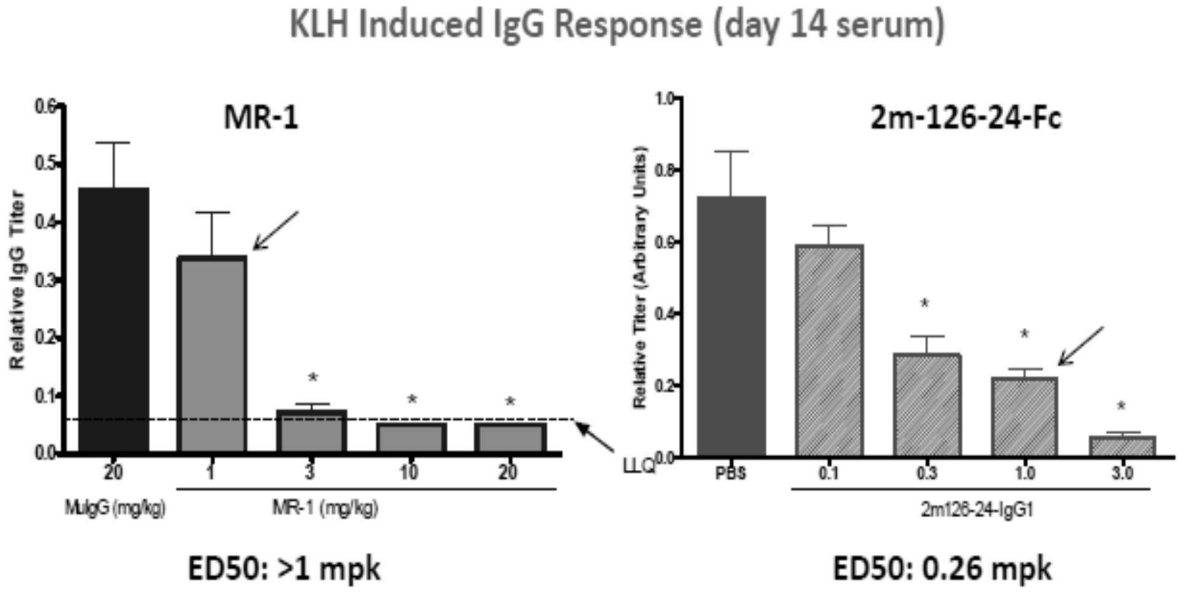

KLH Induced IgG Response (day 14 serum)
MR-1
Relative IgG Titer
0.0
0.1
0.2
0.3
0.4
0.5
0.6
*
*
*
LLQ
20
1
3
10
20
MuIgG (mg/kg)
MR-1 (mg/kg)
ED50: >1 mpk
2m-126-24-Fc
Relative Titer (Arbitrary Units)
0.0
0.2
0.4
0.6
0.8
1.0
*
*
*
PBS
0.1
0.3
1.0
3.0
2m126-24-IgG1
ED50: 0.26 mpk

FIG. 8

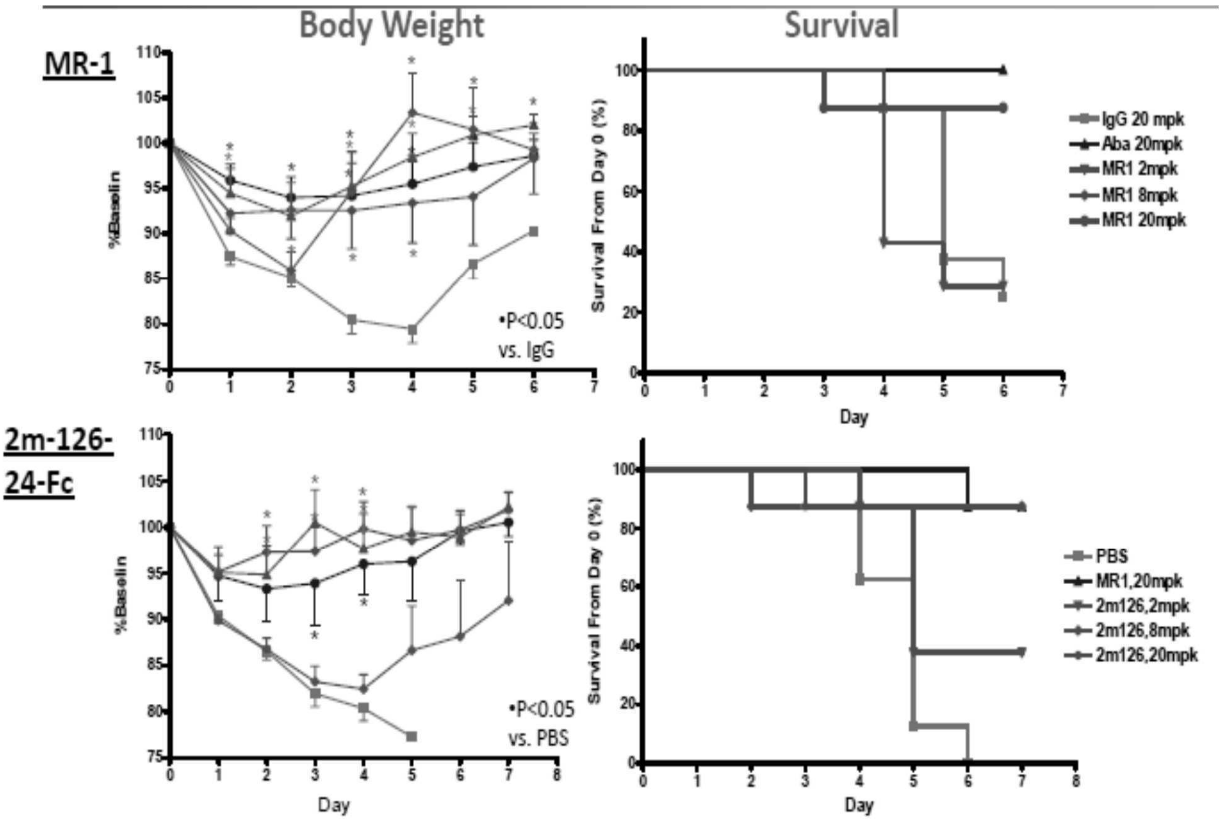
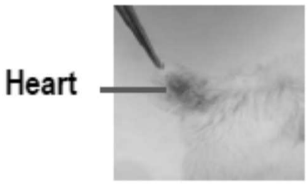
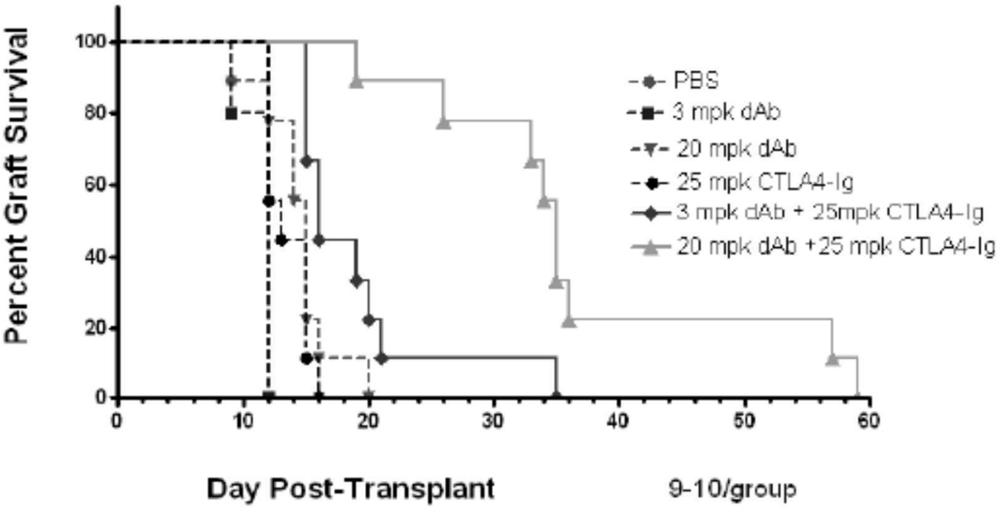

Body Weight
Survival
MR-1
%Baselin
110
105
100
95
90
85
80
75
0
1
2
3
4
5
6
7
•P<0.05
vs. IgG
Survival From Day 0 (%)
100
80
60
40
20
0
Day
IgG 20 mpk
Aba 20mpk
MR1 2mpk
MR1 8mpk
MR1 20mpk
2m-126-
24-Fc
%Baselin
8
Day
•P<0.05
vs. PBS
PBS
MR1,20mpk
2m126,2mpk
2m126,8mpk
2m126,20mpk

FIG. 9



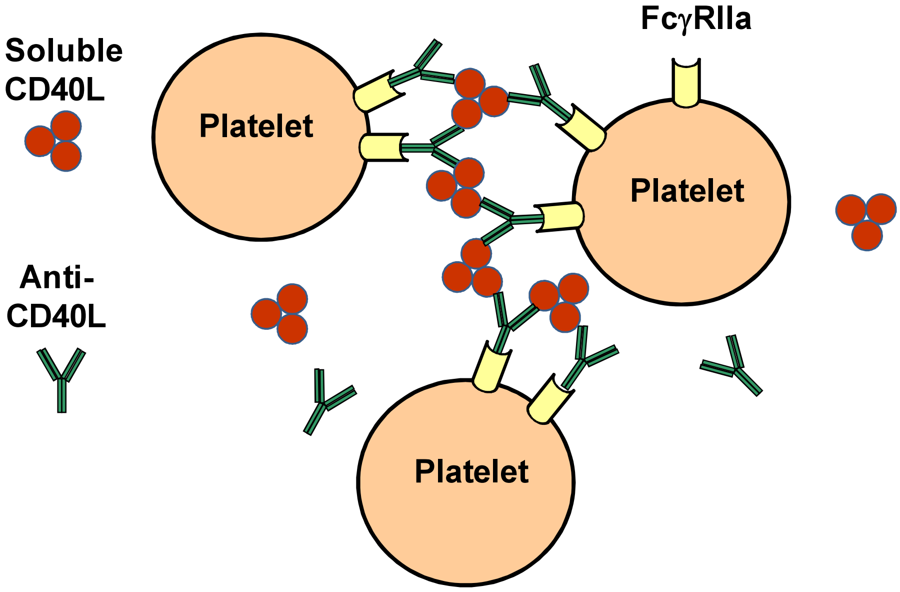
- Insert heart from neonatal C57Bl/6 mice into the pinnae of adult BALB/c mouse ear.
- <u>dosing</u>: 2m126-24-Fc s.c. 1x/wk; CTLA4Ig i.p. 2x/wk

Graft Survival



9-10/group

FIG. 10



Soluble
CD40L
Anti-
CD40L
FcγRIIa
Platelet
Platelet
Platelet

FIG. 11A

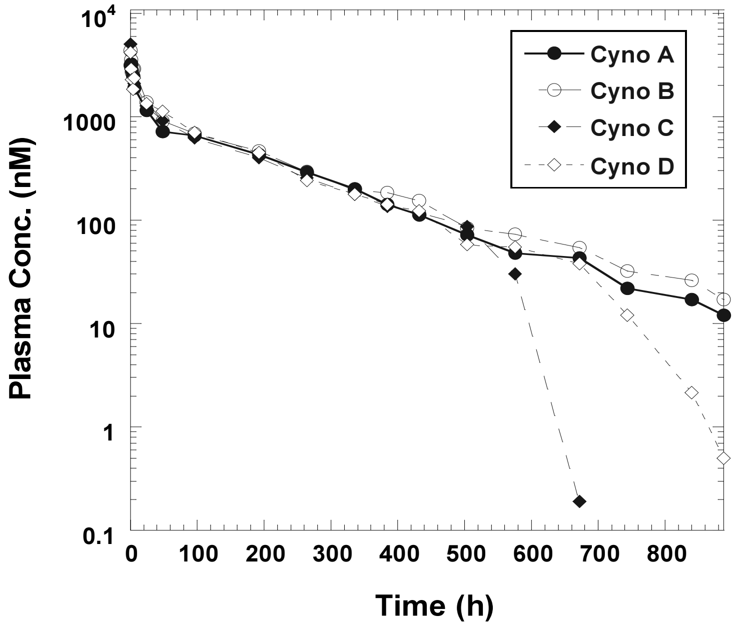


FIG. 11B

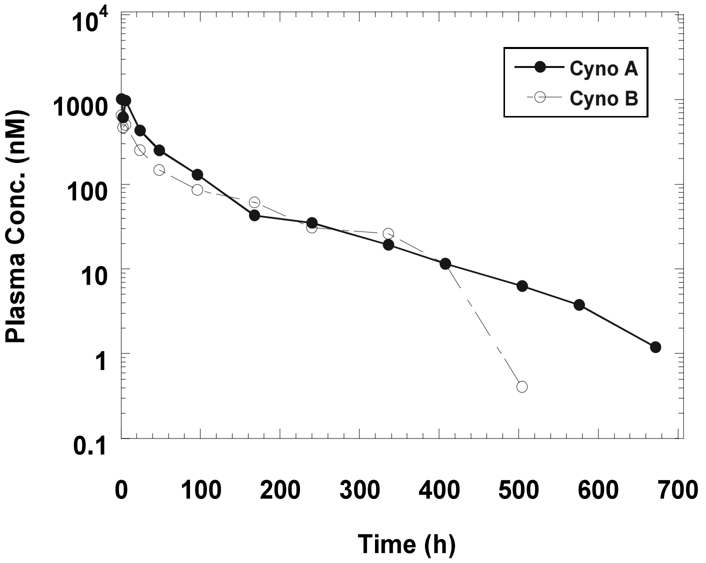
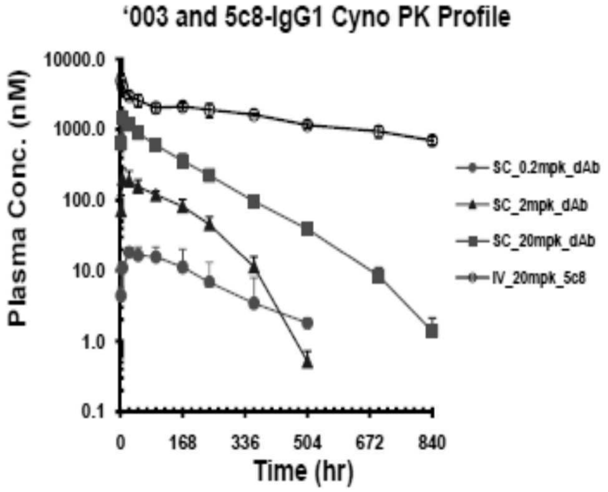
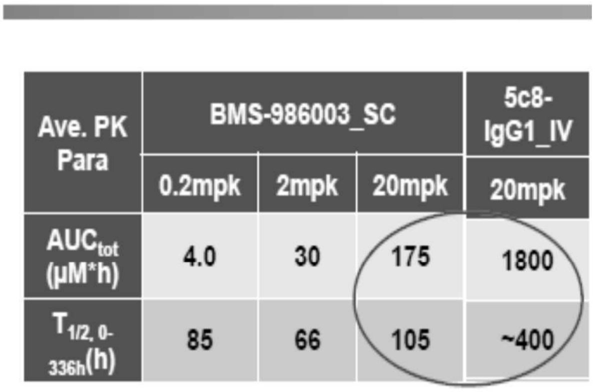


FIG. 12





Ave. PK Para	BMS-986003_SC			5c8-IgG1_IV
	0.2mpk	2mpk	20mpk	20mpk
AUC_{tot} (μM*h)	4.0	30	175	1800
$T_{1/2,\ 0\text{-}336h}$(h)	85	66	105	~400

FIG. 13

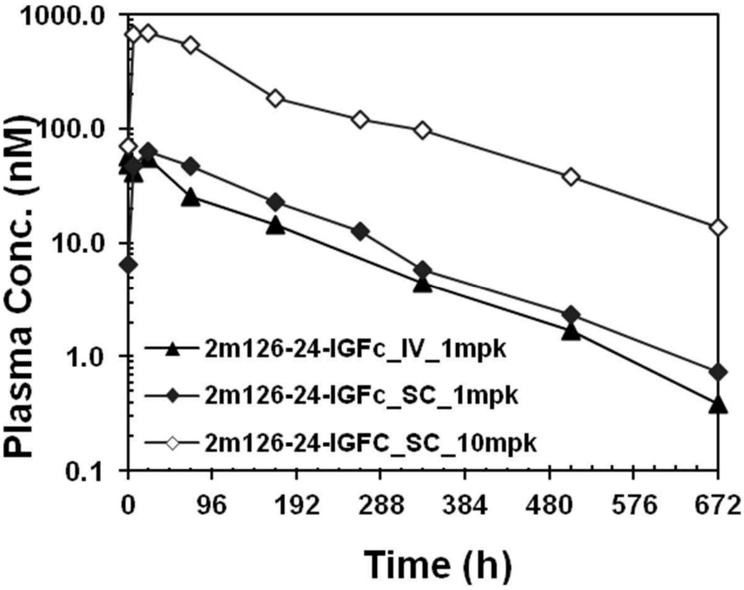
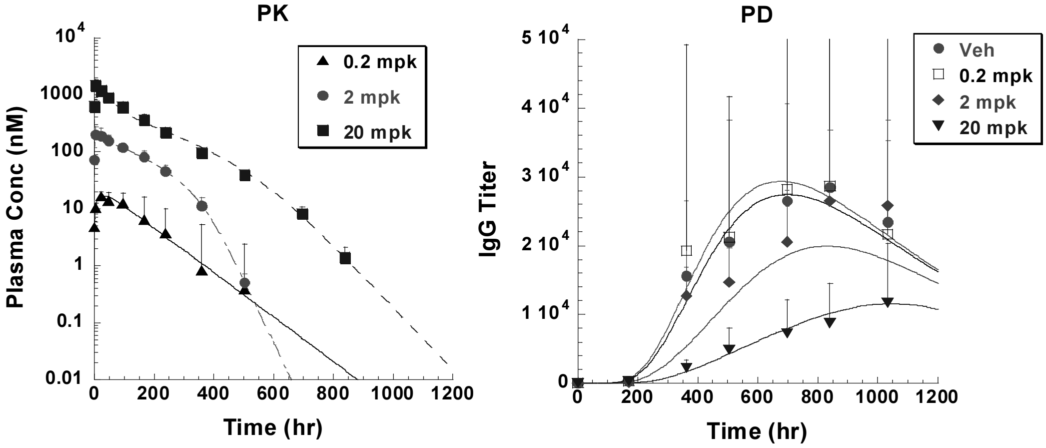

1000.0
100.0
10.0
1.0
0.1
Plasma Conc. (nM)
0
96
192
288
384
480
576
672
Time (h)
2m126-24-IGFc_IV_1mpk
2m126-24-IGFc_SC_1mpk
2m126-24-IGFC_SC_10mpk

FIG. 14

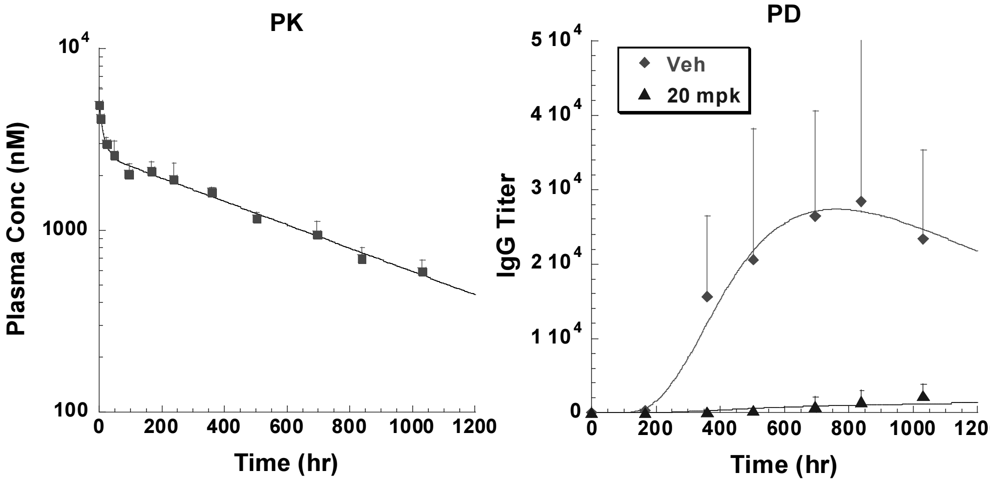
BMS-986003



* Line represents model-fitted curve

0%, 15% 71% inh at 0.2, 2, and 20 mpk, resp (AUC of IgG titer)

5C8-IgG1



*Line represents model-fitted curve

96% inh (AUC of IgG titer)

FIG. 15

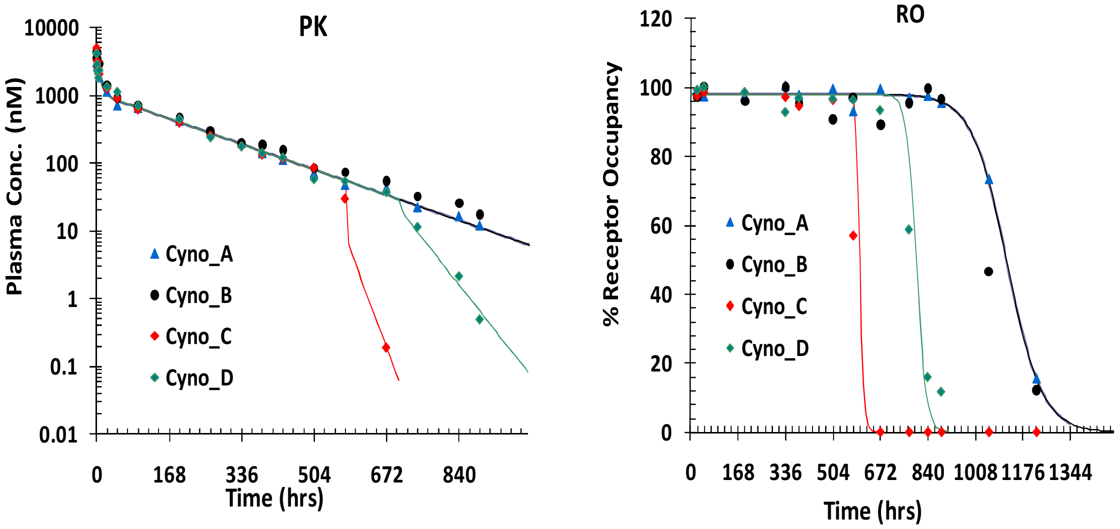

PK
10000
1000
100
10
1
0.1
0.01
Plasma Conc. (nM)
0
168
336
504
672
840
Time (hrs)
Cyno_A
Cyno_B
Cyno_C
Cyno_D
RO
120
100
80
60
40
20
0
% Receptor Occupancy
0
168
336
504
672
840
1008
1176
1344
Time (hrs)
Cyno_A
Cyno_B
Cyno_C
Cyno_D

FIG. 16

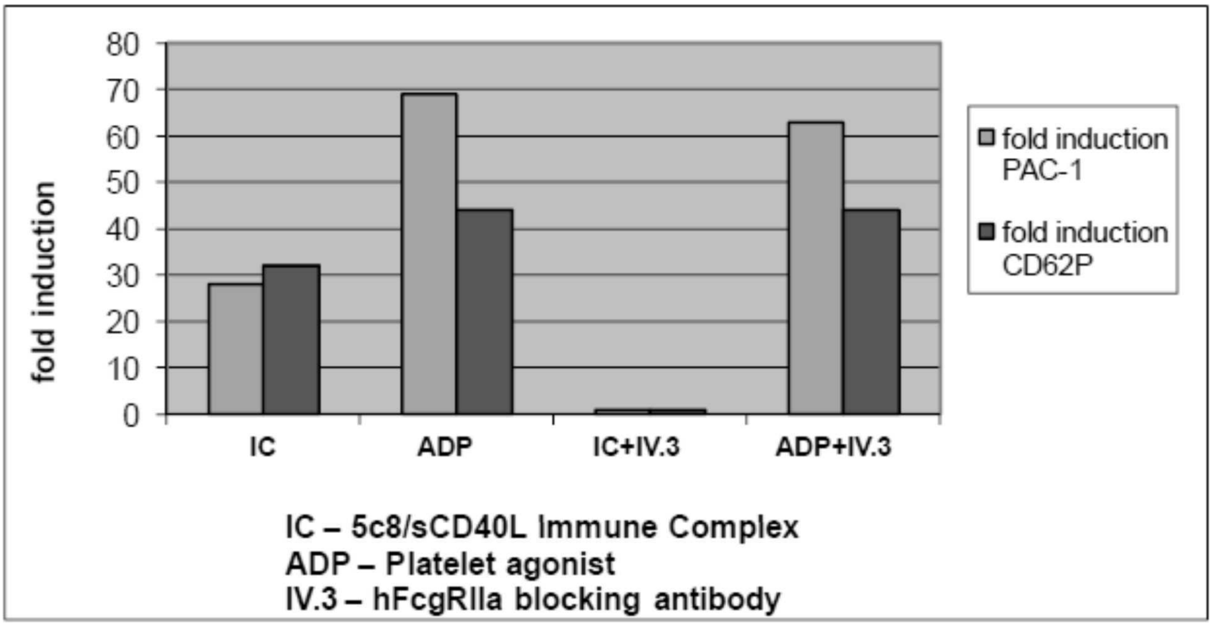

80
70
60
50
40
30
20
10
0
fold induction
IC
ADP
IC+IV.3
ADP+IV.3
fold induction PAC-1
fold induction CD62P
IC – 5c8/sCD40L Immune Complex
ADP – Platelet agonist
IV.3 – hFcgRIIa blocking antibody

FIG. 17

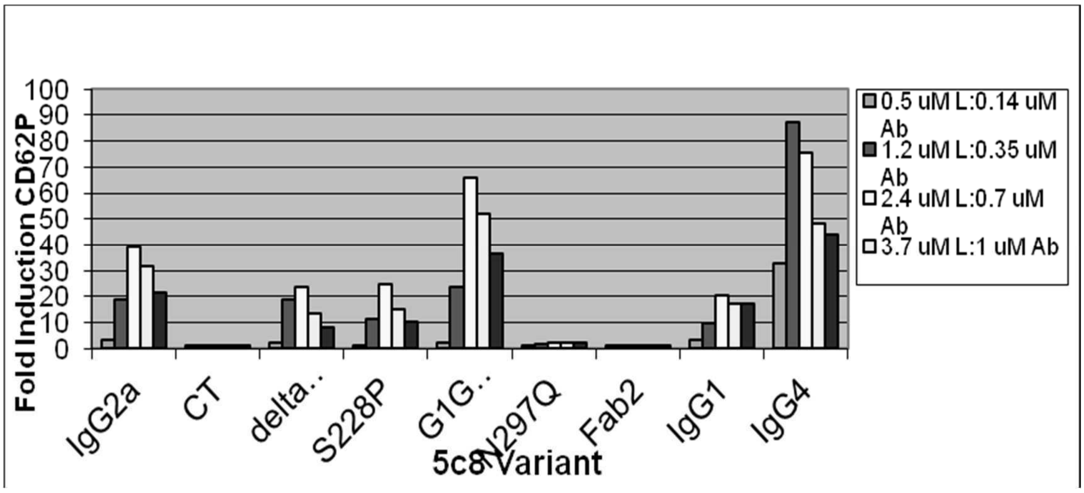

Fold Induction CD62P
100
90
80
70
60
50
40
30
20
10
0
IgG2a
CT
delta..
S228P
G1G..
N297Q
Fab2
IgG1
IgG4
5c8 Variant
0.5 uM L:0.14 uM Ab
1.2 uM L:0.35 uM Ab
2.4 uM L:0.7 uM Ab
3.7 uM L:1 uM Ab

FIG. 18

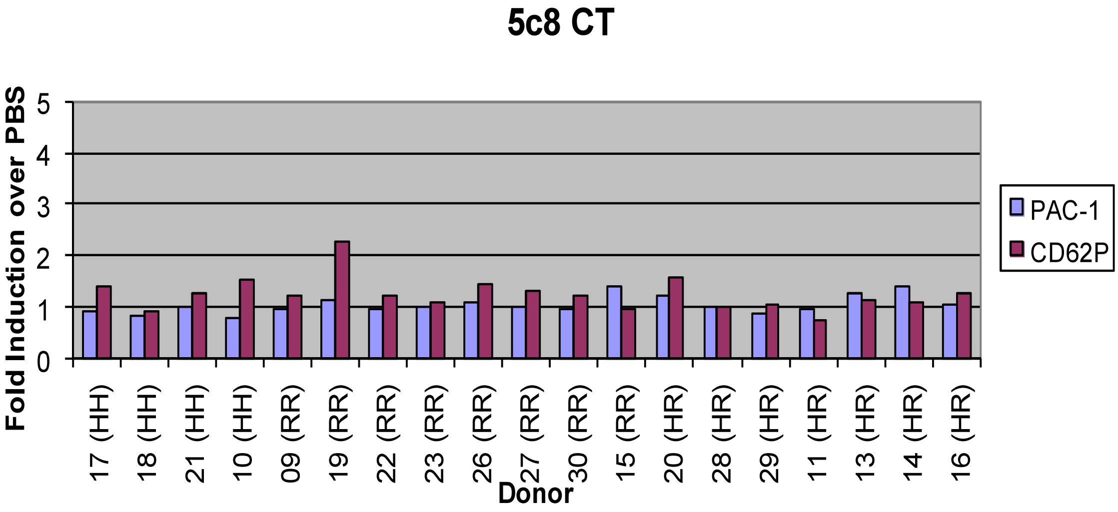

5c8 CT
Fold Induction over PBS
0
1
2
3
4
5
17 (HH)
18 (HH)
21 (HH)
10 (HH)
09 (RR)
19 (RR)
22 (RR)
23 (RR)
26 (RR)
27 (RR)
30 (RR)
15 (RR)
20 (HR)
28 (HR)
29 (HR)
11 (HR)
13 (HR)
14 (HR)
16 (HR)
Donor
PAC-1
CD62P

FIG. 19

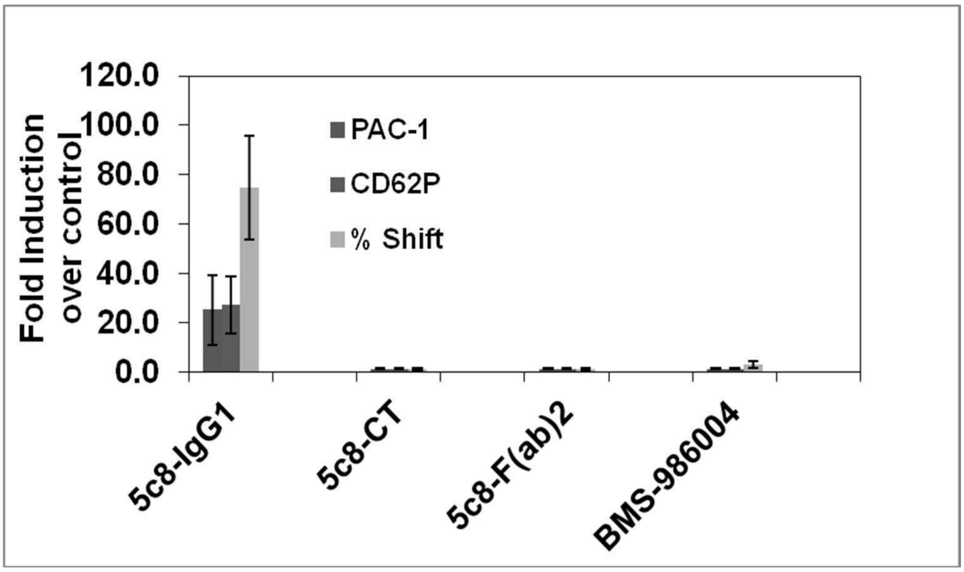
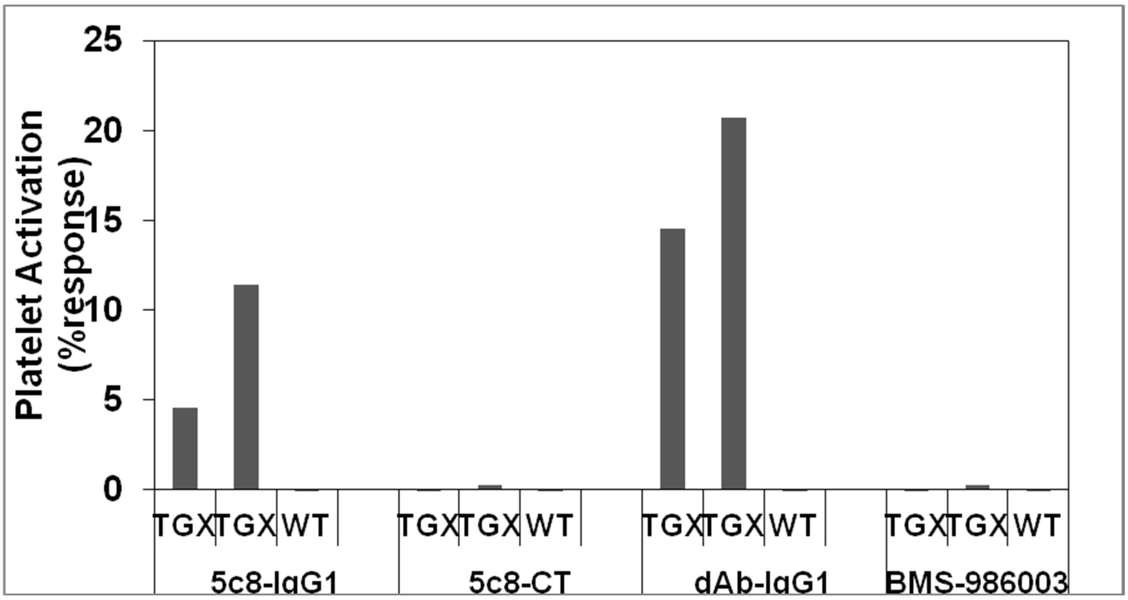

Fold Induction over control
120.0
100.0
80.0
60.0
40.0
20.0
0.0
PAC-1
CD62P
% Shift
5c8-IgG1
5c8-CT
5c8-F(ab)2
BMS-986004

FIG. 20



Platelet Activation (%response)
25
20
15
10
5
0
TGX
TGX
WT
5c8-IgG1
TGX
TGX
WT
5c8-CT
TGX
TGX
WT
dAb-IgG1
TGX
TGX
WT
BMS-986003

FIG. 21

```
                                                  CDR1                  CDR2
BMS2h-572-6         EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQLMGWVRQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-608       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-614       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQLMGWVRQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-619       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQLMGWVRQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-633       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-634       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY 60
BMS2h-572-635       EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY 60
                    ******************************* **** ***********************


                    CDR2                                    CDR3

BMS2h-572-6         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKESNSDYRGQGTLVTVSS 118
BMS2h-572-608       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKESNSDYRGQGTLVTVSS 118
BMS2h-572-614       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSS 118
BMS2h-572-619       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDSRSDYRGQGTLVTVSS 118
BMS2h-572-633       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQGTLVTVSS 118
BMS2h-572-634       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDSRSDYRGQGTLVTVSS 118
BMS2h-572-635       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKVGKDSKSDYRGQGTLVTVSS 118
                    *****************************************   **************
```

FIG. 22

```
                                                 CDR1                 CDR2
BMS2h-719-2        EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-202      EVQLLESGGGLVQPGGSLRLSCAASGFTFKKYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-203      EVQLLESGGGLVQPGGSLRLSCAASGFTFNSYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-213      EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-214      EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-215      EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-218      EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYEMMWVRQAPGKGLEWVSSISSDGSFTYY 60
BMS2h-719-225      EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYEMQWVRQAPGKGLEWVSSISSDGSFTYY 60
                   *****************************  *** *************************


                    CDR2                                  CDR3

BMS2h-719-2        ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTEFDYWGHGTLVTVSS 116
BMS2h-719-202      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTEFDYWGHGTLVTVSS 116
BMS2h-719-203      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTEFDYWGHGTLVTVSS 116
BMS2h-719-213      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCADPFTEMDYWGHGTLVTVSS 116
BMS2h-719-214      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCADPFTEFDYWGHGTLVTVSS 116
BMS2h-719-215      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTELDYWGHGTLVTVSS 116
BMS2h-719-218      AESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTEFDYWGHGTLVTVSS 116
BMS2h-719-225      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAEPFTEFDYWGHGTLVTVSS 116
                   * *********************************** **** *************
```

FIG. 23

```
BMS2h-503-1      DIQMTQSPSSLSASVGDRVTITCRASHHIQRYLSWYQQKPGKAPKLLILWGSQLQSGVPS 60
BMS2h-503-2      DIQMTQSPSSLSASVGDRVTITCRASHDIQRYLSWYQQKPGKAPKLLILWGSQLQSGVPS 60
                 *************************** ********************************

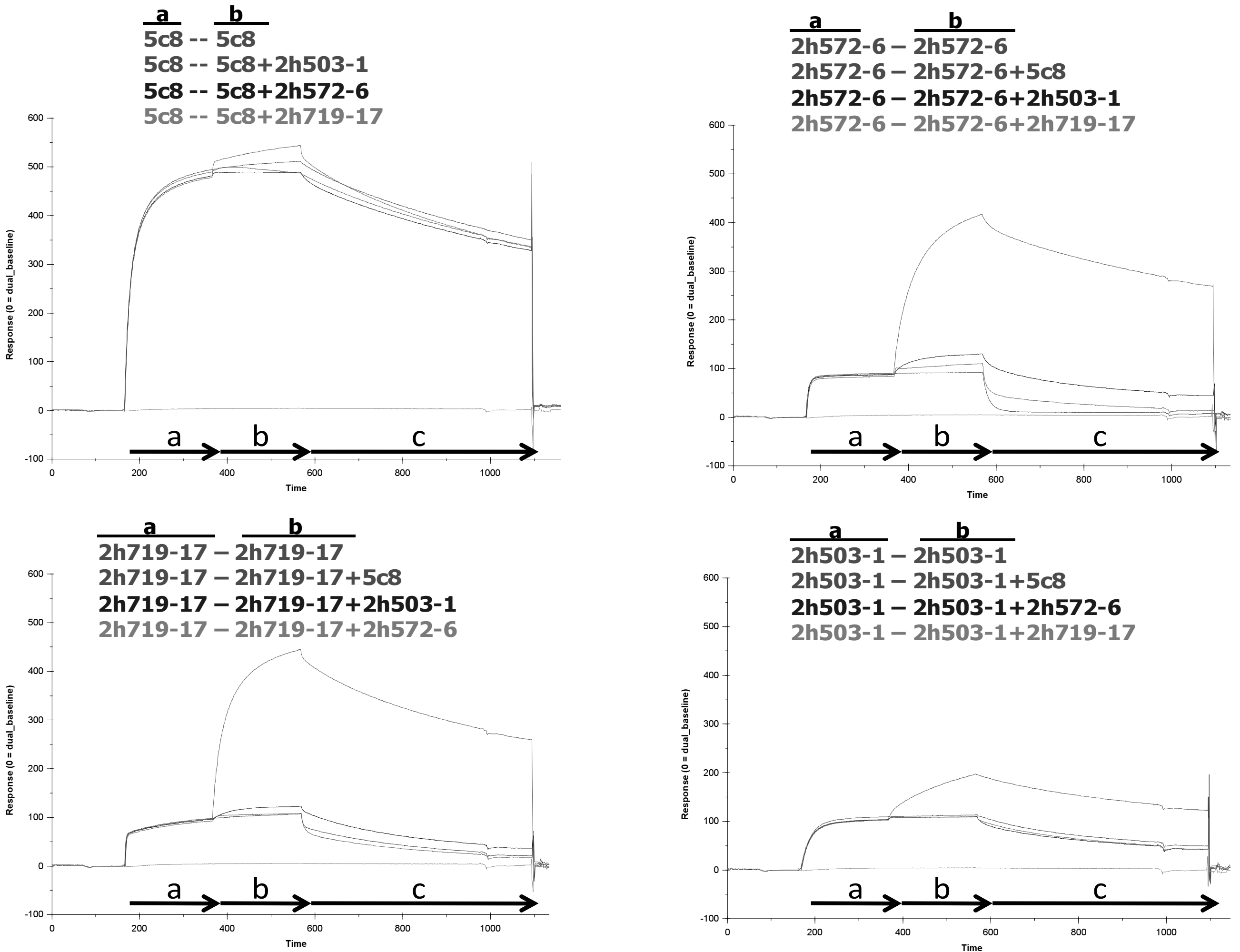
BMS2h-503-1      RFSGSGSGTDFTLTISSLQPEDFATYYCGQWWAPPQTFGQGTKVEIKR 108
BMS2h-503-2      RFSGSGSGTDFTLTISSLQPEDFATYYCGQWWAPPQTFGQGTKVEIKR 108
                 ************************************************
```

FIG. 24

```
BMS2h-116-1312      DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS 60
BMS2h-116-1313      DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS 60
BMS2h-116-1320      DIQMTQSPSSLSAYVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS 60
                    ************* **********************************************

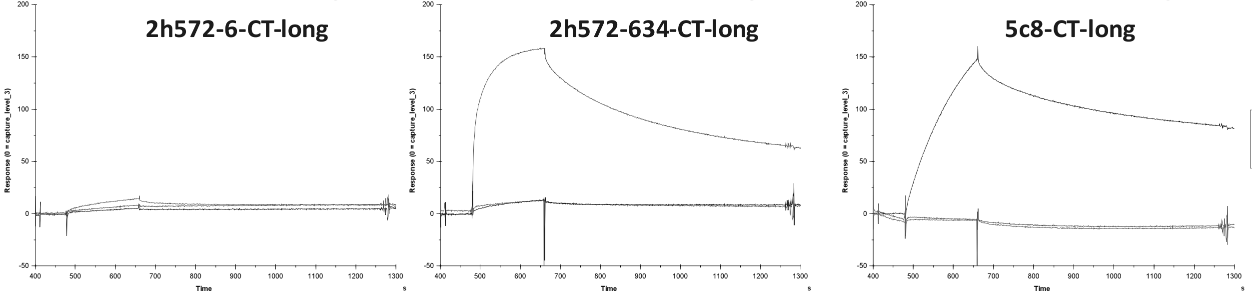

BMS2h-116-1312      RFSGSGSETDFTLTISNLQPEDLATYYCQQYWAFPVTFGKGTKVVIKR 108
BMS2h-116-1313      RFSGSGSETDFTLTISNLQPEDFATYYCQQYWAFPVTFGRGTKVVIKR 108
BMS2h-116-1320      RFSGSGSETDFTLTISNLQPEDFAKYYCQQYWAFPVTFGQGTKVVIKR 108
                    ********************** * ************** ********
```

FIG. 25



BMS Confidential and Proprietary

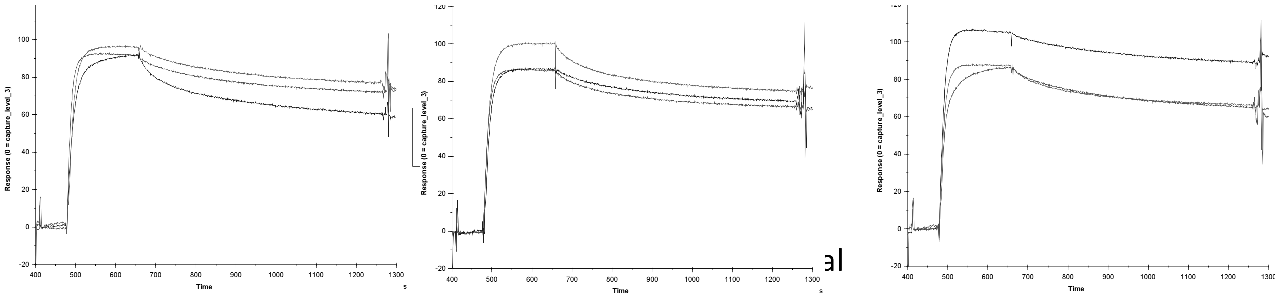
FIG. 26



400nM CD40L monomer binding to:
2h572-619-CT-long
2h572-633-CT-long
2h572-6-CT-long

400nM CD40L monomer binding to:
2h719-202-CT-long
2h572-608-CT-long
2h572-634-CT-long

400nM CD40L monomer binding to:
2h572-614-CT-long
2h572-635-CT-long
5c8-CT-long



17.5nM IZhCD40L trimer binding to:
2h572-619-CT-long
2h572-633-CT-long
2h572-6-CT-long

17.5nM IZhCD40L trimer binding to:
2h719-202-CT-long
2h572-608-CT-long
2h572-634-CT-long

17.5nM IZhCD40L trimer binding to:
2h572-614-CT-long
2h572-635-CT-long
5c8-CT-long

SEQUENCE LISTING

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<110> BRISTOL-MYERS SQUIBB COMPANY
      DOMANTIS LIMITED

<120> ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40L

<130> 200896-0005-WO (489826)

<140>
<141>

<150> 61/655,110
<151> 2012-06-04

<150> 61/546,800
<151> 2011-10-13

<160> 1365

<170> PatentIn version 3.5

<210> 1
<211> 261
<212> PRT
<213> Homo sapiens

<400> 1
Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
1               5                   10                  15


Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
            20                  25                  30


Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
        35                  40                  45


Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
    50                  55                  60


Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65                  70                  75                  80


Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
                85                  90                  95


Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
            100                 105                 110


Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
        115                 120                 125


Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
    130                 135                 140


Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145                 150                 155                 160
```

```
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
                165                 170                 175


Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
            180                 185                 190


Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
        195                 200                 205


Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
    210                 215                 220


Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225                 230                 235                 240


Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
                245                 250                 255


Gly Leu Leu Lys Leu
            260


<210> 2
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"


<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Gln"

<220>
<221> misc_feature
<222> (2)..(2)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<400> 2
Trp Glu Leu Met Gly
1               5


<210> 3
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 3
Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15
```

```
Gly



<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"


<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Glu"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Ser"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Asn" or "Arg"

<220>
<221> misc_feature
<222> (2)..(4)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<400> 4
Lys Asp Ala Lys Ser Asp Tyr
1               5


<210> 5
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 5
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            20                  25                  30


<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
```

```
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"


<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Val"

<220>
<221> misc_feature
<222> (2)..(2)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<400> 6
Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1               5                   10


<210> 7
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 7
Arg Thr Phe Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Lys
            20                  25                  30


Val Gly



<210> 8
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 8
Arg Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1               5                   10


<210> 9
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

```
<220>
<221> VARIANT
<222> (30)..(30)
<223> /replace="Asn"

<220>
<221> VARIANT
<222> (31)..(31)
<223> /replace="Lys" or "Ser" or "Thr"

<220>
<221> misc_feature
<222> (30)..(31)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (35)..(35)
<223> /replace="Gln"

<220>
<221> misc_feature
<222> (35)..(35)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (62)..(62)
<223> /replace="Glu"

<220>
<221> misc_feature
<222> (62)..(62)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (98)..(98)
<223> /replace="Glu"

<220>
<221> misc_feature
<222> (98)..(98)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Met" or "Leu"

<220>
<221> misc_feature
<222> (103)..(103)
<223> /note="Residue given in the sequence has no preference
      with respect to those in the annotations for said position"

<400> 9
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
```

```
            20                  25                  30

Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115


<210> 10
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (28)..(28)
<223> /replace="Asp"

<220>
<221> misc_feature
<222> (28)..(28)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<400> 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His His Ile Gln Arg Tyr
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Leu Trp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Trp Ala Pro Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 11
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (14)..(14)
<223> /replace="Tyr"

<220>
<221> misc_feature
<222> (14)..(14)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (83)..(83)
<223> /replace="Phe"

<220>
<221> misc_feature
<222> (83)..(83)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (85)..(85)
<223> /replace="Lys"

<220>
<221> misc_feature
<222> (85)..(85)
<223> /note="Residue given in the sequence has no preference
      with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Arg" or "Gln"

<220>
<221> misc_feature
<222> (100)..(100)
<223> /note="Residue given in the sequence has no preference
      with respect to those in the annotations for said position"

<400> 11
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Lys Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 12
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"


<220>
<221> VARIANT
<222> (6)..(25)
<223> /replace=" "

<220>
<221> misc_feature
<222> (6)..(25)
<223> /note="Residues given in the sequence have no preference
      with respect to the annotation for said positions"

<220>
<221> misc_feature
<222> (1)..(25)
<223> /note="This sequence may encompass 1 to 5 'Gly Gly Gly
      Gly Ser' repeating units"

<400> 12
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1               5                   10                  15


Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20                  25


<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 13
Thr Val Ala Ala Pro Ser
1               5


<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 14
Ala Ser Thr Ser Gly Pro Ser
1               5


<210> 15
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 15
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Ala Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Asp Glu Trp Gly Leu Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Lys Thr Pro Glu Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115
```

```
<210> 16
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 16
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Gly Glu Gly Ser Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Arg Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 17
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 17
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile His Gly Ser Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Tyr Thr Ser Arg His Asn Ser Leu Gly His Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 18
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 18
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Asp Tyr
            20                  25                  30


Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Val Gly Met Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Gly Gly Thr Ser Gly Arg His Asn Thr Lys Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 19
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 19
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Ser Pro Leu Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Thr Gly Gly Ser Gly Ile Leu Asn Ser Ser Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 20
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 20
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Val Ser Asn Tyr
            20                  25                  30


Asp Leu Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ala Thr Asn Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

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                85                  90                  95


Ala Ala Val Thr Trp Trp Leu Leu Arg His Asn Asp Asn Leu Gly Phe
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 21
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 21
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Ile Ser Tyr Lys
            20                  25                  30


Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Lys Ala Ala Asn Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Gly Ser Gln Lys Lys Arg Thr Tyr Thr Phe Asp Phe Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 22
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 22
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Leu Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Ile Leu Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Leu Ser Trp Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 23
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 23
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asn Pro Met Gly Tyr Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Gly Val Gly Lys Gly Thr Lys Pro His Asn Phe Asp Tyr
            100                 105                 110
```

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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 24
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 24
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Leu Tyr
            20                  25                  30


Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Ser Gly Ser Gly Phe Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Leu His Asp Lys Thr Gln His His Gln Glu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 25
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 25
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Glu Tyr
            20                  25                  30


Pro Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Leu Ile Ser Pro Ser Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asp Glu Ser Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 26
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 26
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Asp Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Gly Ser Ser Gly Tyr Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Arg Met Pro Gly Tyr Phe Pro Gly Phe Ala Arg Gln Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 27
<211> 124
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 27
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Trp Arg Tyr
            20                  25                  30


Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asn Asp Glu Gly Arg Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Lys Arg Val Ser Ser Ser Val Asn Ala Pro Tyr Glu Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 28
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 28
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Tyr
            20                  25                  30


Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Arg Leu Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
```

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Leu Ala Asp Leu Ile Ala Gly His Ala Glu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 29
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 29
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Ser Tyr
            20                  25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Arg Ser Gly Ser Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Val Asp Ala His Val Tyr Tyr Met Glu Pro Phe Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 30
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 30
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Asp Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Thr Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 31
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 31
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Lys Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Gly Asp Gly Lys Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Lys Pro Asp Gln Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 32
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 32
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20   25   30

Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ser Pro Phe Gly Trp Gly Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Tyr Gly Glu Thr Ser Gly Pro Ile Ser Glu Asn Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 33
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 33
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ala Gly Tyr
            20   25   30

```
Gln Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Asn Glu Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Lys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 34
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 34
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr
            20                  25                  30


Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Ile Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

```
<210> 35
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 35
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
            20                  25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Val Asp Asp Gly Leu Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Val Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Asn
        115


<210> 36
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 36
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Gly Tyr
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Leu Gly Ala Thr Thr Tyr Tyr Ala Asp Ser Val
```

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Ala Gly Thr Ser Ser His Ser Val Asp Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 37
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Thr Ser Asp Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Ser Val Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 38
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 38
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Arg Tyr
            20                  25                  30


Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Glu Ala Asp Gly Arg Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Leu Thr Asp Gln His Val Ile Glu Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 39
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 39
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Tyr
            20                  25                  30


Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Pro Asp Gly Asn Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Trp Gly Met Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 40
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 40
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
            20                  25                  30


Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Ile Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Met Lys Ser Pro Tyr Lys Pro Gln Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 41
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 41
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Ala Tyr
            20                  25                  30


Trp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Ser Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Thr Glu Pro Gly Leu Gly Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 42
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 42
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Ser Glu Val Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro His Asp Ser Ser Ile Gly Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110
```

```
Thr Leu Val Thr Val Ser Ser
        115


<210> 43
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 43
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Trp Ser Tyr
            20                  25                  30


Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Met Ala Ser Gly Asp Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Asp Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 44
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 44
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Tyr
            20                  25                  30


Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45


Ser Thr Ile Ser Pro Ile Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Phe Pro Leu Ile Ile Leu Pro Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 45
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 45
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Glu Tyr
            20                  25                  30


Ala Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ile Ile Ser Pro Leu Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Gln Asp Ser Ser Asp Ser Gln Tyr Thr Asn Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 46
<211> 121
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 46
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
            20                  25                  30


Gly Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Leu Gly Leu Trp Thr Tyr Tyr Ala Asp Ser Ala
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Pro Leu Glu Gly Leu Ile Thr Asn Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 47
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 47
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ile Ile Asp Trp Asp Gly Asn Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Asp Asn Val Gly Ile Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 48
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Tyr Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Asp Glu Trp Gly Phe Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Trp Glu Phe Thr Ser Asp Thr Ser Arg Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 49
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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```
<400> 49
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Phe
            20                  25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asn Asp Gln Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Gln Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 50
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 50
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Asp Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Ser Pro Gln Gly Gln Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Ile Arg Gly Gln Ser Arg Ile Pro Met Arg Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 51
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 51
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Tyr
            20                  25                  30


Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Asp Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro His Gly Ser Pro Arg Glu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 52
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 52
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr
```

```
            20                  25                  30

Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Thr Ser Leu Gly Glu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Pro Gly Arg Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115


<210> 53
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 53
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Phe Tyr
            20                  25                  30

Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Trp Ile Asp Ala Thr Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Glu Gly Asn Tyr Gly Ser Ser Tyr Thr Met Gly Val Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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<210> 54
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 54
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Tyr
            20                  25                  30


Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Ser Gly Pro Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Pro Tyr Phe Asp Val Ile Pro Ser Tyr Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 55
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 55
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
            20                  25                  30


Gly Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ser Ile Gln Ser Ser Gly Leu Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Ala Asn Ser Arg Arg Gly Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 56
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 56
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser His Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 57
<211> 122
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 57
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala His Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg Leu Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Ala Thr Pro Val Pro Ile Lys Gly Leu Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 58
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 58
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Gly Arg Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ser Asp Gly Trp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Pro Asp Ser Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 59
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 59
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Arg Gly Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Trp Arg Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 60
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 60
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Arg Tyr
            20   25   30

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ser Arg Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Gly Met Thr Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 61
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 61
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Met Tyr
            20   25   30

Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Met Ile Glu Pro Ala Gly Asp Leu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Tyr Gln Glu Gln Pro Trp Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

```
Leu Val Thr Val Ser Ser
        115


<210> 62
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 62
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Pro Gln Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Met Ile Thr Ser Asp Gly Leu Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Glu Pro Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 63
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 63
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Met Tyr
            20                  25                  30
```

```
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Leu Ser Asp Gly Thr Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Gly Ala Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 64
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 64
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Leu Tyr
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ala Gly Gly His Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Trp Trp Asp Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 65
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<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 65
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asn Arg Ser Gly Met Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Gly His Gln Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 66
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 66
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asn Ala Asn Gly Ile Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Gly Val Trp Arg Trp Gly Thr Gly His Lys Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 67
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 67
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Gln Tyr
            20                  25                  30


Asp Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Gln Asn Gly Thr Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Arg Thr Gly Arg Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 68
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 68
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Thr Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asn Trp Gln Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Phe Gly His Tyr Val Asp Gly Leu Gly Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 69
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 69
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Asp Met Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Pro Gly Thr Ala Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 70
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 70
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Lys Tyr
            20                  25                  30


Lys Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Pro Lys Gly His Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Pro Met Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 71
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 71
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Asn Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Arg Pro Arg Gly Gly Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Arg Arg Glu Gly Tyr Thr Gly Ser Lys Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 72
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 72
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Trp Pro Arg Gly Gln Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asn Ser Arg Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
```

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        115


<210> 73
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 73
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Ser Asp Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Gly Arg Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 74
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 74
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Gly Ile Ser Ser Glu Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Gly Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 75
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 75
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Tyr
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Arg Pro Asn Gly Thr Lys Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Arg Ser Ser Ala His Leu Gln Arg Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 76
<211> 119
<212> PRT
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 76
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
            20                  25                  30


Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg His Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Lys Gly Ser Thr Tyr Pro Arg Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 77
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 77
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Glu Pro Phe Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Tyr Pro Gln Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 78
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 78
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Arg Pro Asp Gly Lys Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Val Tyr Ser Ser Cys Ala Met Cys Thr Pro Leu Leu Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 79
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 79
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asp Ile Gly Pro Arg Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Arg Gly Gln Arg Asp Thr Ser Gln Pro Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 80
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 80
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Ser Gly Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
```

```
            100                 105                 110


Thr Val Ser Ser
        115


<210> 81
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 81
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Ser Asp Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 82
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 82
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Lys Tyr
            20                  25                  30
```

```
Leu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Pro Leu Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Glu Ala Ser Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 83
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 83
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Asn Val Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Lys Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

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<210> 84
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 84
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
            20                  25                  30


Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Arg Gln Gly Phe Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Leu Glu Arg Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 85
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 85
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Tyr
            20                  25                  30


Glu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Ser Glu Trp Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Ala
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Val Gly Gly Thr Gln Tyr Glu Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 86
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 86
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Asn Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 87
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 87
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Leu Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Gly Asp Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Arg Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 88
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 88
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Glu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Lys Pro Gly Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 89
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 89
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Glu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 90
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 90
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Ser Gln Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Arg Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 91
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 91
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Lys Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

```
Thr Val Ser Ser
        115


<210> 92
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 92
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Leu Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 93
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 93
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Tyr
            20                  25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Thr Ile Ser Asp Asn Gly Asn Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 94
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 94
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Arg Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Arg Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 95
<211> 116
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 95
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Arg Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Asp Asp Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Asp Lys Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 96
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 96
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Asp
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Asp Thr Thr Gly Gly Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
```

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Lys Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 97
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 97
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Ser
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Leu Asp Glu Gly Ser Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 98
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 98
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Glu
            20                      25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Thr Asp Asp Gly Asp Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asn Ala Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 99
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 99
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Val Tyr
            20                      25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Val Asn Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 100
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 100
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Thr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Asp Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Gln Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 101
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 101
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Tyr
            20                  25                  30
```

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Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Asp Asp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Leu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 102
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 102
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Val Tyr
            20                  25                  30


Gln Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Phe Ile Val Pro Gly Gly Asp Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Trp Pro Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

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<210> 103
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 103
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asn Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 104
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 104
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Ala Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gln Ile Gly Arg Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
```

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    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Arg Arg Tyr Ala Ile Phe Thr Phe Asp Arg Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 105
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 105
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Gln Tyr
            20                  25                  30


Pro Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Thr Asn Gly Val Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Thr Asp Ile Ile Ser Ser Ser Glu Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 106
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 106
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Asn Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Phe Val Trp Ser Ala Asp Ile Asp Phe Asp Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 107
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 107
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Trp Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ala Ser Trp Gly Gly Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Thr Val Lys Asp Gly Gly Tyr Leu Met Asp Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 108
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 108
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg Asp Gly Ala Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Lys Ala Ala Lys Glu Arg Gly Ser Trp Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 109
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 109
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Ala Tyr
            20                  25                  30


Gln Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Asn Gly Leu Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Leu Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 110
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 110
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Met Tyr
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Pro Arg Gly Val Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Asn Trp Asn Gly Val Asp Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

```
Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 111
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 111
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Tyr
            20                  25                  30


Met Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asn Thr Asn Gly Arg Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asp Ser Asn Met Ser Phe Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 112
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 112
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Tyr
            20                  25                  30


Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

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        35                  40                  45


Ser Ser Ile Asn Ala Ser Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Gly Asn Arg Ser Glu Val Phe Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 113
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 113
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Glu Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Asn Asp Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Arg Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 114
<211> 116
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 114
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Tyr
            20                  25                  30


Leu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Asn Gln Asp Gly Thr Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Ser Ser Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 115
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 115
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Arg Asp Gly His Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Ser Ser Lys Gly Gly Thr Phe Ala Ser Ser Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 116
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 116
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Val
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Thr Asp Asp Gly Leu Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly His Ile Tyr Gly Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 117
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 117
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Leu Tyr
            20                  25                  30


Arg Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ser Asp Gly Asp Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu His Trp Leu Gly Thr Thr Leu Ser Leu Arg Asp Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 118
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 118
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Arg Tyr
            20                  25                  30


Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gln Ile Ser Pro Arg Gly Asn Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Ser Gly Val Ala Gly Ala Glu Ser Pro Glu Tyr Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 119
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 119
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Gly Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Gly Pro Ile Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Gln Asn Ile Tyr Gly Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 120
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 120
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gln Tyr
```

20 25 30

Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Glu Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Glu Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 121
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 121
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Gln Tyr
20 25 30

Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Pro Leu Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Met Ser Lys Leu Leu Leu Ser Arg Glu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 122
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 122
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Met Tyr
            20   25   30

Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ser Pro Arg Gly Val Glu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Thr Asn Trp Asn Gly Val Asp Leu Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 123
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 123
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Arg His
            20   25   30

Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

```
Ser Thr Ile Thr Pro Thr Gly Asn Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Ala His Asp Glu Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 124
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 124
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Val Gly Asp Gly Leu Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 125
<211> 114
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 125
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Thr
            20                  25                  30


Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Arg Asp Thr Gly Leu Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Val Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110


Ser Ser



<210> 126
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 126
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Leu Gly
            20                  25                  30


Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Gly Thr Gly His Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Met Asn Asp Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 127
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 127
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Asp Glu
            20                  25                  30


Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Leu Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Phe Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 128
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 128
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

```
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr
            20                  25                  30


Gln Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Ala Thr Gly Arg Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Thr Arg Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 129
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 129
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Ala
            20                  25                  30


Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Tyr Leu Thr Ser His Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser
        115


<210> 130
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 130
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Ser Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Trp Ser Gln Ala Val Thr Arg Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 131
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 131
Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Glu
            20                  25                  30
```

```
Gly Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Asn Gln Gln Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Ile Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 132
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 132
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Gln
            20                  25                  30


Pro Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Ala Arg Gly Gly Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Phe Asp Ile Ile Ala Trp Asp Pro Phe Ser Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 133
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<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 133
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gln Tyr
            20                  25                  30


Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Pro Ser Gly Phe Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Trp Asn Pro Phe Ile Thr Thr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 134
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 134
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Gln
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Asp Tyr Ser Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 135
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 135
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Ser Asp Gly Gly Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Arg Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 136
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 136
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Glu
            20                  25                  30


Gln Met Thr Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro His Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Arg Thr Leu Val Asp Trp Pro Thr Ser Glu Ser Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 137
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 137
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ser Tyr
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Glu Pro Thr Gly Ile Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Pro His Phe Thr Glu Leu Gly Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 138
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 138
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Glu
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Leu Pro Gly Pro Tyr Thr Phe Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asn Gly Thr Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 139
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 139
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Lys Ile Gly Ala Gln Gly Leu His Thr Tyr Tyr Ala Gly Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gln Thr Thr Met Asp Tyr Glu Arg Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 140
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 140
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Val
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Gly Asn Asn Gly Leu Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Ala Leu Ser Tyr Arg Pro Pro Val Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
```

```
        115                 120


<210> 141
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 141
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Asp
            20                  25                  30


Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Leu Lys Gly Pro Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Arg Asp Gly Leu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 142
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 142
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Ser
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Ser Ile Gly Arg Asp Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Pro Ser Pro Tyr Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 143
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 143
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr
            20   25   30

Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Val Ser His Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Gly Lys Gly Tyr Asn Ala Gln Tyr Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 144
<211> 118
<212> PRT
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 144
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Gln
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Asp Tyr Ser Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 145
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 145
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Tyr
            20                  25                  30


Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser His Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Asp Val Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 146
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 146
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Gln
20 25 30

Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Trp Ser Asp Ser Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 147
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 147

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Gln Ser Asn Gly Asn Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Asn Ser Gln Val Glu Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 148
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 148
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Val Glu
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asn Ile Gly Arg Asp Gly Ser Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Gly Lys His Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr
```

```
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 149
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 149
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Tyr
            20                  25                  30


Arg Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Asp Glu Arg Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Arg Lys Gly Thr Lys Gln Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 150
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 150
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Leu Tyr
            20                  25                  30
```

```
Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Gly Ala Val Gly Glu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Glu Ala Asn Asn Leu Ser Asp Asn Leu Val Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 151
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 151
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Gln
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Ser Val Glu Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115
```

```
<210> 152
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 152
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
            20                  25                  30


Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asn Pro Trp Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Leu Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 153
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 153
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Asp
            20                  25                  30


Met Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Gln Leu Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gln Asn Trp Arg Thr Leu Thr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 154
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 154
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ala Tyr
            20                  25                  30


Gly Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Leu Ser Asp Gly Val Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Ala Arg Gly Ala Asn Phe Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 155
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 155
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Tyr
            20                  25                  30


Met Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Pro His Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Phe Asn Ala Ile Phe Ser Glu Ala Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 156
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 156
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Ser Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

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                85                  90                  95


Ala Glu Trp Ser Gln Ala Val Thr Arg Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 157
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 157
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Leu Tyr
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Met Ile Gly Arg Asp Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Ala Gly Ser Leu Arg Gly Arg Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 158
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 158
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Ala
            20                  25                  30


Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro His Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gln Arg Trp Gly Val Glu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 159
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 159
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Gly Tyr
            20                  25                  30


Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Gly Arg Gly Gly Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Leu Tyr Ile Tyr His Ser Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

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Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 160
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 160
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Gly Met
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Thr Gly Thr Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Tyr His Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 161
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 161
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Met Val
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
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```
Ser Ser Ile Ala Arg Asp Gly Asn Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Ser Pro Thr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 162
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 162
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Gln
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Asp Asp Gly Glu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asp Tyr Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 163
<211> 117
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 163
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr
            20   25   30

Asn Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gln Ile Thr Arg Asp Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Leu Ser Asn Ile Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 164
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 164
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Ser Met Ile Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Thr Pro Tyr Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Asp Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 165
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 165
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Tyr Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Gly Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 166
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 166
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Thr Gly
            20                  25                  30


Pro Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Gly Ile Gly Gly Asp Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Thr Pro Ser Asn Gln Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 167
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 167
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Gln Tyr
            20                  25                  30


Gln Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Pro Ser Gly Phe Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Glu Trp Asn Pro Phe Ile Ser Thr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 168
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 168
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asn Tyr
            20                  25                  30


Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ala Leu Gly Asn Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Thr Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Arg Ser Ala Ile Thr Gly Asn Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 169
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 169
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Glu Tyr
            20                  25                  30
```

```
Gln Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Ser Gly Met Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Trp Arg Ser Val Val Arg Pro Trp Pro Gly Val Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 170
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 170
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Glu
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Pro His Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu His Leu Lys Leu Tyr Glu Ser His Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 171
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 171
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Gly
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Met Ile Pro Met Asp Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 172
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 172
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Phe Met
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg Asp Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
```

```
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Ala Ser Pro Ala Gln Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 173
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 173
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Glu
            20                  25                  30


Pro Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Gly Thr Gly Thr Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Asn Gln Gly Asp Phe Ile Asn Arg Phe His Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 174
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 174
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Ala Tyr
            20                  25                  30


Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Arg Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Pro Pro Pro Ser Ser His Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 175
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 175
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 176
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 176
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Tyr
            20                  25                  30


Met Met Tyr Trp Val His Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Gln Gly His Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Leu Arg Glu Leu Pro Arg Leu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 177
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 177
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Asp Ala Ser Gly Gly Pro Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ala Asn Gly Lys Lys Phe Pro Phe Thr Lys Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 178
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 178
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Ser Val
20 25 30

His Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Leu Thr Gly Val Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ser Ala Thr Thr Arg Gln Ala His Pro Leu Tyr Phe Asp Tyr
100 105 110

```
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 179
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 179
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Glu Gly
            20                  25                  30


Glu Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Thr Asn Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Thr Arg Asp Leu Gly Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 180
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 180
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Tyr
            20                  25                  30


Glu Met Ala Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

35 40 45

Ser Phe Ile Ser Pro Arg Gly His Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Ala Lys Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 181
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 181
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ser Val Asp Gly Ser Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Thr Arg Met Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 182
<211> 124

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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 182
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asn Ile Ser Arg Asp Gly Ser Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Ala Gln Ser Gly Gly Leu Arg Ser Gly Leu Thr Thr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 183
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 183
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Asp Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg Asp Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Pro Lys Gly Ile Ala Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 184
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 184
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro His
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Gly Gly Gly Ser Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Asp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 185
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 185
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Ala Gly
            20   25   30

Glu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Thr Leu Pro Gly Asp Met Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Pro Asn Thr Gly Tyr Thr Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 186
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 186
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
            20   25   30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ser Trp Asp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Gln Asn Thr Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 187
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 187
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Asp Ala
            20                  25                  30


Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Leu Ser Pro Gly Glu Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Gly Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 188
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 188
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Thr Asp
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            20                  25                  30

Gln Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Pro Ser Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Leu Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115


<210> 189
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 189
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Glu Gln Tyr
            20                  25                  30

Gln Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Trp Ile Ser Pro Asp Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Phe Ser Leu Arg Lys Met Glu Lys Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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<210> 190
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 190
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Glu
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Ser Asp Gly Met Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Pro Gly Lys Asn Phe Asp His Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 191
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 191
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
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Ser Ser Ile Thr Thr Gly Gly Glu Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Trp Asn Leu Tyr Thr Glu Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 192
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 192
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gly Gln
            20                  25                  30


Pro Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ala Pro Asp Gly Ile His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asn Leu Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 193
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 193
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Gln Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Ser Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Trp Lys Ala Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 194
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 194
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro His Ser
            20                  25                  30


Thr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Leu Pro Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Ser Asp Glu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 195
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 195
Glu Val Gln Leu Ser Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Gly
            20                  25                  30


Asn Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Ser Asp Gly Val Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Arg Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 196
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 196
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

```
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Met Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro His Gly Val Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Leu His Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 197
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 197
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Thr Met Ala Trp Gly Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Phe Ile Ala Gly Pro Gly Asn Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Ser Thr Ala Thr Tyr Asn Asn Gly Gln Phe Asp Tyr
            100                 105                 110
```

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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 198
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 198
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
            20                  25                  30


Ser Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Gly Ser Gly Arg Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Leu Lys Leu Val Arg Ala Pro Asn Pro Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 199
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 199
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
```

```
Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Lys Thr Gly His Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Ser His Ser Leu Gly Pro Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 200
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 200
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ala Tyr
            20                  25                  30


Arg Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Ser Pro Ser Gly Ser Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Leu Thr Asp Ser Pro Ser Gly His Tyr Glu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 201
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<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 201
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Arg Tyr
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Thr Ala Gln Gly Leu Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Leu Thr Asp Phe Ser Ser Gly His Gln Glu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 202
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 202
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser His Asn Gly Met Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Trp Pro Ser Thr Ser Trp Glu Thr Asp Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 203
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 203
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Glu
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Glu Met Gln Gly Lys Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Arg Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 204
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 204
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Glu
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Cys Ile Asp Asn Leu Gly Ser Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Ile Ser His Gln Tyr Asp Arg Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 205
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 205
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Glu
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Glu Gly Gly Arg Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

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Ala Lys Trp Thr Pro His Lys Gln Leu Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 206
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 206
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ala Asp Glu
            20                  25                  30


Tyr Met Val Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Asp Pro Leu Gly Thr Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Gly Thr Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 207
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 207
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr His
            20                  25                  30


Asp Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Asp Asp Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Met Ser Leu Ile Glu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 208
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 208
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Thr
            20                  25                  30


Pro Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Gly Asp Gly Arg Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Tyr Ala Leu Thr Ser Ser Lys Pro Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
```

```
        115                 120


<210> 209
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 209
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asp Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile His Gly Thr Gly Gly Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Leu Ala Asp Arg Ser Gly Gly Val Val Glu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 210
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 210
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Glu
            20                  25                  30


Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Cys Ile Ser Asn Asp Gly Asn Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Glu Ser Leu Ile Ser Pro Gly Leu Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 211
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 211
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Gly Glu
            20   25   30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Asn Glu Thr Gly Tyr Met Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Leu Ser Thr Arg Gly Val Pro Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 212
<211> 120
<212> PRT
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 212
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Met Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Asn Gln His Ala His Asp Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 213
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 213
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Met Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Ala Leu Thr Glu Pro Met Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 214
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 214
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Leu Gly His Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Glu Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 215
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 215
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Pro Arg Tyr
            20                  25                  30


Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asn Ile Asp Gln Phe Gly Met Lys Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Glu Tyr Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 216
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 216
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Lys Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Met Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Arg Gly Asn Thr Ser Asp Phe Asp Tyr Trp Gly Gln Gly
```

```
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 217
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 217
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Gly Ala Gly His Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Phe Pro Arg Asp Glu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 218
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 218
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Lys Tyr
            20                  25                  30
```

```
Glu Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Gly Leu Asp Gly Ser Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Gly Asp Pro Asn Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 219
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 219
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ser
            20                  25                  30


Glu Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Gly Pro Asp Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Ala Asp Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

```
<210> 220
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 220
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20                  25                  30


Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Asp Thr Asp Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Leu Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 221
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 221
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Glu Asn Ala
            20                  25                  30


Ser Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Glu Gly Gln Gly Asn Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ser Ser Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 222
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 222
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Arg Asn
            20   25   30

Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Thr Pro Thr Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Thr Asp Pro Gly Asn Arg Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 223
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source

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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 223
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 224
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 224
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 225
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 225
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 226
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 226
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Gln Val Thr Val Ser Ser
        115


<210> 227
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 227
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser
        115


<210> 228
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 228
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 229
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 229
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 230
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 230
Glu Val Arg Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 231
<211> 118
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 231
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 232
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 232
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Tyr Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
```

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly His Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 233
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 233
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 234
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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```
<400> 234
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 235
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 235
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Val Gly Lys Glu Ser Lys Phe Asp Tyr Leu Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 236
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 236
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Glu Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Leu Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 237
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 237
Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30
```

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 238
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 238
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
20 25 30

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 239
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 239
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Thr Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Glu Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 240
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 240
Glu Val Arg Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
```

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    50                  55                  60


Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Leu Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 241
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 241
Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 242
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 242
Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 243
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 243
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
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```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 244
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 244
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Pro Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 245
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 245
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp His
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 246
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 246
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp His
            20                  25                  30


Leu Met Ala Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110
```

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Leu Val Thr Val Ser Ser
        115


<210> 247
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 247
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 248
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 248
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Ala Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 249
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 249
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp His
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 250
<211> 118
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 250
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 251
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 251
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Glu
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 252
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 252
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 253
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 253
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20   25   30

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 254
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 254
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20   25   30

Leu Met Gly Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 255
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 255
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 256
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 256
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
```

```
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 257
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 257
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

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<210> 258
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 258
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Lys Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 259
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 259
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Glu Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 260
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 260
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Arg Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 261
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 261
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Tyr Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 262
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 262
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 263
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 263
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Asp Ser Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 264
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 264
Glu Val Gln Leu Leu Glu Phe Gly Gly Gly Leu Val Gln Pro Gly Gly
```

```
1               5                   10                  15


Ser Leu Arg Phe Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Arg Asp Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 265
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 265
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Thr Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110
```

Leu Val Thr Val Ser Ser
        115

<210> 266
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 266
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20   25   30

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Val Lys Val Gly Lys Glu Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 267
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 267
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20   25   30

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Val Gly Lys Asp Ser Ala Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 268
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 268
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
20 25 30

Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Val Gly Asn Asp Ser Tyr Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 269

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<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 269
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 270
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 270
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Ala Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 271
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 271
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 272
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 272
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 273
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 273
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 274
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 274
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Glu
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 275
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 275
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Glu
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 276
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 276
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Glu
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
```

```
        115


<210> 277
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 277
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Leu Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 278
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 278
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 279
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 279
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
            20                  25                  30


Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 280
<211> 120
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 280
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Trp
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Glu Ser Gly Leu Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Gly Ala Pro Gln Tyr Gln Ile Thr Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 281
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 281
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asn Tyr
            20                  25                  30


Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Arg Arg Gly Leu Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Ser His Tyr Met Asn Asn Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 282
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 282
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Asp Tyr
            20                  25                  30


Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Ile Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Pro Tyr Gly Met Glu Asp Gly Leu Thr Trp Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 283
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 283
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
            20                  25                  30


Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Ser Glu Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Ser Asp Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 284
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 284
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Arg Gly Gly Trp Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Thr Ser Gln Ser Ser Thr Gly Ser Phe Asp Tyr Trp Gly
```

```
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 285
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 285
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Arg Tyr
            20                  25                  30


Asp Met Leu Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Ser Pro Thr Gly Ala Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Gly Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 286
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 286
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Pro Tyr
            20                  25                  30
```

```
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Gly Thr Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Thr Gln Asn Ala Thr Leu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 287
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 287
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Val Tyr
            20                  25                  30


Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asp Glu Ser Gly Arg Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Val Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

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<210> 288
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 288
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Phe Tyr
            20                  25                  30


Lys Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Lys Gly His His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Phe Lys Gly Lys Gly Trp Thr Arg Pro Ser Gly Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 289
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 289
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
            20                  25                  30


Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Arg Arg Gly Trp Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Val Leu Leu Asp Ser Thr Lys Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 290
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 290
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Tyr
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ala Arg Gly Pro Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Arg His Trp Leu Arg Asn Gly Arg Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 291
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 291
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Met Gln
            20                  25                  30


Ser Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Asp Asp Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Asp Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 292
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 292
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Ala
            20                  25                  30


Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Thr Asn Asp Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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                85                  90                  95


Ala Lys Ala Gly Asp Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 293
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 293
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            20                  25                  30


Arg Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ser Ser Gly Glu Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Glu Val Pro Met Gly Asn Gln Thr Phe Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 294
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 294
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Gln Gly Ala Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Thr Gly Thr Asp Ser Ser Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 295
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 295
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Cys Ile Gly Pro Gly Gly Lys Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Asp Gly His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

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Thr Val Ser Ser
        115


<210> 296
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 296
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Arg Gly Trp Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Gly Gly Arg Arg Arg Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 297
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 297
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Asp Tyr
            20                  25                  30


Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Thr Ile Ser Pro Met Gly Met Gly Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ser Ser Ala Ile Ser Phe Thr Ser Asp Ile Ser Asn Phe Asp
            100   105   110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 298
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 298
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ser Trp Ser Gly Phe Gln Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Pro Gly Val Ala Arg Met Pro Thr Gly Ile Ala Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 299
<211> 116
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 299
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20   25   30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Asp Ser Ala Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Glu Pro Phe Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 300
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 300
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Tyr
            20   25   30

Pro Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Asp Arg Gln Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Val Arg Arg Gly Leu Pro Arg Pro Ser Arg Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 301
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 301
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Met Gly Thr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Leu Ser Val Tyr Ser Gly Leu Asp Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 302
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 302
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asp Ile Asp Tyr Ile Gly Lys Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Ser Asp Glu Val Gly Val Asn Thr Ser Lys Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 303
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 303
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Arg Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Thr Gly Val Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Gly Phe Glu Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 304
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 304
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Ser His Thr Gly His Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly His Trp Pro Phe Asp Tyr Arg Gly Gln Gly Thr Leu Ile
            100                 105                 110


Thr Val Ser Ser
        115


<210> 305
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 305
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Glu
            20                  25                  30
```

```
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Asp Ile Ser Pro Gly Gly Trp Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Tyr Arg Pro Phe Asp Glu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 306
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 306
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asp Ala Ile
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Arg His Gly Glu Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Asp Ala Trp Ser Arg His Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
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<210> 307
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 307
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Thr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Leu Asp Asn Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Ala Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 308
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 308
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Arg Gln
            20                  25                  30


Ser Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Asp Asp Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
```

    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Gly Asp Pro Trp Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 309
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 309
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Asp Thr
            20   25   30

Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Asp Gly Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Pro Asp Arg His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 310
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 310
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Thr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Ser Asp Asp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Asp Gly Tyr Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 311
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 311
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Gly
            20                  25                  30


Asp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Asn Asp Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Asp Ser Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 312
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 312
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ala Tyr
            20                  25                  30


Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Pro Asn Gly Thr Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Tyr Val Gly Met Arg Trp Asn Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 313
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 313
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Thr Ser Leu Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Gly Arg Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 314
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 314
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Thr Ser Glu Gly Ser Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Pro Asn Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

```
Thr Val Ser Ser
        115


<210> 315
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 315
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Ser Glu Gly His Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Thr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 316
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 316
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45


Ser Thr Ile Asp Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 317
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 317
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asp Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Thr Gly Gln Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Asn Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 318
<211> 124
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 318
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Asp Tyr
            20                  25                  30


Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Pro Leu Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Glu Val Arg Val Gly Arg Gly Val His Pro Pro Lys Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 319
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 319
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Leu Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Ser Asp Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Val Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 320
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 320
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asn Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ala Pro Leu Gly Val Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Lys Lys Val Gly Ala Trp Leu Gln Ser Arg Ser Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 321
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 321
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Asp Tyr
            20                  25                  30


Glu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Gly Ala Ser Gly His Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Leu Asp Met Leu Leu Phe Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 322
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 322
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr
            20                  25                  30


Glu Met Met Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Ala Gly Asn Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Ile Met Leu Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 323
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 323
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Asn Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Ser Met Gly Leu Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Ser Asn Ala Ser Asp Trp Val Val Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 324
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 324
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
```

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            20                  25                  30

His Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ala Asp Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Leu Arg Gly Met Ala Arg Val Trp Gly Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 325
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 325
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
            20                  25                  30

Asp Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Ser Ser Ile Ser Asp Arg Gly Leu Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Phe Thr Glu Ile Pro Leu Asp Trp Leu Glu Val Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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<210> 326
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 326
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Tyr
            20                  25                  30


Lys Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Thr Asn Ser Gly Thr Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Met Tyr Pro Asp Leu Glu Ile Val His Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 327
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 327
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Thr Tyr
            20                  25                  30


Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ala Ile Asp Gln Glu Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asn Ser Gly Thr Arg Pro Gly Leu Arg Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 328
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 328
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asp Ala Ser Gly Tyr Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Leu Leu Lys Leu Ser Leu Asn Pro Asn Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 329
<211> 120
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 329
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile His Asn Thr Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Thr Gln His Arg Phe Val Val Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 330
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 330
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Leu Gly Pro Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Leu Met Gly Glu Tyr Leu Asn Ser Arg Thr Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 331
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 331
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30


Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Asp Ala Asp Gly Trp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Thr Gly His Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 332
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 332
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Gly
            20   25   30

Glu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Arg Ile Val Asp Pro Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ala Gly Asp Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 333
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 333
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Tyr
            20   25   30

Glu Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Thr Pro Ser Gly Gly His Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
                85   90   95

Ala Ile Pro Leu Ser Ser Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
            100   105   110

```
Thr Val Ser Ser
        115


<210> 334
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 334
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Val Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Asn Gly Ala Gly Asp Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Gly Gly Ala Arg Ser Phe Gly Val Pro Pro Asn Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 335
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 335
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Gly
            20                  25                  30
```

```
Glu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Val Asp Pro Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Asp Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 336
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 336
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Thr Leu Tyr
            20                  25                  30


Asn Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Ser Ser Lys Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Thr Ser Ser Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 337
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```
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 337
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Tyr
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Val Asn Asn Gly Leu Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Ala Val His Pro Ser Tyr Arg Ala Glu Leu Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 338
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 338
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Glu Pro Asp Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Asp Asn Phe Thr Met Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 339
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 339
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            20                  25                  30


Met Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ser Leu Gly His Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Ala Glu Phe Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 340
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 340
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 341
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 341
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val
            100   105   110

Thr Val Ser Ser
        115

<210> 342
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 342
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20   25   30

Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 343
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 343
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 344
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 344
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
```

```
        115


<210> 345
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 345
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Leu Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 346
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 346
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 347
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 347
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Lys Arg Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 348
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 348
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Lys Arg Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Arg Ala Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 349
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 349
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Ile Asp Tyr Trp Gly Gln Gly Thr Gln Val
            100                 105                 110


Thr Val Ser Ser
        115
```

<210> 350
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 350

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Gly Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115
```

<210> 351
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 351

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Trp Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 352
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 352
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
```

```
            100                 105                 110


Thr Val Ser Ser
        115


<210> 353
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 353
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Ile Asp Tyr Arg Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 354
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 354
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Lys Tyr
            20                  25                  30
```

```
Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115


<210> 355
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 355
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
            20                  25                  30

Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
```

```
<210> 356
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 356
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 357
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 357
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Met Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 358
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 358
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 359
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 359
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Leu Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 360
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 360
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Glu Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 361
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 361
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30


Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 362
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 362
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            20                  25                  30


Glu Met Met Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 363
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 363
Glu Val Gln Leu Ser Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

```
Thr Val Ser Ser
        115


<210> 364
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 364
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 365
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 365
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Glu Met Asn Ser Met Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 366
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 366
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 367
<211> 116
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 367
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Lys Arg Tyr
            20                  25                  30


Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 368
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 368
Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
```

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 369
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 369
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 370
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

```
<400> 370
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Leu Gly Leu Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Ser Ala Gly Ala Glu Thr His Val Tyr Arg Leu Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 371
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 371
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Val Leu Gly His Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Leu Met Ser Leu Arg Thr Phe Glu Asn Leu Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 372
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 372
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Tyr
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Ala Asn Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Gly Thr Trp Arg Arg His Phe Ala Ile Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 373
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 373
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Leu Tyr
            20                  25                  30
```

```
Asp Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Asp Leu Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asn Gly Phe Arg Val Thr Ser Asn Asp Arg Arg Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 374
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 374
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Gly Gly
            20                  25                  30


Asp Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Met Ile Glu Gly Gly Gly Val Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Leu Asp Leu Arg Thr Gly Gln Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
```

```
<210> 375
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 375
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 376
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 376
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu His Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
```

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 377
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 377
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 378
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 378
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 379
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 379
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Met Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 380
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 380
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Met Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 381
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 381
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Met Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 382
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 382
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Met Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser
        115


<210> 383
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 383
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Thr Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Met Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 384
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 384
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Lys Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 385
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 385
Glu Val Gln Leu Ser Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 386
<211> 118
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 386
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 387
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 387
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Pro Val Thr Val Ser Ser
        115


<210> 388
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 388
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
1               5                   10                  15


Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr Thr
            20                  25                  30


Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
        35                  40                  45


Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Met Leu Tyr Leu
65                  70                  75                  80


Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr Gln
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 389
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 389
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 390
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 390
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Leu Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 391
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 391
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 392
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 392
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
```

20 25 30

Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Gly Asp Arg Gly Thr Trp Thr Tyr Tyr Ala Asp Pro Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 393
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 393
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 394
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 394
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30


Thr Met Gly Trp Val Arg Gln Ala Pro Gly Met Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210> 395
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 395
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Tyr
            20                  25                  30


Lys Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ser Ile Ser Glu Ile Gly Asn Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ile Ala Leu Thr Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 396
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 396
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Ser Tyr
            20                  25                  30


Arg Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Asp Pro Pro Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Leu Asn Leu Ser Phe Pro Tyr Ile Asn Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 397
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 397
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Ser His Ser Gly Arg Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Leu Asp Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 398
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 398
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
            20                  25                  30


Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asn His Asn Gly Ser Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Met Pro Gln Gly Thr Ser Asp Trp Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 399
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 399
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Leu Glu Asp Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 400
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 400
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

```
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Leu Ser Pro Gly Thr Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Glu Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 401
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 401
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Gly
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Met Ile Pro Met Asp Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Glu Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

Thr Val Ser Ser
        115

<210> 402
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 402
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Glu Tyr
            20   25   30

His Met Lys Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ser Arg Asp Gly Met Asn Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ile Gln Leu Ala Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 403
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 403
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
            20   25   30

```
Glu Met Leu Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Leu Pro Ser Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ala Gly Ser Gly Asn Gly Pro Ile Leu Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 404
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 404
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Glu His
            20                  25                  30


Asp Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Gly Ala Glu Gly Val Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Thr Met Ser Asn Gly Ser Gln Ser Arg Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 405
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<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 405
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20   25   30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 406
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 406
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20   25   30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 407
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 407
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 408
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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```
      polypeptide"

<400> 408
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Phe Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 409
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 409
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 410
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 410
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 411
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 411
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
20 25 30

Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 412
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 412
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
20 25 30

Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ala Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser

```
        115                 120


<210> 413
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 413
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 414
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 414
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 415
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 415
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20   25   30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
                85   90   95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 416
<211> 123
<212> PRT
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 416
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Glu Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 417
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 417
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 418
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 418
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 419
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 419
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20   25   30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ser Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
                85   90   95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 420
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 420
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20   25   30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asn
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr

```
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 421
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 421
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Val Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 422
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 422
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30
```

```
Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 423
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 423
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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<210> 424
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 424
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
            20                  25                  30


Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 425
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 425
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Ala
            20                  25                  30


Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Arg Pro Gly Gln Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 426
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 426
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Gly
            20                  25                  30


Thr Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Leu Pro Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Ser Leu Thr Asn Arg Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 427
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 427
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Asp Met Arg Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Asp Ala Val Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ile Pro Gly Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 428
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 428
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Met Tyr
20 25 30

Gly Met Met Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Glu Gly Ala Gly His Ala Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

                85   90   95

Ala Ile Val Leu Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 429
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 429
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Gln Tyr
            20   25   30

Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Pro Val Gly Leu Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Leu Phe Glu Gly Ser Arg Ile Gln Arg Asp Val Gly Phe Asp
            100   105   110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 430
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 430
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Lys Tyr
            20                  25                  30


Gln Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Arg Gly Ser Gly Leu Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val His Thr Thr Leu His Thr Glu Val Ile Gly Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 431
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 431
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr
            20                  25                  30


Thr Met Tyr Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Ser His Ser Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ile Ser Gly Leu His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

```
Thr Val Ser Ser
        115


<210> 432
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 432
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Gly Val Glu Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Leu Arg Leu Tyr Arg Leu Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 433
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 433
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Lys Tyr
            20                  25                  30


Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Lys Ile Asn Ser Asp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Leu His Gly Arg Gly Phe Val Ile Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 434
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 434
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30


Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Met Gly Leu Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Tyr Ser Val Ala Pro His Gly Tyr Pro Leu Gly Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 435
<211> 122
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 435
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asp Tyr
            20                  25                  30


Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Asp Asn Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Met Ser Leu Ala Thr Tyr Leu Gln Phe Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 436
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 436
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Glu Tyr
            20                  25                  30


Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Ala Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Ser Ser Asp Gly Leu Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
```

```
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Val Ser Ala Leu Ala Pro Phe Asp Ile Gly Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 437
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 437
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Glu Tyr
            20                  25                  30


Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asn Phe Ala Gly Arg Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Ser Leu Pro Leu Asp Ile Phe Ser Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 438
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 438
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 439
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 439
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65                  70                  75                  80


Leu Arg Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Glu Thr Ser Gly Tyr Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 440
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 440
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Ser Gly Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 441
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 441
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30
```

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Glu Thr Ser Ser Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 442
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 442
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20   25   30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Glu Thr Ser Gly Tyr Tyr Glu Tyr Trp Gly His Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

```
<210> 443
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 443
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Gly Asp Tyr
            20                  25                  30


Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Ser Gly Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 444
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 444
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser His Ile Ser Ser Asn Gly Arg Phe Ile Tyr Tyr Ala Asp Ser Val
```

```
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Ser Gly Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 445
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 445
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Glu Tyr
            20                  25                  30


Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asn Gly Leu Gly Asn Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Glu Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ile Gln Leu Pro Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 446
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 446
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Asp
            20   25   30

Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Phe Ile Asn Val Asp Gly Arg Glu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Glu Trp Ser Pro Gly Arg Val Gln Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 447
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 447
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gly Trp
            20   25   30

Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ala His Glu Gly Gly Glu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Val Pro Gly Ser Pro Leu Phe Asp Tyr Trp Gly Gln Arg
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 448
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 448
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gln Gly
            20                  25                  30


Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Gly Ser Asn Gly Pro Arg Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Gly Glu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 449
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 449
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Gln Ser
            20                  25                  30


Asp Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Gly Asn Asn Gly Glu Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Asn Trp Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 450
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 450
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Leu Ser
            20                  25                  30


Thr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Gly Gly Asp Gly Ser His Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Gly Thr Gln Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
```

Thr Val Ser Ser
115

<210> 451
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 451
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Thr Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Val Thr Gly Tyr Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 452
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 452
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```
        35                  40                  45


Ser Tyr Ile Asp Pro Leu Gly Arg Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Asp Leu Ser Ser Leu Gln Tyr Gly Val Ser Pro Asn Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 453
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 453
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe His Tyr
            20                  25                  30


Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Gly Pro Val Gly Arg Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Met Ile Gln Ser Pro Leu Phe Lys Asp Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 454
<211> 120
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 454
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
            20                  25                  30


Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Arg Ile Asp Ser Gly Gly Asn Gln Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Ala Ser Leu Trp Lys Trp Arg Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 455
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 455
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Tyr
            20                  25                  30


Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Leu Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys His Ala Thr Ser Gln Glu Ser Leu Arg Ser Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 456
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 456
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20                  25                  30


Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Leu Pro Asp Ala Phe Trp Thr Arg Gly Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 457
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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```
<400> 457
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Thr Tyr
            20                  25                  30


Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Asp Arg His Gly Leu Ala Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Pro Gly Ser Ser Trp Gln Thr Val Phe Gly Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 458
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 458
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ser Tyr
            20                  25                  30


Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp His His Gly His Ser Thr Tyr Tyr Ala Asp Ser Ala
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Leu Leu Arg Val Ser Met Ile Phe Gly Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 459
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 459
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Gln Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Trp Ile Ser Ser Ser Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Thr Ser Arg Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 460
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 460
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Glu Tyr
```

```
            20                  25                  30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Ser Pro Pro Gly Arg Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Val Ile Leu Gly Tyr Thr Asn Arg Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 461
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 461
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asn Tyr
            20                  25                  30

Gly Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Asn Ser Ser Gly Met Glu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Phe Phe Arg Leu Asn Asp His Asn Ser Val Phe Gly Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

```
<210> 462
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 462
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asp Tyr
            20                  25                  30


Lys Met Met Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Val Gly Ser Gly Ser Met Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 463
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 463
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Asn Tyr
            20                  25                  30


Ala Met Gly Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ser Ile Asp Glu His Gly Thr Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Ser Leu Asp Arg Val Trp Ile Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 464
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 464
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
            20                  25                  30


Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Tyr Ser Ala Gly Ser Pro Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Tyr His Arg Glu Pro Ile Leu Phe Gly Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 465
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 465
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Asp Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Gly His Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 466
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 466
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Tyr
            20                  25                  30


Thr Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Glu Ile Asp Arg Thr Gly Glu Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Pro Gly Phe Ala Ser Leu Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 467
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 467
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Thr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Lys Ile Ser Pro Ser Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Pro Phe Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 468
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 468
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
```

```
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Ala
            20                  25                  30


Glu Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ala Arg Gly Leu Thr Thr Tyr Tyr Ala Asp Pro Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Glu Ala Thr Ser Ala Met Tyr Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 469
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 469
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
            20                  25                  30


Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Leu Gly His Phe Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Gly Phe His Glu Tyr Thr Glu Gly Phe Asp Tyr Trp Gly
            100                 105                 110
```

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 470
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 470
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Arg Ala
20 25 30

Gly Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Gly Arg Gly Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 471
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 471
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Arg Tyr
20 25 30

```
Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Asp Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Ser Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 472
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 472
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Phe Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Leu Tyr
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Val Gly Phe Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly His Glu Gly Ser Tyr Thr Pro Arg Ser Ala Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 473
```

```
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 473
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ala Tyr
            20                  25                  30


Pro Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ala Pro Leu Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Pro Glu Gly Leu Gln Ile Asp Ser Gln Asn Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 474
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 474
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Leu Tyr
            20                  25                  30


Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Asp Ser Ser Gly Ser Asp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Pro Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 475
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 475
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Gln Tyr
            20                  25                  30


Gln Met Ala Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ala Ser Asp Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Gly Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 476
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 476
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gln Tyr
            20   25   30

Asp Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Trp Ile Asp Glu Ala Gly His Glu Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Gly Met Asp Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 477
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 477
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Asp Tyr
            20   25   30

Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Thr Gly Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Lys Ala Arg Tyr Tyr Tyr Leu Ser Gln Ile Lys Asn Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 478
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 478
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ile Tyr
            20                  25                  30


Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Pro Leu Gly Leu Val Thr Tyr Tyr Ala Asp Pro Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Lys Glu His Gly Asp Val Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 479
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 479
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Leu Tyr
            20                  25                  30


Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Thr Gly Leu Leu Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Lys Arg Ser Gly Lys Thr Asp Asp Thr Asn Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 480
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 480
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Glu Tyr
            20                  25                  30


Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Val Gly Asp Gly Asn Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gln Asp Arg Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
```

```
        115


<210> 481
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 481
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Pro Ile Gly Val Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asn Ala Tyr Asp Arg Lys Ser Asn Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 482
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 482
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Arg Tyr
            20                  25                  30


Val Met Val Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
        35                  40                  45
```

```
Ser Gly Ile Thr Pro Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Leu Gly Arg His Phe Asp Pro Leu Leu Pro Ser Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 483
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 483
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Thr Pro Gly Gly Phe Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Thr Ser Ser Gly Glu Leu Gln Leu Val Glu Asp Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 484
<211> 351
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 484
gaggtgcagc tgttggagtc tgggggaggc ttagtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatt gcttatgata tgagttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatgg attgatgagt ggggtctgca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagacg 300

cctgaggagt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 485
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 485
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatgaga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg attgatggtg agggttctga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccgggg 300

aggagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 486
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 486
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag cgttatccta tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attcatggtt ctggtagtgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggccg 300

tatactagtc ggcataatag tcttgggcat tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 487
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 487
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatg gattatccta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgggcctg ttggtatgag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatggg 300

gggactagtg gtaggcataa tactaagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 488
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 488
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gagtatccta tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagtt atttctcctc ttggttttac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggact 300

ggtgggagtg gtattttgaa ttcttctttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 489
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 489
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt tagggttagc aattacgatt tgacctgggt ccgccaggct 120

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ccagggaagg gtctagagtg ggtatcaacc attagtgcca caaacggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attattgcgc ggcagtgacg      300

tggtggttgt tgcgtcataa cgacaacttg gggttttggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 490
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 490
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt tagcattagc tataagaata tggcctgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtatcagcc attaaggcgg caaacggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attattgcgc gacagggagt      300

cagaagaagc ggacctacac gttcgacttt tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 491
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 491
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagg ttgtatgaga tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attgatattt tgggttcgag gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatctg      300

tcgtggcagg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 492
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 492
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg tcttatacga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attaatccta tgggttatca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacatggg 300

gtggggaagg gtactaagcc gcataatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 493
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 493
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag ctgtatagga tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagag attagtggta gtggttttcc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtctg 300

catgataaga ctcagcatca tcaggagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 494
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 494
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatt gagtatccta tgcggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactt atttctccgt ctggtgtgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat 300

gagtctagta cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 495
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 495
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag cggtatgata tggattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgggagtt cgggttatcc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaaggatg 300

cctggttatt ttcctgggtt tgctcggcag tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 496
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 496
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttgg cggtatgcta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attaatgatg agggtcggga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagcgg 300

gtgtctagtt ctgtgaatgc tccgtatgag tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 497
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 497
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg aattatagta tgagttgggt ccgccaggcc 120 ccagggaagg gtctagagtg ggtctcatcg attgatcgtc ttggtacgca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagtgctg 300

gctgatctta ttgctgggca tgcggagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 498
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 498
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg tcgtatgata tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg atttcgaggt ctggttctat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ttgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgtt 300

gatgcgcatg tttattatat ggagcctttt tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 499
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 499
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag aggtatcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attagttctg atggtggggg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300

actgtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 500
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 500
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacatttccg aagtatgaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgatggtg atggtaagtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccggat 300

cagttttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 501
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 501
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct tattattcga tgtattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg atttcgcctt ttggttgggg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagga cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggg 300

gagacgagtg gtccgatttc tgagaatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 502
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 502
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccggatt cacctttgcg ggttatcaga tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attactaatg agggtgtttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300

aagtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 503
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 503
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gagtatgaga tggtgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct attacgtcgg atggtctgag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaccgggt 300

attcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 504
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 504
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gattatgata tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgttgatg atggtcttat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat 300

gttgcttttg actactgggg tcaggggacc ctggtcaccg tctcgaac 348

<210> 505
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 505
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatt ggttatgcta tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attggtcctt tgggtgcgac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgcct 300 gctggtacga gtagtcatag tgtggatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 506
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 506
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg gattatgaga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attactagtg atggtgtttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgtcg 300

gttcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 507
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 507
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgt aggtatgtta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgg attgaggctg atggtcgtac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggctt 300

acggatcagc atgttattga gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 508
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 508
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttgat ggttatcgta tggggtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg attgctccgg atggtaatta tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattttgg      300

gggatgcagt ttgactactg gggtcaggga accctggtca ccgtctcgag c               351


<210> 509
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 509
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgct tcgtatccga tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt attggtccta ttggttttac tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaatgaag      300

tcgccttata agccgcagtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 510
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 510
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt caccttttg gcttattgga tggtttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct atttctccgt cgggtacgca tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgtcgaggac accgcggtat attactgtgc gaaatatact      300

gagccggggt tgggttcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 511
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polynucleotide"

<400> 511
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg aattatgaga tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagtg atttctgagg tgggttctct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctcat 300

gatagttcga ttgggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 512
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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ccagggaagg gtctagagtg ggtctcatct attatggctt cgggtgatga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatgggat 300

cgggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 513
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 513
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ccagggaagg gtctggagtg ggtctcaact atttctccta ttggtctgac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatttcct 300

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<210> 514
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<220>
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tcctgtgcag cctccggatt cacctttatg gagtatgcga tgatttgggt ccgccaggct       120

ccagggaagg gtctagagtg ggtctcaatt atttctccgc ttggtttgtc tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag       300

gattcgtctg atagtcagta tacgaatttt gactactggg gtcagggaac cctggtcacc       360

gtctcgagc                                                               369


<210> 515
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
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ccagggaagg gtctagagtg ggtctcaagt attggtcctc tgggtctttg gacatactac       180

gcagactccg cgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctccg       300

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<210> 516
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
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ccagggaagg gtctagagtg ggtctcaatt attgattggg atggtaattc tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg       300
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gataatgttg gtatttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
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ccagggaagg gtctagagtg ggtctcagcg attgatgagt ggggttttgc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacattgg 300

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tcgagc 366

<210> 518
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<213> Artificial Sequence

<220>
<221> source
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polynucleotide"

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ccagggaagg gtctagagtg ggtctcatct attaatgatc agggttctct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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cagtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 519
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<220>
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polynucleotide"

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

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tcgagc 366

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<220>
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ccagggaagg gtctggagtg ggtctcatat attagttctg atggttattc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgcat 300

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<210> 521
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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ccagggaagg gtctagagtg ggtctcaacg attactagtt tgggtgagag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300

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<210> 522
<211> 369
<212> DNA
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<220>
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggtaat   300

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gtctcgagc   369

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<212> DNA
<213> Artificial Sequence

<220>
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ccagggaagg gtctagagtg ggtctcatcg attggtcctt ctggtccgaa tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctccg   300

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tcgagc   366

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      polynucleotide"

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ccagggaagg gtctagagtg ggtctcatct attcagtcgt cgggtttgcg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacgggct   300

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ccagggaagg gtctagagtg ggtctcatct attactagtc atggtgggtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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aaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

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<220>
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ccagggaagg gtctagagtg ggtctcatcg attggtaggc tgggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtgct 300

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tcgagc 366

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ccagggaagg gtctagagtg ggtctcaagt attgattcgg atggttgggt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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tcgttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

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polynucleotide"

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ccagggaagg gtctagagtg ggtctcaggt attaatcggg gtggtactcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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aggagggggt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

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ccagggaagg gtctggagtg ggtctcaggg atttcgaggg atggttatcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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actgcgtcgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

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<213> Artificial Sequence

<220>
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag 300

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ccagggaagg gtctagagtg ggtctcaatg attacttctg atggtcttga tacatattac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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ccagggaagg gtctagagtg ggtctcaacg attttgtctg atggtacgga tacatactac 180

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gctatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

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ccagggaagg gtctagagtg ggtctcatct attgatgcgg ggggtcatga gacatactac 180

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagattgg 300

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<210> 535
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ccagggaagg gtctagagtg ggtctcaact attaatgcga atggtattcg gacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagg      300

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg      300

tttggtcatt atgttgatgg tcttgggttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


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<220>
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ccagggaagg gtctagagtg ggtctcatct attactgata tgggtgattc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggg      300

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<210> 539
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<213> Artificial Sequence

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ccagggaagg gtctagagtg ggtctcaagt attactccga agggtcattc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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tcgagc 366

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ccagggaagg gtctggagtg ggtctcaagt atttggccga ggggtcagaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggaat   300

agtcggtatg tttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc   354

<210> 542
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 542
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttttct gattatgaga tgatgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaact attacttcgg atggtatttc tacatactac   180

gcagactccg tgaagggccg gttcaccatc ttccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaagtggg   300

aggtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 543
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 543
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttttcg ggttatcaga tggcttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaggt attagttcgg agggtcttac tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgggg   300

cgtaggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 544
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 544
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttact aattatagta tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attcgtccta atggtactaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacggtcg 300

tctgcgcatc ttcagaggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 545
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 545
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt aattattcga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attggtcgtc atggtgggcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagggg 300

agtacttatc ctaggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 546
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 546
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccggatt caccttttcg cattatgaga tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attgagcctt ttggtggtgg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagtgtat 300

cctcagggtt cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 547
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

```
      polynucleotide"

<400> 547
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt aattatacta tggggtgggt ccgtcaggct      120

ccagggaagg gtctagagtg ggtctcatct attcggcctg atggtaagat tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagtttat      300

tcttcgtgtg cgatgtgtac tccgcttttg tttgactact ggggtcaggg aaccctggtc      360

accgtctcga gc                                                          372


<210> 548
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 548
gaggtgcagc tgttggagtc tgggggggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag cggtattcga tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagat attgggccga ggggtttttc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgggt      300

cgtggtcagc gtgatactag tcagccgttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 549
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 549
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgct tcttatcaga tggcttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attacttcgg gtggtcttag tacgtactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300

aggggttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348
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<210> 550
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 550
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggtgggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgct tcttatgaga tgacttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaggg atttcttctg atggtctgtc tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg   300

gtgttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 551
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 551
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc   60

tcctgtgcag cctctggatt cacctttgat aagtatttga tgtcgtgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcaggt attgagcctc tgggtgatgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggct   300

tcgggggatt ttgactactg gggtcaggga accctggtca ccgtctcgag c   351

<210> 552
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 552
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc   60

tcctgtgcag cctccgggtt cacctttact gagtatgaga tgtcttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagt attgataatg tgggtagtag tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg   300

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aagcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                348


<210> 553
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 553
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgct gattatgaga tgtggtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagcg atttctaggc agggttttgc tacatactac      180

gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatctg      300

gagcgggatg attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 554
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 554
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgcg aattatgaga tggggtgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagtt atttctgagt ggggttattc tacatactac      180

gcagactccg cgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttgtg      300

ggtgggactc agtatgagtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 555
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 555
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcat aattatgaga tgtcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt atttcttcgg gtggttcttc tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300

gttaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 556
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 556
gaggtgcagc tgttggagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttggg ctgtatgaga tgacgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt attacgggtg atggtatttc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggg      300

aggaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 557
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 557
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt aattatcaga tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt attactagtg agggtggttc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt      300

aagaattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 558
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 558
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60
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tcctgtgcag cctccggatt cacctttagt gattatcaga tggcgtgggt tcgccaggct 120

ccagggaagg gactagagtg ggtctcaagt attactagtg agggtggttc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacagtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300

aagaatttcg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 559
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 559
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aattatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attacgtcgc agggtactag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

cgttcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 560
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 560
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgt agttatgaga tgacttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct attacgtcgg atggtggtac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

aagacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 561
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 561
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat ttgtatgaga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attactagtg atggtgtttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat 300

tctccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 562
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 562
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg cattatgata tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attagtgata atggtaatgg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300

cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 563
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 563
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt cgttatcaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct atttcttctg atggtggggg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg 300

cgggcgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 564
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 564
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg aggtatcaga tggcttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaact atttctgatg atggtgattc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactggat 300

aagttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 565
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 565
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatgatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct attgatacga cgggtgggca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300

aaggagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 566
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 566
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gagagtgaga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attcttgatg agggttctgg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

aaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 567
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 567
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagcg attactgatg atggtgatga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctaat 300

gcgggtgctt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 568
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 568
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gtgtatgata tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg attgttaatg atggttcttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

aaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 569
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 569
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt aatacggaga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attgcggatg atggttctag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300 caggcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 570
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 570
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gagtatcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg atttcggatg atggttcttc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

ctttattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 571
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 571
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gtgtatcaga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcattt attgtgcctg gggtgattt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaacgtgg 300

ccggagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 572
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 572
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aattatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attacgagtg atggtacttc gacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctaat      300

ccgccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 573
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 573
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag gcgtatgata tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcacag attgggaggg atggttcttt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctcgt      300

cggtatgcta tttttacttt tgatcggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 574
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 574
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag cagtatccga tggtgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaacg atttctacta atggtgtgag gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggacg      300

gatattattt cgtcttcgga gtttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 575
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 575
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttt aattatgata tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttttt 300

gtgtggtcgg ctgatattga ttttgatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 576
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 576
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg tggtatgata tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacat attgcgagtt ggggtggtaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgacg 300

gtgaaggatg gggggtatct gatggatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 577
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 577
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gagtatgcta tggcgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaagt attgggcggg atggtgcggt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggaag 300

gcggcgaagg agcggggttc ttggtttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 578
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 578
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcag gcttatcaga tgcagtgggt ccgccaggct   120

ccagggaagg gtcttgagtg ggtctcaact attagtccta atggtctttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggttg   300

agttcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 579
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 579
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgct atgtattcga tggcttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaggt atttcgcctc gtggtgttga gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactaat   300

tggaatggtg tggatctgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc   360

<210> 580
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 580
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcct acgtatatga tgagttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaact attaatacga atggtcgtga tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat   300 agtaatatgt cgtttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc   357

<210> 581
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 581
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgag ggttattcga tgacgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatct attaatgcgt cgggtactct gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatggt   300

aataggtctg aggttttttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc   360

<210> 582
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 582
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttttt gagtatgaga tgacgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatct attgcgaatg atggttcgac tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat   300

cggcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 583
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 583
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcag gattatttga tggcgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcagag attaatcagg atggtactgt tacatactac   180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaagttct      300

ccgtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 584
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 584
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat aattatgcga tgtcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct attagtcggg atggtcatgt gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactttct      300

tctaaggggg ggacgtttgc tagttctttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 585
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 585
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt gctgttccga tgacgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagcg attacggatg atggtcttcg tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcat      300

atttatgggg attattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc        357


<210> 586
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 586
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag ctttatagga tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct attagtagtg atggtgatac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacattgg 300

ttgggtacta cgttgtcttt gagggatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 587
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 587
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttat cgttatacga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacag atttcgccta ggggtaatat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtggt 300

gtggcggggg cggagtcgcc tgagtatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 588
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 588
gaggtgcagc tgttggagtc tgggggaggt ttggtgcagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttg ggttattata tgagttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgggccga ttggtggtgg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctcag 300

aatatttatg gtccttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 589
<211> 348

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 589
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag cagtatgata tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagag attagtcgtg atggtgggcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagagtat 300

ccttattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 590
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 590
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg cagtatagta tggtgtgggt ccgccaggct 120

ccagggaagg gtcttgagtg ggtctcaact atttcgcctc tgggttcttc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaatgagt 300

aagttgttgc tgtcgaggga gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 591
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 591
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct atgtattcga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt atttcgcctc gtggtgttga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactaat 300 tggaatggtg tggatctgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc   360

<210> 592
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 592
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttacg cgtcatggta tggcgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaacg attacgccta ctggtaatac tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatgct   300

catgatgagg ggtattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc   357

<210> 593
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 593
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttggt ccgtatgaga tgacttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatcg attgttggtg atggtctgga tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat   300

cgggtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 594
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 594
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttggt agtacgccta tgatgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcagag attagggata cgggtctggc tacatactac   180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gagtgtttcg      300

tttgactact ggggtcaggg aaccctggtc accgtctcga gc                         342


<210> 595
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 595
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcat ctgggggata tgcattgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg attagtggga cgggtcatac tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctatg      300

aatgatcagg ggtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 596
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 596
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttatg gatgaggata tgttgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagg attaattcgc tgggtactca tacatactac      180

gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatcgttt      300

atgatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                  348


<210> 597
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 597
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60
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tcctgtgcag cctccggatt cacctttcgt aattatcaga tgcattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgatgcga ctggtcgggc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gagatctact 300

aggtcatttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 598
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 598
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg aatgcggata tggtgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttat 300

ttgacttcgc attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 599
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 599
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg gattattcta tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccgt cgggtcttac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggtct 300

caggcggtta ctcggtcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 600
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 600
gaggtgcagc tgttggagtc tgggggagac ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gatgagggta tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagag attaatcagc agggttcggc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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gggatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 601
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 601
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tcctgtgcag cctccggatt cacctttact gatcagccga tggtgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attggggcgc gtggtgggcc tacatactac 180

gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggttt 300

gatattattg cttgggatcc ttttagtttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 602
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 602
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tcctgtgcag cctccggatt cacctttaat cagtatccta tgatgtgggt tcgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attactcctt ctggtttttt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggaat 300

ccttttatta ctacgtttga ctactggggt cagggaaccc tggtgaccgt ctcgagc 357

<210> 603
<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 603
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tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttgat 300

tattcgcttc gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 604
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 604
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct tcttatgaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attggtagtg atggtgggcc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac tccgcggtat attactgtgc gaaacctgat 300

agggcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 605
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 605
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tcctgtgcag cctccggatt caccttttct gcggagcaga tgacttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccgc atggtgattc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggcgg 300

actttggttg attggcctac gagtgagtcg tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 606
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 606
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tcctgtgcag cctccggatt cacctttacg tcttatgaga tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgagccta ctggtattac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctcat 300

tttactgagc ttggttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 607
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 607
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tcctgtgcag cctccggatt cacctttgag ggggagcaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attacgctgc ctggtccgta tacattctac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggaat 300

gggacgtttt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 608
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 608
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tcctgtgcag cctccggatt cacctttggt aattatgcga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaaag attggggcgc agggtcttca tacatactac 180

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gcaggctccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagacg      300

acgatggatt atgagaggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 609
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 609
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tcctgtgcag cctccggatt cacctttgat gaggttgata tgtcgtgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcagct attggtaata atggtcttaa gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggct      300

ctgtcgtata ggcctcctgt ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 610
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 610
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tcctgtgcag cctccggatt cacctttcag gatgatacta tgtcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaacg attacgctta agggtccgtc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagg      300

gatgggttgt attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 611
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 611
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tcctgtgcag cctccggatt cacctttgct tcgtctccga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attggtcggg atggtagtac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccttcg 300

ccttatcggc ggtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 612
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 612
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gattattcga tggtttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attgtgagtc atggtggtac tacatactac 180

gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaag 300

ggttataatg cgcagtattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 613
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 613
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tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttgat 300

tattcgcttc gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 614
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 614
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gattatgata tgatttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attagttcgc atggtgatag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgat 300

gtttttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 615
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 615
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaatggtcg 300

gattcttttg actacagggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 616
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 616
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gattatgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg attcagtcta atggtaatat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctaat 300

tctcaggttg agtattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 617
<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 617
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tcctgtgcag cctccggatt cacctttggg gtggagccta tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaaat attggtcgtg atggttcgat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgggg 300

aagcatggta cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 618
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 618
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg gagtatcgga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatgg attgatgagc ggggttcgct tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaggcgg 300

aagggtacta agcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 619
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 619
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tcctgtgcag cctccggatt cacctttgag ttgtatgcta tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attggtgctg tgggtgagac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggct 300

aataatcttt ctgataatct tgtgtttgac tactggggtc agggaaccct ggtcaccgtc 360

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tcgagc                                                                366


<210> 620
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 620
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct     120

ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac     180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat     240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggtcg     300

gttgagtggt ttgactactg gggtcaggga accctggtca ccgtctcgag c              351


<210> 621
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 621
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttaat agttatacga tgaattgggt ccgccaggct     120

ccagggaagg gtctagagtg ggtctcaagt attaatcctt ggggtagtcg gacatactac     180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat     240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtctg     300

gtgctgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                  348


<210> 622
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 622
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttgat ggtgatatga tgtcttgggt ccgccaggct     120

ccagggaagg gtctagagtg ggtctcatcg attactcagc ttggtagtag gacatactac     180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagaat 300

tggcggactc ttacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 623
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 623
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttaat gcttatggga tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attctttctg atggtgttat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtgct 300

cggggtgcga atttttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 624
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 624
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg cattatatga tggtgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct attacgcctc atggtacgag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatttaat 300

gctattttta gtgaggcgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 625
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 625
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg gattattcta tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccgt cgggtcttac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggtct 300

caggcggtta ctcggtcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 626
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 626
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat ctttatgcga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaatg attgggaggg atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac acggcggtat attactgtgc gaaattggct 300

ggttcgctga ggggtcgttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 627
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 627
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat aaggctagta tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attacgcctc atggttcgtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagcgg 300

tggggtgttg agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 628
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 628
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcag gggtatagta tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgctgggc gtggtggtgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtttg 300

tatatttatc atagtctgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 629
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 629
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggctc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct ggtatggaga tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct attactggga ctggtagtac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttat 300

catccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 630
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 630
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg atggtggcta tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgctcggg atggtaatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagtttcg 300

ccgactggtt ttgactactg ggtcaggga accctggtca ccgtctcgag c 351

<210> 631
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 631
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg catcaggata tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg attacggatg atggtgagag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgat 300

tatgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 632
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 632
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gagtataata tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacag attacgaggg atggttctag gacatactac 180

gcagactccg tgaggggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac tccgcggtat attactgtgc gaaactgtcg 300

aatattgggt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 633
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 633
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gattattcta tgatttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attacgccgt atggttctta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaactgat 300

tatttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 634
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 634
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat acgtatagta tgatgtgggt ccgccaggct 120

ccagggaagg gtcttgagtg ggtctcaact attactcctt atggtagttc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggggt 300

ctggtgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 635
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 635
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgactc 60

tcctgtgcag cctccggatt cacctttact acgggtccta tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagcg attggtattg gggtgatac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtct attactgtgc gaaattgact 300

ccgtctaatc agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 636
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 636
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag cagtatcaga tgatgtgggt tcgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attactcctt ctggtttttt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggaat 300

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ccttttatta gtacgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc        357


<210> 637
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 637
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcct aattatgata tggtttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg atttctgctt tgggtaatgt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaacga acagcctgcg tgccgaggac actgcggtat attactgtgc gaaatggcgt      300

agtgctatta ctggtaattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 638
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 638
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag gagtatcaga tgtcttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaact atttcgccgt cgggtatgaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggcgg      300

tcggttgttc gtccttggcc gggtgtgttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 639
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 639
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat gatgagagta tggcgtgggt ccgccaggct      120
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ccagggaagg gtctagagtg ggtctcatcg attactcctc atggtacttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttcat 300

cttaagttgt atgagtctca ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 640
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 640
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag ggtggtgaga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaatg attccgatgg atggtagtgc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300

agtacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 641
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 641
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat tttatgccga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgggaggg atggtgctta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttgct 300

tcgccggcgc agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 642
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 642
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gatgagccta tgctgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgggggta cgggtacgac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaat 300

cagggtgatt ttattaatcg gtttcactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 643
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 643
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcat gcgtataata tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg atttctccgc ggggttctta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggccg 300

ccgccttcgt ctcattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 644
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 644
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gggtatgaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attacgagtg atggtacgag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300

ctgcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 645
<211> 357

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 645
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag ggttatatga tgtattgggt ccaccaggct      120

ccggggaagg gtctagagtg ggtctcatct atttctcctc agggtcattt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacttcgt      300

gagcttcctc gtctgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 646
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 646
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt agttatgcta tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg attgatgcga gtggtggtcc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgaat      300

gggaagaagt ttccttttac taagtatttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 647
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 647
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcct agtgtgcata tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attaatctga cgggtgttga tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtgct      300
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actactaggc aggcgcatcc gttgtatttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 648
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 648
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag gagggtgaga tgtattgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaacg atttcgacta atggtcttac tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctact      300

cgtgatctgg gttttgccta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 649
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 649
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag gagtatgaga tggcttgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcattt atttctcctc gtggtcattt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggct      300

aagacttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 650
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 650
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat acgtatgaga tgctttgggt ccgccaggct      120
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ccagggaagg gtctagagtg ggtctcacgt atttctgttg atggtagtat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaacgcgg 300

atgcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 651
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 651
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt tcgtatgcta tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaaat atttctcgtg atggttcgaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcgcag 300

tctgggggc ttcggtcggg tttgactacg tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 652
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 652
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag actccggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgggaggg atggtgctta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300

ccgaagggta ttgcgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 653
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

      polynucleotide"

<400> 653
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttagt ccgcatgcta tggcttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcaggt attgatgggg ggggttcgat gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggat   300

cctccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 654
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 654
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgcgcag cctccggatt cacctttcat gcgggggaga tgcattgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatcg attacgctgc ctggtgatat gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgaat   300

actgggtata cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc   354

<210> 655
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 655
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttggg aattatggta tgtcgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagt atttcgtggg atggttctct tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaaatacg   300

cggctttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 656
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 656
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcat gatgcggata tgctgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaggt attttgtctc cgggtgagga tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttggt   300

ctgccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 657
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 657
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcgt actgatcaga tgaattgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagt atttctccta gtggtgcgta tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtctt   300

ggtgcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 658
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 658
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt catctttgag cagtatcaga tggtttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatgg atttcgcctg atggtacgca tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttagt   300

ttgcgtaaga tggagaagtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc   360

<210> 659
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 659
gaggtgcagc tgttggaatc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcag gatgagcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attgcgtctg atggtatgtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc gcaacctggg 300

aagaattttg accactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 660
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 660
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gattatgcga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attactactg gggtgagcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgttgg 300

aatctgtata cggagtcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 661
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 661
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt ggtcagccga tggattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgctcctg atggtattca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatttg 300 ggtcagggtt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 662
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 662
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag cggtatcaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt atttctccta gtggtacgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggaag 300

gcgctttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 663
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 663
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct cattcgacta tgtattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactt attttgccgt cgggtagtcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattttct 300

gatgagcgtt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 664
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 664
gaggtgcagc tgtcggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gatgggaata tggattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt atttctagtg atggtgtgac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagg 300

ggtcaggggt ttgactactg ggtcaggga accctggtca ccgtctcgag c 351

<210> 665
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 665
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cttccggatt cacctttgat gattatatga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attagtccgc atggtgttta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggttg 300

catacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 666
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 666
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg aattatacga tggcgtgggg ccgccaggct 120

ccagggaagg gtctagagtg ggtctcattt attgctggtc cgggtaatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300

agtactgcga cgtataataa tggtcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 667
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 667
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg gagtatagta tggtgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct attagtggga gtggtcgtgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggctt 300

aagctggtta gggctcctaa tccgtttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 668
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 668
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt aattatcaga tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt atttctaaga ctggtcattc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcttcg 300

cattcgttgg ggcctctttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 669
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 669
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg gcgtatagga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgg atttcgcctt ctggttcggg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactttg 300

acggattcgc cgtcggggca ttatgagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 670
<211> 369

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 670
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgcg cggtatgaga tggggtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcacgg attactgctc agggtcttgg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca actccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatctt   300

actgatttta gtagtgggca tcaggagttt gactactggg gtcagggaac cctggtcacc   360

gtctcgagc   369

<210> 671
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 671
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgat gattatggta tgtcgtgggt ccgccaggtt   120

ccagggaagg gtctggagtg ggtctcaggt attagtcata atggtatgtt gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatattgg   300

ccgtctacta gttgggagac tgattttgac tactggggtc agggaaccct ggtcaccgtc   360

tcgagc   366

<210> 672
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 672
gaggtgcagc tgttggagtc tgggggaggc tcggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttggg aatgagccta tggcttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagt attgagatgc agggtaagaa tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagg      300

ggtcaggggt ttgactactg gggtcaggga accctggtca ccgtctcgag c               351


<210> 673
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 673
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatgt attgataatc tgggtagtcc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaaacgatt      300

tctcatcagt atgataggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 674
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 674
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg attgatgagg ggggtcggtg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggacg      300

ccgcataagc agttgtcgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 675
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 675
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cagctttgct gatgagtata tggtttgggc ccgccaggct      120
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ccagggaagg gtctagagtg ggtctcagag attgatccgt tgggtactgg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggg      300

acggcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 676
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 676
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc       60

tcctgtgcag cctccggatt cacctttttct acgcatgata tgatgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg atttctgatg atggtattag tacatactac      180

gcagactccg tgaagggccg gttcaccatt tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctgat      300

atgtctctta ttgagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 677
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 677
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat ggtactccga tggtttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attagtggtg atggtaggaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccttat      300

gcgcttactt cgtctaagcc ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 678
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polynucleotide"

<400> 678
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gattatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgg attcatggga ctggtggtca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctttg 300

gctgatagga gtgggggggt tgttgagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 679
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 679
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gcggagacga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgt attagtaatg atggtaatac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagtct 300

ctgattagtc ctggtctttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 680
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 680
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact ggtgagtata tgaattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attaatgaga ctggttatat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc gaaactttct 300

acgagggggg tgccttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 681
<211> 360

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 681
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttagg tcgtatgata tgggttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaacg atttcgccta tgggtgtttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctaat   300

cagcatgctc atgatccttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc   360

<210> 682
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 682
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttagt gattatgata tgggttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcaagt atttcgccta tgggtacgtt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgct   300

ttgactgagc ctatgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc   357

<210> 683
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 683
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcgt gattatgata tgggttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaact atttctcctc ttggtcattt tacatactac   180

gcagactccg tgaagggccg gtccaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagctgag   300

gaggcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 684
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 684
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60

tcctgtgcag cctccggatt cgcctttcct aggtatggta tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaaat attgatcagt ttggtatgaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagagtat 300

gcttcgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 685
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 685
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aagtatgata tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg atttcgccta tgggtgtttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgg 300

ggtaatactt cggattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 686
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 686
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt aattatgata tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact atttctgggg cgggtcattt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtttt 300

ccgcgtgatg agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 687
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 687
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg aagtatgaga tgaggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagag attggtctgg atggttcgcc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgggg 300

gatccgaatg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 688
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 688
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg actagtgaga tggattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaggt attgggcctg atggtttgac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgcg 300

gattggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 689
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 689
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gagtatgata tgtattgggt ccgccaggct 120 ccagggaagg gtctagagtg ggtctcatgg attgatactg atggtgggga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300

ctgaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 690
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 690
gaggtgcagc tgttggagtc tgggggaggc ctggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccggatt cacctttgag aatgcttcta tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgaggggc agggtaatgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagttcg 300

tcttggtctt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 691
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 691
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg cgtaatgaga tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attacgccga ctggtacgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacggat 300

cctggtaata ggtattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 692
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 692
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 693
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 693
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag gggaccctgg tcaccgtctc gagc 354

<210> 694
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 694
gaggtgcagc tgttggagtc tggtggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 695
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 695
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctcaggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagattccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaacccagg tcaccgtctc gagc 354

<210> 696
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 696
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 697
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 697
gaggtgcagt tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaaggaccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgctaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtaggg 300

aaggagagta attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 698
<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 698
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggc attgagggtc ctggtgatgt tacatactac 180

gcagactcag tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 699
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 699
gaggtgcggc tattggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caactttaat tggcagctga tgggttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcagtat attactgtgc gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 700
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 700
gaggtgcagc tgttggagtc tgggggaggc ttggtacggc ctggggggtc actgcgtctc 60

tcctgtgtag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 701
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 701
gaggtgcagc tgttggagtc tgggggaggc ttggtacaga ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctataat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgatgac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attttgacta ccggggtcac ggaaccctgg tcaccgtctc gagc 354

<210> 702
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 702
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgcaaggct 120

cctgggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 703
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 703
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggcc 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 704
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 704
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtcttgagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta agtttgacta cctgggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 705
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 705
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagaatccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta atcttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 706
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 706
gaggtgcagc tgtttgagtc tgggggaggc tcggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg      300

aaggagagta attctgacta ccggggtcag ggaccctgg tcaccgtctc gagc             354


<210> 707
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 707
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

acctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcgggt attgagggtc ctggtgatgt tacatactac      180

gcagactccg tgaagggccg gttcatcatc tcccgcgaca attccaagaa cacgctatat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg      300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 708
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 708
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac      180

gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccacgaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg      300

aaggagagtg aatttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 709
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 709
gaggtgcggc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc acccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta atcttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 710
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 710
gaggtgcagc tgttggtgtc tgggggaggc ctggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 711
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 711
gaggtgcagc tgttggtgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240

ctgcaaatga acggcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 712
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 712
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 713
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 713
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctca tggggtgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 714
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 714
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcacctga tggggtgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta gttctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 715
<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 715
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tggcacctga tggcctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 716
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 716
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct 120

ccagggaagg gtctcgagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 717
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 717
gaggtgcagc tgttggagtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctga tggcctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 718
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 718
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tggcacttga tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 719
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 719
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctca tggggtgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 720
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 720
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 721
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 721
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tggcagctca tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 722
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 722
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca agtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 723
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 723
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcgggct 120 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtcggg 300

aaggacagca agtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 724
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 724
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtcggg 300

aaggacagca actcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 725
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 725
gaggtgcagc tgttggagtc tgggggaggc ttggcacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca agtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 726
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 726
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300

aaggacgcca agtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 727
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 727
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggcc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300

aaggacaaga actcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 728
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 728
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300

aaggagagca agtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 729
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 729
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg   300

agggacagca agtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 730
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 730
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac   180

gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtcggg   300

aagtacagca actcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 731
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 731
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc   300

aaggacagca ggtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 732
<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 732
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg   300

aaggacgaca gctcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 733
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 733
gaggtgcagc tgttggagtt tgggggaggc ttggtacagc ctggggggtc cttgcgtttt   60

tcctgtgcag cttccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct   120

ccagggaagg gtttagagtg ggtttcaggt attgagggtc caggtgatgt tacatattac   180

gcagattccg tgaagggccg gttcaccatt tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcttgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg   300

agggacagca attccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 734
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 734
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg   300

aaggacagca cctcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc   354

<210> 735
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 735
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg 300

aaggagagca gctcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 736
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 736
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc ttccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggc 300

aaggacagcg cgtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 737
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 737
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtcggc      300

aacgacagct actcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc            354


<210> 738
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 738
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctctggatt cacctttaat tggcagctga tgggttgggt ccggcaggct      120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acggcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg      300

aaggacagca gctcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc            354


<210> 739
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 739
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct      120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcgatat attactgtgt gaaagtgggc      300

aaggacagcg cgtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc            354


<210> 740
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 740
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct      120
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ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300

aaggacgcca agtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 741
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 741
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca ggtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 742
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 742
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca agtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 743
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 743
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300

aaggacgcca agtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 744
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 744
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca ggtcggacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 745
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 745
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca agtccgacta ccggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 746
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 746
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggatgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggtcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctacaaatga acagcctgcg tgccgaggac tccgcggtat attactgtgc gaaagttggg 300

aaggagagta attttgacta cctgggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 747
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 747
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgtag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggcg 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtcggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtttc gagc 354

<210> 748
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 748
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300

aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 749
<211> 360

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 749
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gggtgggaga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgatgagt ctggtcttaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggtgcg 300

ccgcagtatc agattacatt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 750
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 750
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct aattatggga tgtattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatat atttcgcgga ggggtttgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgtcg 300

cattatatga ataatgggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 751
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 751
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgtg gattatacga tggcttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct attagtccga ttggtacttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcct 300

tatgggatgg aggatggtct gacgtggttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 752
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 752
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gcgtatgata tgcagtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaacg attacgtcgg agggtctttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctagt 300

gatttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 753
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 753
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gggtatgata tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact atttctcgtg gggttggtt cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggacg 300

agtcagtcgt ctacggggag ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 754
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 754
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgt cggtatgata tgctttgggc ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcagag atttcgccta cgggtgctct tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttggt      300

tcgacttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 755
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 755
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttttt ccgtattata tgagttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct atttcgggta cgggtgggct tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgacg      300

cagaatgcga cgctttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 756
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 756
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag gtttatacta tggcgtgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcaacg attgatgagt ctggtcgtga tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt      300

gtttggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 757
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 757
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgcg ttttataaga tggggtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaacg attactccta agggtcatca tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttttt      300

aagggtaagg gttggactcg tccgagtggg tttgactact ggggtcaggg aaccctggtc      360

accgtctcga gc                                                          372


<210> 758
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 758
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaat gagtatagta tgatgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct attgggaggc gtggttggct tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgtg      300

ctgctggatt ctactaagtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 759
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 759
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat gagtatccga tgacttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaact atttctgcgc gtggtccttt tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg      300

cattggcttc gtaatggtcg ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 760
<211> 348
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 760
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt atgcagtcga tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attactgatg atggtactag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300

cgggtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 761
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 761
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gcggctgata tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactg attactaatg atggtatttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300

gatcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 762
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 762
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat aagtatagga tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attgatagtt ctggtgagct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagaggtt 300

ccgatgggga atcagacttt ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 763
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 763
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gattatacta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attacgtctc agggtgcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctacg 300

ggtacggatt cgtcgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 764
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 764
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gattatgaga tgtcttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatgt attgggccgg ggggtaagcc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtggat 300

gggcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 765
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 765
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt cagtatgata tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg atttcttcga ggggttggct tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtccg 300

gggggtcgtc ggcggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 766
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 766
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttctg gattatgcga tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaact atttctccga tgggtatggg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagt 300

gctatttcgt ttacttctga tatttctaat tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 767
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 767
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gattatccga tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt atttcttggt ctggttttca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggt 300

gttgcgagga tgcctactgg gattgctttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 768
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 768
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gcttatgaga tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attgatagtg ctggtacttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtct attactgtgc ggaacctttt 300

gggatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 769
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 769
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gagtatccga tgaagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgatcggc agggtgatcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacggtg 300

cggaggggtc ttcctcgtcc gagtcgttat tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 770
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 770
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gattatgata tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaagt atttcgccta tgggtacgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtctg 300

agtgtgtatt cgggtcttga ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 771
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 771
gaggtgcagc tgttggagtc tgggggaggc ctggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttct cattatgata tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcagat attgattata ttggtaagac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tctcgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcttcg 300

gatgaggtgg gtgttaatac ttccaagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 772
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 772
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg cggtatgata tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact atttctccta ctggtgtgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtttt 300

gaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 773
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 773
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gcttatccga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactg atttctcata cgggtcatgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcat      300

tggccttttg actaccgggg tcagggaacc ctgatcaccg tctcgagc                   348


<210> 774
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 774
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc caggggggtc cctgcgcctc       60

tcctgtgcag cctccggatt cacctttgag gatgagtgga tgagttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagat attagcccgg gtggttggac tacatactac      180

gccgactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttat      300

cgtccgtttg atgagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 775
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 775
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggagt cacctttgat gctattgaga tgtcttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcatcg atttcgcgtc atggtgagta tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagatgct      300

tggtctcggc attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 776
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 776
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat agtacggata tgagttgggt ccgccaggct      120
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ccagggaagg gtctagagtg ggtctcaggt attttggata atggtagtaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat      240

ctgcaaatga atagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggggcg      300

agggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 777
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 777
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cttccggatt cacctttggt aggcagagta tgcagtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt attgatgatg atggtttttc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat      300

ccgtggggtt ttgactactg ggtcagggga accctggtca ccgtctcgag c               351


<210> 778
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 778
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtacag cctccggatt cacctttagt gatacgcaga tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggt attgatgatg gggtgtgag tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat      300

cgtcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 779
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 779
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg agtacgacga tggggtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcagtg atttcggatg atggtggttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttgat 300

ggttatggtg tttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 780
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 780
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg agtggggata tgaattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attacgaatg atggtacgtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctgat 300

tctgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 781
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 781
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gcttatgcta tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatat attagtccga atggtacggc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatatgtg 300

gggatgcgtt ggaattcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 782
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 782
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt caccttttcg agttatgaga tggcttgggt ccgccaggct       120

ccagggaagg gtctagagtg ggtctcatct attacgagtc ttggtacttc tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt       300

aggaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348


<210> 783
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 783
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt cacctttaat gagtatgaga tgacgtgggt ccgccaggct       120

ccagggaagg gtctagagtg ggtctcaacg attactagtg agggtagtgg gacatactac       180

gcagactccg taaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctaat       300

ggtaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348


<210> 784
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 784
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt caccttttct gattatgaga tgttgtgggt ccgccaggct       120

ccagggaagg gtctggagtg ggtctcaact attactagtg agggtcattc tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggg       300

acttcgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348


<210> 785
<211> 348
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 785
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gattatgaga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgattctg atggtagttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300

gtgaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 786
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 786
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag gattatgaga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct atttcttcta ctggtcagtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300

aataagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 787
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 787
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttctt gattatggta tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct atttcgcctc ttggtcttag tacatactac 180

gcagactccg tgaagagccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaggtg 300

agggtgggta ggggtgttca tcctccgaag tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 788
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 788
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat ttgtatgaga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attactagtg atggtgtttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggg 300

gtgatttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 789
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 789
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag aattatgcta tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgctccgc tgggtgttcc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaagaag 300

gttggggcgt ggctgcagtc gcggagtttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 790
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 790
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatg gattatgaga tgcattgggt ccgccaggct 120 ccagggaagg gtctagagtg ggtctcaacg attggtgctt ctggtcatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatctt 300

gatatgctgc tgtttgggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 791
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 791
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gagtatgaga tgatgtgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacgt attgctggta atggttctcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gataatgctt 300

tctcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 792
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 792
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttat aattatgata tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgattcga tgggtcttgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggtct 300

aatgcgagtg attgggttgt tttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 793
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 793
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg tcgtatcata tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attgcggata cgggtgatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac actgcggtat attactgtgc gaaattgcgt 300

gggatggctc gggtttgggg gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 794
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 794
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt tattatgata tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg gatctcatct atttcggatc gtggtcttca gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatttacg 300

gagattccgt tggattggtt ggaggtgttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 795
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 795
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg agttataaga tgttgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attactaatt ctggtactga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgatg 300

tatccggatt tggagattgt gcattttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 796
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 796
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag acttatcgta tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagct attgatcagg agggttctgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatagt 300

gggacgaggc cggggcttcg gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 797
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 797
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60

tcctgtgcag cctccggatt cacctttagt agttatgata tgctttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacgg attgatgcga gtggttattt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaattgttg 300

aagctgtcgt tgaatcctaa ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 798
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 798
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120 ccagggaagg gtctagagtg ggtctcatcg attcataata ctggtttgtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggact 300

cagcatcgtt ttgttgtttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 799
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 799
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag ggttatccta tgtcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attagtcctt tgggtcctga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaactgttg 300

atgggggagt atttgaattc taggacgttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 800
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 800
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat acgtatagta tgtcttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatgg attgatgctg atggttgggt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaactggg 300

catacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 801
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 801
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg gatggggaga tgggttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagg attgtggatc ctggtgattc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300

gatcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 802
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 802
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct gagtatgaga tgaagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attactccgt cgggtggtca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gatacctctt 300

tctagttttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 803
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 803
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct aattatgtga tgatttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactt attaatggtg ctggtgatat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggggt 300

gcgcgttcgt ttggggttcc gcctaatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 804
<211> 348

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 804
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttacg gatggggaga tgggttgggc ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagg attgtggatc ctggtgattc tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt   300

gatcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 805
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 805
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgtag cctccggatt cacctttacg ctgtataata tgtcttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcagtt atttctagta agggtgatag tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaacgagt   300

agtgtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 806
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 806
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgag gcgtattata tgagttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaggt attgttaata atggtttgtt gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggct   300

gttcatcctt cgtatagggc ggagttgttc gactactggg gtcagggaac cctggtcacc   360

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gtctcgagc                                                          369


<210> 807
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 807
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt tcgtatgaga tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcacgt attgagcctg atggtagtaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtccg      300

gataatttta ctatgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 808
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 808
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaat aagtatatga tggggtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct attgatagtc ttggtcatta tacatactac      180

gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcggag      300

tttccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 809
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 809
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgacgtgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 810
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 810
gaggtgcagc tgttggagtc tgggggaggc atggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcagggaacc caggtcaccg tctcgagc 348

<210> 811
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 811
gaggtgcagc tgttggagtc tgggggaggc atggtgcagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 812
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 812
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgcaaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccgagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt 300

actgagtttg actattgggg tcagggtacc ctggtcaccg tctcgagc 348

<210> 813
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 813
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggacccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 814
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 814
gaggtgcagc tgttggagtc gggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcgtgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240

ctacagatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggacccgttt 300

actgagcttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 815
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 815
gaggtgcagc tgttggagtc tgggggaggc ttggtacggc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atttctgtgc agatccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 816
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 816
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cgcctttaag aggtatgaga tgacatgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcatatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt 300

actgagattg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 817
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 817
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cccctttaag aggtatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actaccgggc tcagggaacc ctggtcaccg tctcgagc 348

<210> 818
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 818
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgtcgtgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcttct atttcgtcgg atggttcttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt   300

actgagattg actactgggg tcagggaacc caggtcaccg tctcgagc   348

<210> 819
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 819
gaggtgcagc tgttggagtc tgggggaggc ttggtacatc ctggggggtc cctgcgtctc   60

tcctgtgcag cttccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgacgaggat accgcggtat attactgtgc ggaaccgttt   300

actgagtttg actacggggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 820
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 820
gaggtgcagc tgttggagtc tgggggaggc tgggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctcaggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt   300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 821
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 821
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 822
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 822
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cactctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagattg actaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 823
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 823
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aagtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

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actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc                  348


<210> 824
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 824
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttaac agctatgaga tgatgtgggt ccgccaggct     120

ccagggaagg gtctagagtg ggtctcatct atttcgtcgg atggttcttt tacatactac     180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat     240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt     300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc                  348


<210> 825
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 825
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct     120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac     180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat     240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccattt     300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                  348


<210> 826
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 826
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct     120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac     180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggacccgttc 300

acggagatgg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 827
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 827
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggacccgttc 300

acggagttcg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 828
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 828
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggagccgttc 300

acggagttgg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 829
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 829
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggcc 120

ccagggaagg gtctggagtg ggtctcatcg atttcgtccg acggttcctt cacgtactac 180

gccgagtcgg tcaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 830
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 830
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac acgtatgaga tgcagtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 831
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 831
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaac aagtatgaga tgatgtgggc ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 832
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 832
gaggtgcagc tgtcggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 833
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 833
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccagact 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcagtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcaagc 348

<210> 834
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 834
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctggaaatga acagcatgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg acaactgggg tcagggaacc ctcgtcaccg tctcgagc 348

<210> 835
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 835
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc agaaccgttt 300

actgagtttg actactgggg tcagggaacc caggtcaccg tctcgagc 348

<210> 836
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 836
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caactttaag aggtatgaga tgacgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc agacccgttt 300

actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 837
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 837
gaggtgcagc tgttggagtc tgggggagac ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actacagggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 838
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 838
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaag aggtatgaga tgtcgtgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt   300

actgagtttg actactgggg tcggggaacc ctggtcaccg tctcgagc   348

<210> 839
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 839
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgag gcgtatccta tgtcgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagt atttcccctc ttggtttgtg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttagt   300

gctggggcgg agactcatgt ttatcggctt tttgactact ggggtcaggg aaccctggtc   360

accgtctcga gc   372

<210> 840
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 840
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttggt aattatgaga tgatgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatct attggggtgt tgggtcatac gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttatg 300

tcgttgagga cgtttgagaa tctttttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 841
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 841
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg aagtatccta tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attgatgcta atggtaatag gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggact 300

tggcgtaggc attttgcgat tttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 842
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 842
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat ctgtatgata tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct atttctgatc tgggtacgct tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatggt 300

tttagggtta cgagtaatga tcgtaggttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 843
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 843
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact ggtggggata tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaatg attgagggtg gtggtgtgac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacttgat 300

cttcggacgg gtcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 844
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 844
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 845
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 845
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcatctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat atttctgtgc ggatccgtcg 300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 846
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 846
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg   300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc   354

<210> 847
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 847
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga gcagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg   300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc   354

<210> 848
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 848
gaggtgcagc tgttggagtc tgggggtggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttcccg gcttatacta tgggttgggt ccgccaggct   120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgtcgaggac accgcggtat attactgtgc ggaaccgtcg   300

gatcctacta tgtttgtcta ctggggtcag ggaacccttg tcaccgtctc gagc   354

<210> 849
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 849
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcg gcttatacta tgggctgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctctctt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300

gatcctacta tgtttgtcta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 850
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 850
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag catccggatt cacctttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtca 300

gatcctacta tgtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 851
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 851
gaggtgcagc tgttggagtc tgggggggc atggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcatgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg 300 gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 852
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 852
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtcacactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300

gatcctacta tgtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 853
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 853
gaggtgcagc tgttggagtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgcgc ggaaccgtcg 300

gatcctacta agttagacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 854
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 854
gaggtgcagc tgtcggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

acctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg 300

gatcctacta agtttgtcta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 855
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 855
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc agatccgtcg 300

gatcctacta agtttgtcta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 856
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 856
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgcgc ggaaccgtcg 300

gatcctacta agtttgtcta ctggggtcag ggaaccccgg tcaccgtctc gagc 354

<210> 857
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 857
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttcg gcttatacta tgggttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcgctt attggggatc gtggttcttg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa catgctgtat      240

ctgcaaatga aaagcctgcg tgccgaggac accgcggtat attactgcgc ggatccgtcg      300

gatcctacta agtttgtcta ctggggtcaa ggaacccagg tcaccgtctc gagc            354


<210> 858
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 858
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcg gcttatacta tgggttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180

gcagactccg tgaagggccg gttcaccatc ttccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg      300

gatcctacta agtttgtcta ctggggtcag ggaaccctgg tcaccgtctc gagc            354


<210> 859
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 859
gaggtgcagc tgttggagtc tgggggaggc ttgttacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcg gattatacta tgggttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg      300

gatcctacta agttcgacta ctggggtcgg ggaaccctgg tcaccgtctc gagc            354


<210> 860
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polynucleotide"

<400> 860
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcc 300

gatcctacta agtttgtcta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 861
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 861
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggtacttg gacatattac 180

gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat 240

ctgcaaatga acagcctgcg tgccgaggac actgcggtat attattgtgc ggatccgtcg 300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 862
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 862
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 863
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 863
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120

ccagggatgg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300

gatcctacta agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 864
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 864
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ccggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aattataaga tgtattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaagt atttcggaga taggtaatct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatagctctg 300

acgcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 865
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 865
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg agttatcgta tgtattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatat attgatccgc cgggtagtcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtttg 300

aatttgtcgt ttccttatat taattttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 866
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 866
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgag cggtatgaga tgctgtgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcacgt atttctcatt cgggtcggac gacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaattggat   300

ggtccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 867
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 867
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttaag aggtattata tggattgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaagg attaatcata atggttctgt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaatgccg   300

cagggtactt ctgattggta ttattttgac tactggggtc agggaaccct ggtcaccgtc   360

tcgagc   366

<210> 868
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 868
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt caccttttct aagtatgata tgtcttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaact attctggagg atggtctgac tacatactac   180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300

cgtttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 869
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 869
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt caccttttcg gattatccta tgacgtgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcaact attctgtctc cgggtacgga gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgag      300

aaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 870
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 870
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag ggtggtgaga tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaatg attccgatgg atggtagtgc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt      300

gaggtgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 871
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 871
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60
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tcctgtgcag cctccggatt cacctttagg gagtatcata tgaagtgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attagtaggg atggtatgaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatacagctt      300

gctttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 872
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 872
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc       60

tcctgtgcag cctccggatt cacctttcgt gattatgaga tgctttgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggt attcttccgt cgggtggggc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggt      300

tcggggaatg ggcctattct tttgactac tggggtcagg gaaccctggt caccgtctcg       360

agc                                                                    363


<210> 873
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 873
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag gagcatgata tgttttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggg attggggctg agggtgtttg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgacg      300

atgtctaatg gttctcagtc gcgttttgac tactggggtc agggaaccct ggtcaccgtc      360

tcgagc                                                                 366


<210> 874
<211> 369
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 874
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 875
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 875
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtttcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 876
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 876
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc ccttcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acaacctgcg tgccgaagac accgcggtat attactgtgc gaaaattcgt 300 aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 877
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 877
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca atttcaagaa cacgctgtat 240

ctgcagatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 878
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 878
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagattccg tgaagggccg gttcaccatc tcccgcgaca attccatgaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 879
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 879
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cttgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aacactgaga tggcttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 880
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 880
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccgggtt cacctttgat aatactgaga tggcttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 881
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 881
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc caggggggtc cctgcgtctc 60

tcctgtgcag cctctggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cgcgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtctgggaac cctggtcacc 360

gtctcgagc 369

<210> 882
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 882
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 883
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 883
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcctggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa caggctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggcac cctggtcacc 360

gtttcgagc 369

<210> 884
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 884
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaaattcgt      300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctcgtcacc      360

gtctcgagc                                                              369


<210> 885
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 885
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgaggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt      300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 886
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 886
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaggt attagtgagg atggtaatcg tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgcagaggac tccgcggtat attactgtgc gaaaattcgt      300

aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 887
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 887
gaggtgcagc tgttggagtc tgggggaggc ttggtagagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

cctgggaagg gtctcgagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga gcagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 888
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 888
gaggtgcagc tgttggagtc tgggggaggc ctggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attagtgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 889
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 889
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gctgactccg tgaagggccg gttcatcatc tcccgcgaca attccaagaa cacgctgaat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

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gtctcgagc                                                            369


<210> 890
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 890
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc     60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct    120

ccagggaggg gtctagagtg ggtctcaggt gttactgagg atggtaatcg tacatactac    180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt    300

aatctgcatt gggatgtggg gaggcaattt gactactggg gtcagggaac cctggtcacc    360

gtctcgagc                                                            369


<210> 891
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 891
gaggtgcagc tgttggagtc agggggaggc ttggtacagc ctggggggtc cctgcgtctc     60

tcctgtgaag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct    120

ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac    180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat    240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attattgtgc gaaaattcgt    300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc    360

gtctcgagt                                                            369


<210> 892
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 892
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc     60
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tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtgatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagag ctcgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctccagc 369

<210> 893
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 893
gaggtgcagc tgttggagtc tgggggaggc tcggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cactctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 894
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 894
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg tcggctgaga tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggt atttcgaggc ctggtcaggt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 895
<211> 357

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 895
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat gatggtacta tggggtgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcactt attttgccgt cgggtagtcg tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacattcg      300

ctgactaatc gtccgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc         357


<210> 896
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 896
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt aagtatgata tgcggtgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagat attgatgctg ttggtactcg gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gataccgggg      300

gggacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 897
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 897
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag atgtatggta tgatgtgggc ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatct attgagggtg cgggtcatgc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac actgcggtat attactgtgc gatagtgctt      300

ggtatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348
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<210> 898
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 898
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctcgggatt cacctttttg cagtatccga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact atttctcctg ttggtttgac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaattgttt 300

gaggggtcga ggattcagcg tgatgtgggt tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 899
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 899
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag aagtatcaga tgggttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attcgggggt ctggtcttgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgcat 300

actacgctgc atacggaggt gattgggttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 900
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 900
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc cggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt cagtatacga tgtattgggc ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcagag atttctcata gtggttctaa tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatcgggg      300

ctgcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                  348


<210> 901
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 901
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt caccttttcg gattatgcga tggcttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcacgt attggtgtgg agggtgggga tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgttg      300

cggctttatc gtctggggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 902
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 902
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgct aagtatgata tgacgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaaag attaattctg atggtggtct tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggttg      300

catggtaggg ggtttgttat ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 903
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polynucleotide"

<400> 903
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg cggtatgata tggtgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacgg attaattcta tgggtctggc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagattat 300

tcggttgcgc cgcatgggta tcctttgggt tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 904
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 904
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag gattattcga tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attactgata atggtacgtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatatg 300

tcgcttgcta cttatctgca gttttttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 905
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 905
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatg gagtatgata tgctttgggt ccgccaggct 120

ccagggaagg ctctagagtg ggtctcacgt atttcgtcgg atggtctttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300

agtgcgcttg ctccttttga tattggtttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 906
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 906
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag gagtataata tggcttgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaagt attaattttg ctggtcggac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactgtct 300

cttcctttgg atattttttc ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 907
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 907
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 908
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 908
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240

ctgcgaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttattatg aatactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 909
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 909
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60

tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttattttg aatactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 910
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 910
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggcc 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

agttattttg aatactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 911
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 911
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccgggtt cacctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttattatg agtactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 912
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 912
gaggtgcagc tgttggagtc tgggggaggc ttggtccagc ctggggggtc cctgcgtctc 60

tcctgtgctg cctccggatt cgcctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttattttg aatactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 913
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 913
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tatatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300

ggttactttg aatactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 914
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 914
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg gagtatgtta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attaatggtt tgggtaatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggag accgcggtat attactgtgc gatacagctg 300

cctaattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 915
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 915
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt aatgatggga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcattt attaatgttg atggtaggga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaatggtct 300

cctgggcggg ttcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 916
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 916
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt ggttgggata tggcgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attgctcatg agggtggtga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatgtt 300

cctgggtctc ctctgtttga ctactggggt cagagaaccc tggtcaccgt ctcgagc 357

<210> 917
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 917
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat cagggttgga tgtattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaggg attggttcga atggtcctcg gacatcctac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgggg 300

gagtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 918
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 918
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg cagagtgata tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagtt attggtaata atggtgagtt tacatactac 180

gcagactcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagataat 300

tggctgttgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 919
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 919
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat cttagtacta tgtattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attggtgggg atggtagtca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaggtacg 300

cagtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 920
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 920
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gcgtatacga tggagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attggggtta cgggttatga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtggt 300

cagggttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 921
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 921
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gattatggga tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatat attgatcctc tgggtcgtct tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagatttg 300

tcgtcgctgc agtatggggt gtcgcctaat tttgactact ggggtcaggg aaccctggtc 360

accgtctcga gc 372

<210> 922
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 922
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttt cattattcta tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attggtccgg ttggtcggga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatgatt      300

cagtcgccgt tgtttaagga ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 923
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 923
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag tggtatgata tgtattgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcacgt attgatagtg gggtaatca gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcgtcg      300

ctttggaagt ggaggttgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 924
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 924
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag gagtatggta tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaact atttctccgc tgggtatttc gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgct      300

acgtctcagg agtctttgcg gtcttttgac tactggggtc agggaaccct ggtcaccgtc      360

tcgagc                                                                 366


<210> 925
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 925
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttagt aagtatgaga tgatgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcct      300

ctgcctgatg cgttttggac taggggtttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 926
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 926
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttggt acttattcta tggcgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaact attgatcggc atggtttggc tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactcct      300

ggttcttctt ggcagactgt tttggctac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363


<210> 927
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 927
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag tcgtatccta tgggttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaagt attgatcatc atggtcattc gacatactac      180

gcagactccg cgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgctt      300

agggtttcga tgatttttgg ttttgactac tggggtcagg gaaccctggt caccgtctcg      360

agc                                                                    363
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<210> 928
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 928
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgtg cagtatggga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgg attagtagta gtggtacgta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctacg tgccgaggac accgcggtat attactgtgc ggaaacgtct 300

aggatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 929
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 929
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcgg cctccggatt cacctttcgg gagtatgata tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactt atttcgcctc ctggtcgtac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagttgtg 300

attctgggtt atacgaatag gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 930
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 930
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct aattacggga tgttgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attaattctt cgggtatgga gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatttttt      300

cgtctgaatg atcataattc tgtgtttggt tttgactact ggggtcaggg aaccctggtc      360

accgtctcga gc                                                          372


<210> 931
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 931
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttaag gattataaga tgatgtggat ccgccaggct      120

ccagggaagg gtctagagtg ggtctcatcg attgttgggt ctggttcgat gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcct      300

ggttattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348


<210> 932
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 932
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcat aattatgcta tggggtgggt ccgccgggct      120

ccagggaagg gtctagagtg ggtctcaagt attgatgagc atggtactat tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagt      300

ctggatcggg tttggatttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 933
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 933
gaggtgcagc tgttggagtc tggggggggc ttggtacagc ctggggggtc cctgcgtctc       60
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tcctgtgcag cctccggatt cacctttgct gattatccga tgacttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt atttattctg cgggttctcc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaactttat 300

catcgggagc cgattctttt tgggtttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 934
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 934
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag aggtatcaga tggcgtgggt ccgccaggct 120

ccggggaagg gtctagagtg ggtctcaacg attagttctg atggtggggg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300

catcggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 935
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 935
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt tcttatacta tgatgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagag attgatcgga cgggtgagcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacctggg 300

tttgcttctc ttccttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 936
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 936
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttacg gattatacta tgtattgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaaag atttctccga gtggtcgttc tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatccg   300

tttgggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc   348

<210> 937
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 937
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttgat gatgcggaga tgttttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcatct attgatgctc gtggtttgac gacatactac   180

gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcgacg   300

tcggctatgt atccttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc   357

<210> 938
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 938
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60

tcctgtgcag cctccggatt cacctttcgt gattatgata tgggttgggt ccgccaggct   120

ccagggaagg gtctagagtg ggtctcaact atttctcctc ttggtcattt tacatactac   180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatctggg   300

tttcatgagt atactgaggg gtttgactac tggggtcagg gaaccctggt caccgtctcg   360

agc   363

<210> 939
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 939
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat cgtgcgggta tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcactg attgggcgtg gtggtgatat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 940
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 940
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt cgttatcaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct atttcttctg atggtggggg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgtct 300

cgtcggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 941
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 941
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtt cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag ttgtatccga tggcgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatcg atttctccgg ttggttttct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggcat 300

gaggggtcgt atactccgcg gtcggctttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 942
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 942
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgtg gcgtatccta tggcgtgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcaact attgcgcctc tgggtggtaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacggccg 300

gaggggctgc agattgattc tcagaatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 943
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 943
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg ttgtatcaga tggcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attgattctt ctggtagtga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgag 300

cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 944
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 944
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg cagtaccaga tggcttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgcgtcgg atggtgtttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggt 300

cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 945
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 945
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag cagtatgata tgaggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatgg attgatgagg cgggtcatga gacatactat 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg 300

gatgggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 946
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 946
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgtt gattatccga tgggttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg atttctacgg ggggtttttc gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgcgg 300

tattattatc ttagtcagat taagaatttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 947
<211> 360
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 947
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgat atttatggga tgacttgggt ccgccaggct      120

ccagggaagg gtctggagtg ggtctcaagt atttcgcctc ttggtcttgt tacatactac      180

gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactgaag      300

gagcatgggg atgttccttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360


<210> 948
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 948
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttgag ctttatccga tgagttgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaact atttctccta cgggtttgtt gacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttaag      300

aggagtggga agactgatga tactaatttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 949
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 949
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc       60

tcctgtgcag cctccggatt cacctttcgg gagtatgata tgctgtgggt ccgccaggct      120

ccagggaagg gtctagagtg ggtctcaacg attgtggggg atggtaatgg tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacaggat      300

cgtcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                   348
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<210> 950
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 950
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt cacctttgag gagtatggta tgagttgggt ccgccaggct       120

ccagggaagg gtctagagtg ggtctcaacg atttcgccta ttggtgttac tacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatgct       300

tatgatcgga agtctaattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc       360


<210> 951
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 951
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt cacctttgat cggtatgtga tggtgtgggt ccgccaggct       120

ccagggaagg atctagagtg ggtctcaggt attactccga gtggtaggag gacatactac       180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagga cacgctgtat       240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgttg       300

gggcgtcatt ttgatcctct tctgccttcg tttgactact ggggtcaggg aaccctggtc       360

accgtctcga gc                                                           372


<210> 952
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 952
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc        60

tcctgtgcag cctccggatt cacctttgag gattatgcta tgagttgggt ccgccaggct       120

ccagggaagg gtctagagtg ggtctcaact attactccgg gtggtttttg gacatactac       180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaacgtct      300

agtggggagt tgcagttggt tgaggatttt gactactggg gtcagggaac cctggtcacc      360

gtctcgagc                                                              369


<210> 953
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 953
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Lys His Ser
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Arg His Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 954
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 954
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20                  25                  30
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Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Ala Leu Phe Pro Tyr
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 955
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 955
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln His Ile Gly His His
            20   25   30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr His Arg Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Trp Asp Arg Pro Pro Tyr
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 956
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

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<400> 956
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Arg Ala Val Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 957
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 957
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Arg Phe Ser Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
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<210> 958
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 958
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ala Arg Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 959
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 959
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn His Arg
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
```

65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Val Arg Pro Asn
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 960
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 960
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20   25   30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Ser Pro His
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 961
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 961
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20   25   30

```
Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ala Val Arg Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 962
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 962
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly His Arg
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Tyr Arg Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 963
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 963
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Pro Met
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Gly Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Ser Ile Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 964
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 964
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
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<210> 965
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 965
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Ile Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 966
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 966
Asp Ile Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 967
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 967
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 968
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 968
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30
```

```
Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Thr Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 969
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 969
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 970
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 970
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Lys Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 971
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 971
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Arg Gly Thr Lys Val Val Ile Lys Arg
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            100                 105


<210> 972
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 972
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 973
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 973
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Met Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Thr Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 974
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 974
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Tyr Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Lys Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 975
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 975
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
```

```
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Val Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Val Ile Lys Arg
            100                 105


<210> 976
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 976
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 977
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 977
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Thr Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 978
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 978
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Asp Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Val Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95
```

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 979
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 979
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 980
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 980
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Glu Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Ser Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 981
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 981
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Arg Val Glu Ile Lys Arg
            100                 105


<210> 982
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 982
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 983
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 983
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Ile Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 984
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 984
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Val Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
            100                 105


<210> 985
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 985
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Asp Pro Asp
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95
```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 986
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 986
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Pro Asp
20 25 30

Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gln Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 987
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 987
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Met Pro Ile Gly Pro Asp
20 25 30

Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly

```
    50                  55                  60


Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 988
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 988
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Thr
            20                  25                  30


Leu Thr Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Gly Ser Glu Leu Gln Ser Gly Val Pro Pro Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Cys Ile Ser Ser Pro Cys
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 989
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 989
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Ile Gly Asp Ser
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Phe Ser Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Thr Ser Pro Thr
                85                  90                  95


Thr Phe Gly Arg Gly Thr Lys Val Lys Ile Lys Arg
            100                 105


<210> 990
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 990
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr His Gly Tyr Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 991
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 991
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Met Ile Asp Gln Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Gly Tyr Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 992
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 992
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Tyr Thr Ser
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


His Tyr Gly Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Val His Gln Ala Pro Thr
                85                  90                  95
```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 993
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 993
Asp Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ile Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Leu Ser Ser Ser Met Pro His
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 994
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 994
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

```
Tyr Asp Ser Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Gln Asn Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 995
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 995
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Arg Gln
            20                  25                  30


Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Thr Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gln Ser Lys Gly Pro Leu
                85                  90                  95


Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 996
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 996
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Thr Asp
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Met Gly Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 997
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 997
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Glu Glu Met
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Phe Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His His Thr Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 998
<211> 108
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 998
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Met Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Lys Leu Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 999
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 999
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Met Asp Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Lys Leu Pro Val
```

```
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1000
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1000
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1001
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1001
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Asp Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Ser Ala Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Leu Leu Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1002
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1002
Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Lys Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Thr Asn Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1003
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1003
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

```
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Glu Ala Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Ser Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Met Ser Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1004
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1004
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Ser Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Met Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Asp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1005
<211> 108
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1005
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asp Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Ser Ser Phe Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1006
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1006
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Glu Gly Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His His Leu Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1007
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1007
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Thr Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Arg Trp Ile Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1008
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1008
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Asp Ala Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1009
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1009
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Thr Thr Ser
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Val Thr Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1010
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1010
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile His Thr Asn
            20   25   30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ala Asn Pro Val
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
            100   105

<210> 1011
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1011
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile His Thr Asp
            20   25   30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Val Ser Pro Val
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 1012

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<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1012
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Asn Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Leu His Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1013
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1013
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Arg Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Tyr Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1014
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1014
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Glu Ser Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Ala Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Gln Trp Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1015
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1015
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Gly Asn Thr
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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        35                  40                  45


Tyr Leu Ser Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Lys Lys Pro Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1016
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1016
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Lys Asn Arg
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Glu Val Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Arg Gln Ser Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1017
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1017
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Gly Glu Glu
            20                  25                  30


Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Thr Leu Gln Ser Glu Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln His
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Glu Trp Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1018
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1018
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Ser Gly Gly
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Thr Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Ser Ala Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

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<210> 1019
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1019
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Gln Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Val Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Met Asn Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1020
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1020
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Gln
            20                  25                  30


Leu Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Leu Arg Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1021
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1021
Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Ser Thr Ser
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Glu Tyr Asn Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1022
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1022
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Gly Glu Ser
            20                  25                  30
```

```
Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Phe Ala Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His His Met Leu Pro Ser
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1023
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1023
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Ile Gly Asp Ser
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Phe Ser Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Met Asp Ile Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1024
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1024
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp His Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Ile Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1025
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1025
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gln Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Leu Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

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<210> 1026
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1026
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr His Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Phe Asn Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1027
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1027
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Cys Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Gly Leu
            20                  25                  30


Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Gly Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
```

```
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Lys Ala Phe Glu Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1028
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1028
Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly His Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asn Val Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser His Asn Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1029
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1029
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln His Ile Glu Asn Asp
            20                  25                  30
```

```
Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Leu Gln Pro Thr
                85                  90                  95


Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1030
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1030
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Glu Gly Ser
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Arg Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gln Leu Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1031
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 1031
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Asn Gly Lys
            20                  25                  30


Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ala Phe Ala Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Gln Ala Val Tyr Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1032
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1032
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Tyr Gln Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

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<210> 1033
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1033
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Glu His Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Gln Gln Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1034
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1034
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Gln Ile Glu Glu Ser
            20                  25                  30


Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ala Asp Val Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Val Val Glu Pro Arg
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1035
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1035
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Tyr Ile Gly Leu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Arg Gln Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1036
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1036
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
            20                  25                  30
```

```
Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1037
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1037
Asp Ile Gln Leu Thr Gln Ser Pro Thr Ser Leu Ser Ala Thr Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg His Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1038
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1038
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
            100                 105


<210> 1039
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1039
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Val Ser Thr Pro Ile Gly Thr Met
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Pro Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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            100                 105


<210> 1040
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1040
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Cys Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1041
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1041
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
            20                  25                  30


Ile Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Val Arg Pro Pro Ala
                85                  90                  95


Thr Phe Gly Lys Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1042
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1042
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Tyr Ile Asp Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Val Val Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1043
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1043
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
```

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            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Val Asp Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Asp Arg Trp Ser Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1044
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1044
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Arg Ile Gln His Met
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly His Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ser Cys Ala Trp Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1045
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1045
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Gly Ile Asp Gly Asp
            20                  25                  30


Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ala Asp Ser Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Ala Val Arg Pro Met
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1046
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1046
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Gly Ile Asp Thr Asp
            20                  25                  30


Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ala Asp Ser Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Ala Val Arg Pro Met
                85                  90                  95
```

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1047
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1047
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Tyr Thr Ile Pro Val Ala
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ala Asp Ala Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Trp Pro Gly Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1048
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1048
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ala Thr Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Thr Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Tyr Asn Pro Ser
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1049
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1049
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Val Pro Ile Thr Glu Gly
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gln Ala Asn Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Glu His Val Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1050
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1050
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Met Ile Leu Tyr Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Thr Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Glu Thr Val Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1051
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1051
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Asn Gly Leu
            20                  25                  30


Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Met Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ala Arg Ile Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
            100                 105


<210> 1052
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1052
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Leu Ile Arg Thr Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gln Ser Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Asp
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1053
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1053
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Ser
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Phe Gly Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu His Thr Pro Ser
                85                  90                  95
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1054
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1054
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Glu Ala Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr His Ser Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Phe Asn Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1055
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1055
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Glu Tyr Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Gly Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
```

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    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Glu Val Gln Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1056
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1056
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Asp Thr Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1057
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1057
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Trp Ile Gly Met Ser
            20                  25                  30


Leu Glu Trp His Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Arg Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Arg Trp Pro Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1058
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1058
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Ser Asn Ala
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Leu Gly Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Thr Gln Val Trp Asp Arg Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1059
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1059
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Met Ser Ala
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Thr Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Leu Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1060
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1060
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Gly Ile Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ser
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ala Ser Asn Pro Pro
                85                  90                  95
```

```
Thr Phe Gly Arg Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1061
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1061
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Met Ile Gly Asp Trp
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Arg Ser Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Phe Trp Pro Arg
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1062
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1062
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Leu Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Val Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1063
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1063
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu His Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
                85                  90                  95


Thr Tyr Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1064
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1064
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Ala Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Phe
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Gly Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Val Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1065
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1065
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Thr Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1066
<211> 108
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1066
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu His Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1067
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1067
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu His Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
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                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1068
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1068
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Ser Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Val Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1069
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1069
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu His Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
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```
Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1070
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1070
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asp Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1071
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1071
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Glu Asp
            20   25   30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35   40   45

Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 1072
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1072
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Glu Asp
            20   25   30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35   40   45

Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gln Tyr Pro Pro
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 1073
<211> 108

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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1073
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Glu Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85                  90                  95


Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1074
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1074
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
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```
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1075
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1075
Glu Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Ser Ile Asp Lys Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Trp Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85                  90                  95


Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1076
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1076
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Glu Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45
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```
Tyr Ser Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Lys Gln Tyr Ser Gln Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1077
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1077
Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Lys Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Trp Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1078
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1078
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Tyr Ile Asn Ala Glu
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Ala Met Trp Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1079
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1079
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Leu Asp Ile Asn Asn Gly
            20                  25                  30


Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Leu Gly Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Val Arg Ser Arg Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1080
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<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1080
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Leu Ser Ala
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Ser Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Tyr Ser Leu Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1081
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1081
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Glu Ser Tyr
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Arg Tyr Val Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Phe Arg Ala Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1082
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1082
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Val Ser Glu Ser Ile Asn Ala Glu
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ser Gly Phe Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Phe Ala Met Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1083
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1083
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Met Met Ile Arg Phe Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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        35                  40                  45


Gly Gly Gly Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln His Glu Arg Trp Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1084
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1084
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Leu
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Leu Thr Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Val Tyr Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1085
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1085
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ser Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Lys Val Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1086
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1086
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His His Ile Gln Arg Tyr
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Trp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Trp Ala Pro Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1087
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1087
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His His Ile Gln Arg Tyr
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Leu Trp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Trp Ala Pro Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1088
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1088
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Asp Ile Gln Arg Tyr
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Leu Trp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Trp Ala Pro Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1089
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1089
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Tyr Ile Asp Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Ala Val Val Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1090
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1090
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ala Phe Asp
            20                  25                  30
```

```
Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Leu Gln Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1091
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1091
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ala Thr Leu
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Trp Gln Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1092
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1092
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Val Asp Glu
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Trp Ser Thr Tyr Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1093
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1093
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Asp Gly Val Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Asp Trp Asp Trp Pro Arg
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

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<210> 1094
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1094
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Arg Asp Trp
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Asp Trp Gly Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Thr Trp Asp Asp Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1095
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1095
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Arg Asp Trp
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Asp Trp Gly Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
```

```
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Thr Trp Tyr Asp Pro Leu
                85                  90                  95


Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1096
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1096
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ile Asp Ile His Gly Gly
            20                  25                  30


Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Val Gly Val Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Val Trp Arg Arg Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1097
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1097
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser
            20                  25                  30
```

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Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ser Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ala Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1098
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1098
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gln Ile Glu Thr Asn
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Tyr Leu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1099
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      polypeptide"

<400> 1099
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ala
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Leu Gly Ser Asp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Gln Tyr Phe Pro Thr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1100
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1100
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Tyr Gly Gly
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Glu Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu His Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr His Lys Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

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<210> 1101
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1101
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Gly Val Trp
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser Phe Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Phe Ser Ser Pro Ser
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1102
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1102
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Pro Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Glu
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Gln Phe Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1103
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1103
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Asn Ile Thr Gly Pro
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Pro Gly Trp Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Val Trp Gly Glu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1104
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1104
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ala Tyr Gly
            20                  25                  30
```

```
Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Gly Gly Arg Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Pro Gly Met Pro Pro Asp
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1105
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1105
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Gln Ile Val Gly Gly
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Arg His Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Gly Val Trp Ala Pro Gly
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1106
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1106
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Pro Ala Ile Ala Ala Lys
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Ala Asp Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Ala Gly Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1107
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1107
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Thr Ile Ala Asp Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Ala Tyr Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Glu Gly Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
```

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            100                 105


<210> 1108
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1108
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Tyr Gly Phe
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Leu Ala Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1109
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1109
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Trp
            20                  25                  30


Leu Met Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Trp Gly Ser Phe Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asp Thr Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1110
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1110
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Thr Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ser Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Ser Tyr Tyr Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1111
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1111
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Phe Gly Trp
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            20                  25                  30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Thr Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Ser Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1112
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1112
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Asn Ile Gly Ala Asp
            20                  25                  30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Gly Gly Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Asn Gly Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1113
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1113
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Tyr Asp Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ser Gly Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Leu Gly Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gln
            100                 105


<210> 1114
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1114
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Arg Ile Tyr Asn Gly
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Arg Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Val Gly Glu Ala Pro Ser
                85                  90                  95
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1115
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1115
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Phe Ile Asn Glu Glu
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Ser Trp Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Pro Gly Gly Gly Pro Gly
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1116
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1116
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asp Ile Leu Asp Glu
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Gly Gly Gly Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp His Gly Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1117
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1117
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Tyr Thr Gly
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Arg Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Met Gln Val Gly Thr Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1118
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1118
Asp Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ser Arg Arg
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ser Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Gly Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Tyr Pro His
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1119
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1119
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Pro Gln Asp
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Val Gly Ile Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Ser Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1120
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1120
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Asp Gly Met
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Pro Gly Phe Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Val Glu Ala Pro Trp
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1121
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1121
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Tyr Ile Ala His Pro
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Pro Gly Ser Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Val Val Val Pro Trp
                85                  90                  95
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1122
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1122
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Thr Ile Glu Gly Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Met Gly Gly Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Val Gly Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1123
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1123
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Phe Ile Arg Asp Glu
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Gly Gly Ser Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
```

```
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Arg Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1124
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1124
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Pro Ile Tyr Gly Gly
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Gly Gly Gly Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Val Trp Gly Gly Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1125
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1125
Asp Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Ser Gly Cys
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Asp Gly Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Trp Trp Glu Tyr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1126
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1126
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Pro Ile Val Arg Asp
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


His Gly Val Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Glu Ala Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1127
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1127
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asp Ile Gly Asp Trp
20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Val Trp Ala Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Trp Gly Thr Pro Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1128
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1128
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Asn Arg Ile Glu Tyr Gly
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Ser Gly Ser Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ser
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Glu Ala Ala Pro Ala
85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1129
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1129
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Gly His Phe
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Leu Gly Gly Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Val Glu Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1130
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1130
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Ile Tyr Ser Asp
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

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Asp Gly Trp Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu His Arg Ala Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1131
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1131
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Phe Ile Thr Asp Arg
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Val Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Ser Glu Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1132
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1132
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Lys Ile Gly Ser Glu
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Gly Arg Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp Glu Pro Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1133
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1133
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Gly Asn Gly
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Gly Glu Gly Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Leu Trp His Thr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1134
<211> 108
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1134
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Tyr Gly Trp
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Gly Gly Trp Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Asp Tyr Thr Leu Pro Gly
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1135
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1135
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Lys Asp Trp
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Phe Ala Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr
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                85                  90                  95


Thr Ser Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1136
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1136
Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Leu Ile Ser Ser His
            20                  25                  30


Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
        35                  40                  45


Tyr Asp Ala Ser Glu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Arg Ser Leu Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1137
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1137
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Gly Ala
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45
```

```
Tyr Gln Ile Ser Val Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Arg Ser Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1138
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1138
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ala Ala
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Leu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Phe Arg Leu Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1139
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1139
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

```
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Gly Gly Arg
            20                  25                  30


Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Ser Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ala Glu Ala Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1140
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1140
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Ser
            20                  25                  30


Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile
        35                  40                  45


Tyr Tyr Ser Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Leu Ser Ser Pro Tyr
                85                  90                  95


Thr Val Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1141
<211> 108
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1141
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Glu
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Trp Thr Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Leu Glu Thr Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1142
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1142
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Trp Asp Ala
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Arg Gly Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
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```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Tyr Arg Trp Pro His
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1143
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1143
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln His Ile Glu Asp Ser
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Tyr Gly Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Tyr Lys Phe Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1144
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1144
Asp Ile Gln Thr Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Asn Ser Ser
            20                  25                  30


Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Asp Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Trp Gly Ser Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1145
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1145
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Pro Val Gly
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Trp Tyr Tyr Pro Asn
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1146
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1146
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Tyr Gly Trp
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Leu Thr Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile His Ser Ser Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1147
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1147
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Ile Asp Thr Ser
            20                  25                  30


Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Gly Ser His Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Val Leu Pro Leu
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1148
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<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1148
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asp Ala
            20                  25                  30


Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Tyr Ser Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg His Ser Thr Pro Ala
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1149
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1149
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Glu Ser
            20                  25                  30


Leu Met Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Val Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Trp Lys Ala Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1150
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1150
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Val Glu Asp
            20                  25                  30


Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Ala Lys Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Arg Arg Arg Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1151
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1151
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Pro Met
            20                  25                  30


Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
```

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        35                  40                  45


Tyr Ala Gly Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Leu Val Thr Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1152
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1152
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Ala
            20                  25                  30


Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Tyr Gly Ser Val Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Phe Gln Glu Pro Val
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1153
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1153
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gln Ile Ser Asp Glu
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Val Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Leu Ser Phe Pro Ser
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 1154
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1154
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gagcaagtca gaatattaag cattcgttac ggtggtacca gcagaaacca      120

gggaaagccc ctaggctcct gatctatcat cgttcccagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag gttaggcatc gtccttatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1155
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1155
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atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca      120
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gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag gttgctttgt ttccctatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1156
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1156
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atcacttgcc gggcaagtca gcatattggt catcatttaa ggtggtacca gcagaaacca      120

gggaaagccc ccaagctcct gatctatcat aggtcccatt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattctg ctacgtacta ctgtcaacag tgggataggc cgccttatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1157
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1157
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atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag gtgcgggctg tgccttatac gtttggccaa      300

gggaccaagg tggaaattaa acgg                                             324


<210> 1158
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1158
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag gttcgttttt ctccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1159
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1159
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atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tcttatgcta ggcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1160
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1160
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atcacttgcc gggcaagtca aagtattaat cataggttat attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggtccaggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaggattttg ctacgtacta ctgtcaacag tataaggtta ggcctaatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1161
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1161
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atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatttatcat cggtccaagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acttattcgt ctcctcatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1162
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1162
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctacaacct 240

gaagattttg ctacgtacta ctgtcaacag agggcggtga ggccttttac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1163
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1163
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggtccaagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acttattatc gtcctcttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1164
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1164
gacatccaga tgacccagtc tccagcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggatattgat cctatgttaa ggtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgcg ggttccattt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag actagtatta ggccttatac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1165
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1165
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1166
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1166
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gcctattggt cctgatatac tgtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatcag acgtccatct tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1167
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1167
gacatccaga taacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccatat tgcgaagtgg agtcccatca 180

cgtttcagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatcttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1168
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1168
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagcttct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagaggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1169
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1169
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca acctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctctt gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagcggatc tgggactgat ttcactctca ccatcagcag tctgcaacct 240 gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1170
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1170
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atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa   300

gggaccaagg tggtaatcaa acgg   324

<210> 1171
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1171
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct   240

gaagatcttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggcaaa   300

gggaccaagg tggtaatcaa acgg   324

<210> 1172
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1172
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca   120 gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccga 300

gggaccaagg tggtaatcaa acgg 324

<210> 1173
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1173
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gagcaagtca gcctattggt cctgatttac tgtggtaccg gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg tgtcccatca 180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggtaatcaa acgg 324

<210> 1174
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1174
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccatta tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1175
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1175

gacatccaga tgacccagtc tccatcctcc ctgtctgcat atgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgagacagat ttcaccctca ccatcagcaa tctgcaacct 240

gaagattttg ctaagtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggtgatcaa acgg 324

<210> 1176
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1176
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240

gtagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tagtaatcaa acgg 324

<210> 1177
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1177
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggttcca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1178
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1178
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atcacttgcc gggcaagtca gcctatcggt cctgatttac tgtggtaccg gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1179
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1179
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattgat cctgacttac tgtggtacca gcagaaacca 120

ggtaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagtt ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggcat ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1180
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1180
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atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaagcca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1181
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1181
gacatccaga tgacccagtc tccatcatcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattgaa cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ctcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1182
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1182
gacatccaga tgacccagtc accatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggctagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagcg gcagtgaatc cgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatattg caacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaggg tggaaatcaa acgg 324

<210> 1183
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1183
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atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccttca 180

cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1184
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1184
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcgcc 60

atcacttgcc gggcaagtca gcctattggt cctgatatac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattctg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggtcaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1185
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1185
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccgtca 180

cgtttcagtg gcagtggatc tgtgacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tgggaatcaa gcgg 324

<210> 1186
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1186
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattgat cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc taggacagat ttcactctca ccatcagcag tctgcaacct 240 gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1187
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1187
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcgg tctgcaacct 240

gaagattttg ctacgtacta ctgtcagcag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1188
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1188
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtat gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180

cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1189
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1189
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtggattggg gatacgttaa cgtggtacca gcagaaacta 120 gggaaagccc ctaagctcct gatctatggt ggttccgagt tgcaaagtgg ggtcccacca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tgtattagta gtccttgtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1190
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1190
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtttattggt gattctttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatttt tcttccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcatactt cgcctactac gttcggccga 300

gggaccaagg tgaaaatcaa acgg 324

<210> 1191
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1191
gacatccaga tgacccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gactattgag actaatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat tcttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240

gaagatttag ctacgtacta ctgtcaacag tatcatgggt atcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1192
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1192

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gatgattgat caggatttag agtggtacca gcagaaacca       120

gggaaagccc ctaagctcct gatctataat gcgtcctggt tgcaaagtgg ggtcccatca       180

cgtttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag tatcatggtt atcctattac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1193
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1193
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gacgatttat acttcgttaa gttggtatca gcagaaacca       120

gggaaagccc ctaagctcct gatccattat ggttccgtgt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattctg ctacgtacta ctgtcaacag gttcatcagg ctcctacgac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1194
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1194
gacatccgga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gtggattggg gattctttag cgtggtacca gcagaagcca       120

gggaaagccc ctaagctcct gatctatggt atttccgagt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattctg ctacgtacta ctgtcaactg tctagtagta tgcctcatac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1195
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1195
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggagattgag acgaatttag agtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgat tcgtcccatt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tatcatcaga atcctccgac gttcggccaa   300

ggaaccaagg tggaaatcaa acgg   324

<210> 1196
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1196
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gtggattggg aggcagttag tttggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatggg gcgaccgagt tgcaaagtgg ggtcccatca   180

cgttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag cagtcgaagg gtcctcttac gttcggccat   300

gggaccaagg tggaaatcaa acgg   324

<210> 1197
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1197
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggggattggt actgatttaa attggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatatg ggttcctatt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag atttattctt ttcctattac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1198
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1198
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggatattgag gagatgttac attggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatttt ggttccctgt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtagatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag catcatactc gtccttatac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1199
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1199
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggatattggg atggatttag agtggtacca gcagatacca   120

gggaaagtcc ctaagctcct gatctatgat gcgtcctatt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tatcataagc ttcctgcgac gtttggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1200
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1200
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca ggatattatg gataatttag agtggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgcg gcgtcctggt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag tatcataagt tgcctgtgac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1201
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1201
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gagcaagtca gaatattggg gaggatttag agtggtacca gcagaaacca 120

gggaatgccc ctaagctcct gatctatagt gcgtcccatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattctagtt atcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1202
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1202
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ccgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gccgattgat gaggatttag agtggtacca gcagaaacca 120

gggaatgccc ctaagctcct gatctatagt gcgtcctatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag actgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcatcttc tgcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1203
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1203
gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattaat gaggatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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aaagattttg ctacgtacta ctgtcaacag tatcatacta atcctactac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1204
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1204
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattgag gcggatttag agtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatcat tcttccgagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcatatgt cgcctgtgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1205
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1205
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattgat agtgatttag agtggtacca gcagaaacca      120

gggaaagccc ctatgctcct gatctattct tcgtccgatt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcatagtc tgcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1206
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1206
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatatttcg gatgatttag agtggtacca gcagaaacca      120
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gggaaagccc ctaagctcct gatctataat tcgtcctttt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tggggcagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcatagtt tgcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1207
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1207
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattgag ggtaatttag agtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat tcgtcccagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcatcatc ttcctacgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1208
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1208
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gagtattgat acggatttag agtggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat gggtcctggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcggtgga ttcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1209
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1209
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattagt actgatttag agtggtacca gcagaaacta 120

gggaaagccc ctaagctcct gatctatgat gcttcccttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattcgagtc tgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1210
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1210
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctattacg acgtctttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcgtccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattgggtta cgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1211
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1211
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacctgcc gggcaagtca gaatattcat acgaatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat ggttccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattcggcta atcctgttac gttcggccaa 300

gggaccaagg tgggaatcaa acgg 324

<210> 1212
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1212
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtggattcat acggatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat ggttccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatagtgtgt cgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1213
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1213
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattgat aataatttag agtggtacca gcagaaacca 120

ggggaagccc ctaagctcct gatctatgat gggtcccttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctta ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcatcttc atcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1214
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1214
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgat acgaatttag agtggtatca gcagaaacca 120

ggggaagccc ctaagctcct gatctatgat cgttccacgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgattctt atcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1215
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1215
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gtctattgag tctaatttag agtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctataat gcgtccgagt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcgacct   240

gaagattttg ctacgtacta ctgtcaacag tatgatcagt ggcctacgac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1216
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1216
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact   60

atcacttgcc gggcaagtca ggctattggt aatactttac ggtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatctt agttccaggt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag ctgaagaagc ctccttatac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1217
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1217
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc   60

atcacttgcc gggcaagtca gaagattaag aatcggttag cgtggtacca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgag gtttcccatt tgcaaagtgg ggtcccatca   180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcggcag tctgcaacct   240

gaagattttg ctacgtacta ctgtcaacag aggaggcagt cgccttatac gttcggccaa   300

gggaccaagg tggaaatcaa acgg   324

<210> 1218
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1218
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtga ggatattggg gaggagttat tttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattcg gcgtccacgt tgcaaagtga ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacat 240

gaagattttg ctacgtacta ctgtcaacag gtttatgagt ggccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1219
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1219
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcctatttct gggggtttaa ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct acttccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag ctttattctg ctccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1220
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1220
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgat caggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctataat gtttccctgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattctatga atcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1221
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1221
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattggg aatcagttaa agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag gcttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatttga ggcctcagac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1222
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1222
gacatccaga tgacccagtc tccatccttc ctgtctgcat ctgtaggtga ccgtgtcacc 60

atcacttgcc gggcgagtca gaagatttct acgtctttag agtggtatca gcagaaacca 120

gggaaagccc ctaggctcct gatctatgat tcttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgagtata atcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1223
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1223
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattggg gagagtttac attggtacca gcagaaacca 120

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gggaaagccc ctaggctcct gatctatttt gcttccctgt tgcaaagtgg ggtcccatcg      180

cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag catcatatgc ttccttctac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1224
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1224
gacatccaaa tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gtttattggt gattctttat cttggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatttt tcttccattt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatatggata ttcctattac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1225
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1225
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattgat cataatttag agtggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat agttccatgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcattcta ttcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1226
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1226
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcagattgag acgaatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat ggttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcatagtt tgcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1227
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1227
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattggt aataatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctatcat gggtcctggt tgcaaagtgg ggtcccatcg 180

cgtttcagtg gcagtggatc tgggacagat ttcactctta ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatttta atcctactac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1228
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1228
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ctgtgtcacc 60

atcacttgcc gggcaagtca gaatattgat ggtctgttat ggtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgcg gggtccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag aaggcttttg agccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1229
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1229
gacatccaga tgacccagac tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattggt catgatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctataat gtgtcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatagtcata atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1230
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1230
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact 60

atcacttgcc gggcaagtca gcatattgag aatgatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct gcttcccatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcatcttc agcctacgac gttcggccca 300

gggaccaagg tggaaatcaa acgg 324

<210> 1231
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1231
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact 60

atcacttgcc gggcaagtca ggttattgag ggtagtttaa attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat aggtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gccgtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acttatcagc ttcctttgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1232
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1232
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg tcctattaat ggtaagttat tttggtacca gcagaaacca 120

ggcaaagccc ctaagctcct gatcgcgttt gcttccgctt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgtgcag caggctgtgt atcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1233
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1233
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggctattgag acgaatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gggtcccttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagaggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcattatc agcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1234
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1234
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgag catgatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattcg gcgtcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcagcagc agcctactac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1235
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1235
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc gcagattgag gagtctttat ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgcggat gtttccctgt tgcaaagtgg agtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgctcag ggtgtggtgg agcctcgtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1236
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1236
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtatattggt ctggatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattttcggc agcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1237
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1237
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctcctgcgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1238
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1238
gacatccagt tgacccagtc tccaacctcc ctgtctgcaa ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacct      120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggactgat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag catgtgcgtc atcctgcgac gttcggccaa      300

gggaccaagg tggaaatcaa gcgg                                             324


<210> 1239
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1239
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtggacag catgtgcgtc ctcctgcgac gttcggccaa      300

gggaccaagg tgggaatcaa acgg                                             324


<210> 1240
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1240
gacatccaga tgacccagtc tccgtcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggtaagtac gccgattggt actatgttag attggtacca gcagaaacca      120
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gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccacca 180

cgtttcagtg gcagcggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1241
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1241
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gctgtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1242
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1242
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtac gccgattggt actatgatag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctcctgcgac gttcggcaaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1243
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1243

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacatgcc gggcaagtca gtatattgat actaatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctatgat ggttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca tcatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatcaggttg tgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1244
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1244
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcgtggat tcttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag gatcgttggt ctcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1245
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1245
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc gcggattcag catatgttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggg cattccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgcgcaa tcgtgtgcgt ggcctctgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1246
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1246
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtag gggtattgat ggtgatttat ggtggtacca gcagaaacca       120

gggaaagccc ctaagctcct gatcgcggat tcttccctgt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtgggcag ggggctgttc ggcctatgac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1247
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1247
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtag gggtattgat actgatttat ggtggtacca gcagaaacca       120

gggaaagccc ctaagctcct gatcgcggat tcttccctgt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtgggcag ggggctgttc ggcctatgac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1248
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1248
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atcacttgcc gggcaagtta tactattccg gttgctttag attggtacca gcagaaacca       120

gggaaagccc ctaagctcct gatcgctgat gcgtccttgt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtgcgcag ggttggccgg ggcctcagac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1249
<211> 324
<212> DNA
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1249
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atcacttgcc gggcaagtca gagtattgcg acggacttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat acttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatagttata atccttcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1250
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1250
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtgt gcctattact gagggtttat cgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccaggct aattcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tgggagcatg ttcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1251
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1251
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag tatgattctt tatggtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggt acttccgcgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tgggagacgg ttcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1252
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1252
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atcacttgcc gggcaagtca gcctattaat gggcttttaa tttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgcg atgtccagtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag ttggctcgga ttccttttac gttcggccaa 300

gggaccaagg tgggaatcaa acgg 324

<210> 1253
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1253
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gagcaagtca gctgattcgg acttatttag cgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag tcttctcagt tgcaaagtgg tgtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tataattctt atcctgatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1254
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1254
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtggattggg gattcgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatttt ggttcctatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatttgcata ctccttcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1255
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1255
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgag gcggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat tcttccgagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatggtttta atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1256
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1256
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc tcctattgag tatggtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggggg gggtccgcgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tgggaggttc agcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1257
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1257
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcggattgat actgatttag agtggtacca gcagaaacca 120

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gggaaagccc ctaagctcct gatctatgat agttcacagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatcatagtg cgcctgcgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1258
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1258
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtgg gtggattggt atgtctttag agtggcacca gcagaaacca      120

gggaaagccc ctaagctcct gatccgtggg gcttcctctt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtagtcag tctcggtggc cgcctgtgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1259
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1259
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtcg taatatttcg aatgctttat cgtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatccttggg gcttcctggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtactcag gtgtgggata ggccttttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1260
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1260
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattatg tcggctttat cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct acttccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag gtttatttgc tgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1261
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1261
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggagattggg attgatttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcttcttatt tgcaaagtgg ggtcccatca 180

cgtttcagta gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgcttcta atcctcctac gttcggccga 300

gggaccaagg tggaaatcaa acgg 324

<210> 1262
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1262
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gatgattggg gattggttaa attggtacca gcagaaacca 120

gggaaagccc ctaaactcct gatctatcgt agttccgagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag ttgtattttt ggcctcgtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1263
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1263
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggcgattgag cttaatttag agtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatgttt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1264
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1264
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggccagtca ggcgattgag cataatttag agtggtacca gcagaagcca 120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctccaacct 240

gaagatttag ctacgtacta ctgtcaacag tatgatgctt atcctcctac gtacggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1265
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1265
gacatccaga tgacacagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg ggcgatagag actaatttag agtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gttctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcggtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtctacag tatgatgttt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1266
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1266
gacatccaga tgacccagtc tccatcctcc ctgtctgcaa ctgtaggaga ccgtgtcacc 60

atcacttgtc gtgcaagtca ggcgattgag actaatttag agtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagac ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1267
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1267
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggcgattgag cataacttag agtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgtttcagtg gcagaggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1268
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1268
gacatccaga tgaaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtctcc 60

atcacttgca gggcaagtca ggctattgag cataatttag agtggtacca gcagaaacca 120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180

cgcttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

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<210> 1269
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1269
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca ggcgattgag tctaatttag agtggtacca gcaaaaacca       120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag tatgatgttt atcctcctac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1270
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1270
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gtgcaagtca ggcgattgag cataatttag agtggtacca gcagaaacca       120

gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1271
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1271
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gggtattgat gaggatttag agtggtacca gcagaaacca       120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca       180

cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240
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gaagattttg ctacgtacta ctgtcaacag tattttcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1272
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1272
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattttcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1273
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1273
gacatccaga tgacccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60

atcacttgca gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattctcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1274
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1274
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattgaa gaggatttag agtggtacca gcagaaacca 120 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagcgg ggtcccatca 180

cgtttcagtg ggagtggctc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tattttcagt atcctccgac gttcggccat 300

gggaccaagg tggaaatcaa acgg 324

<210> 1275
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1275
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtactt ctgtcaacag tattttcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1276
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1276
gagatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atgacttgcc gggcaagtca gagtattgat aaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagagg ggtcccatca 180

cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcgacct 240

gaagattttg ctacgtacta ctgtcaacag tattttcagt atcctccgac gttgggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1277
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1277

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcgg tctgcaacct 240

gaagatatcg ctacgtacta ctgtaaacag tattctcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1278
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1278
gacatccaga tgacccagtc cccaccctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattgat aaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagagg ggtcccatca 180

cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacca ctgtcaacag tattttcagt atcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1279
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1279
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtga gtatattaat gctgagttag cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggg agttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtctgcag aatgcgatgt ggcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1280
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1280
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtct ggatattaat aatggtttaa tttggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcttgggt gcgtccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgttcgcag gtgcgttctc ggccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1281
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1281
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattctg agtgcgttag cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggg agttccgttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc agggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag aattatagtc ttcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1282
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1282
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc tcctattgag tcgtatttaa ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcaggtat gtgtccgtgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tggtttcggg cgcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1283
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1283
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggtaagtga gtctattaat gctgagttac attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctctggg ttttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgtgcag tttgcgatgt ggccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1284
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1284
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtat gatgattagg tttgggttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggt gggtcctctt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag catgagcggt ggcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1285
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1285
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattggt actcttttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt acttccgttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag atggtttatc gtccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1286
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1286
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gactattgag actaatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat tcttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatgataagg ttcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1287
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1287
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca tcatattcag aggtatttat cgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcctttgg ggttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tggtgggctc ctcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1288
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1288
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca tcatattcag aggtatttat cgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcctttgg ggttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagattttg ctacgtacta ctgtgggcag tggtgggctc ctcctcagac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1289
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1289
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca tgatattcag aggtatttat cgtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcctttgg ggttcccagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag tggtgggctc ctcctcagac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1290
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1290
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacatgcc gggcaagtca gtatattgat actaatttag agtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat ggttccctgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag ggggctgttg tgcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1291
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1291
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattgct tttgatttag agtggtatca gcagaaacca      120
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gggaaagccc ctaagctcct gatctattcg gcgtccatgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggtcagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tataatcttc agcctcctac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1292
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1292
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gaatattgct acgctgttac gttggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct ggttccatgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag atgtggcagc gtccttatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1293
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1293
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gcctattgtt gatgagttag attggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct gcgtccattt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcatcag tggtctactt atcctacgac gttcggccaa      300

gggaccaagg tggaaattaa acgg                                             324


<210> 1294
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1294
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gacatccaga tgacccaatc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtacca gcagaaacca 120

gggaaagccc ctaagctcct aatcgatggt gtttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag gattgggatt ggcctcgtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1295
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1295
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag gaatattcgt gattggttac ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgattgg gggtccgtgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgctcag acgtgggatg atcctctgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1296
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1296
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ttgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag gaatattcgt gattggttac ggtggtacca acagaaacca 120

gggaaagccc ctaagctcct gatcgattgg gggtccgagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgctcag acgtggtatg atcctctgac gttcggccac 300

gggaccaagg tggaaatcaa acgg 324

<210> 1297
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1297
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtat tgatattcat ggtggtttaa cttggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcgtgggg gtttccggtt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct      240

gaagattttg ctacgtacta ctgtgcgcag gtgtggcgta ggccttttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1298
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1298
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca ggatattggg agttcgttat cttggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct tcttccctgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag acttatgctc ttcctgttac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1299
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1299
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gcagattgag acgaatttag agtggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat ggttcctggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tataagtatc tgcctgtgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1300
<211> 324
<212> DNA
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1300
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggtga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattggg tctgcgttaa ggtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatttg ggttccgatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acgcagtatt ttcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1301
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1301
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggcgatttat gggggttac ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggg gagtccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcatcct 240

gaagattttg ctacgtacta ctgtcaacag gtttatcata agccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1302
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1302
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacgtgcc gggcaagtca gcgtattggg gtgtggttag attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat ggttcctttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag actttttcga gtccttctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1303
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1303
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcccc 60

atcacttgcc gggcaagtca gtggattggg gatgagttat attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatagt tcttccactt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tcgtttcagt ttccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1304
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1304
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag taatattacg gggccgttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccctggt tggtccactt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag gtgtgggggg agcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1305
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1305
gacatccaga tgacccagtc tccatcctcc ctgtctgcgt ctataggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcgtattgct tatggtttac attggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcgggggg cggtccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgtgcag cctgggatgc cgcctgatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1306
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1306
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtaa gcagattgtt ggtggtttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggcgt cattctgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgtgcag ggggtttggg ctcctgggac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1307
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1307
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcc tgctattgct gctaagttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtgcg gattccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ctgtgggcgg ggcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1308
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1308
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg tactattgct gatgggttag attggtacca gcagaaacca 120 gggaaagccc ctaagctcct gatcggggcg tattccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ctttgggagg gtcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1309
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1309
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gaggatttat gggtttttag attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggg gtgtcctcgt tgcaaagtgg ggtcccatca 180

cgttttagtg gcagcggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag actttggcgt ggccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1310
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1310
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atcacttgcc gggcaagtca ggatattcgg gattggttaa tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattgg ggttcctttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag ctgtatgata ctccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1311
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1311

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gaatattaat acgggtttag attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat agttccgctt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag acgtcgtatt atccttatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1312
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1312
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gaagattttt ggttggttag attggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatggg acttccaagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag gtttattcgc ttccttatac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1313
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1313
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagttc gaatattggg gcggatttag attggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcgggggg gcgtccgggt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag ctgtggaatg ggcctcctac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1314
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1314
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atcacttgcc gggcaagtag tccgatttat gatggtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctctggt gcttcctggt tgcaaagtgg ggtcccatca 180

cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ttgtggttgg gtcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acag 324

<210> 1315
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1315
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc gcgtatttat aatggtttac attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggt cggtccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgctcag gtgggggagg ctccttctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1316
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1316
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag gtttattaat gaggagttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctcgtgg tcttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgtgcag ccgggggggtg gtcctgggac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1317
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1317
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag ggatattctg gatgagttag attggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcggtggg gggtccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ctgtggcatg ggcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1318
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1318
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag tcctatttat acgggtttac attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggg cggtccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtatgcag gttgggacgg ctcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1319
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1319
gacatccgga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gaatatttct aggcggttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct tcttcccggt tgcaaagtgg ggtcccatca 180

cgtttcggtg gcagtggatc tgggacggat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acgtatagct atcctcatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1320
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1320
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag tccgattccg caggatttat attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgttggg atttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag ttgtggagtg cgcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1321
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1321
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtaa gtctattgat gggatgttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccctggt ttttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tcggttgagg cgccttggac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1322
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1322
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg gtatattgct catcctttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcccgggt tcgtccgttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagattttg ctacgtacta ctgtggtcag tcggttgtgg tgccttggac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1323
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1323
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtcg gacgattgag ggtggtttag attggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcatgggg ggttccggtt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag ttgtgggtgg gtcctcctac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1324
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1324
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtaa gtttattagg gatgagttat attggtacca gcagaaacca      120

gggaaagccc ctaggctcct gatcggtggt tcgtccttgt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgggcag ctgtggcggg cgcctgcgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1325
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1325
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtaa gccgatttat ggtggtttag agtggtacca gcagaaacca      120
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gggaaagccc ctaggctcct gatcgggggg ggttccgtgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag gtgtgggggg gtcctgttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1326
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1326
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atcacttgcc gggcaagtcg gccgattagt ggttgtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgatggg gcttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag tggtgggagt atcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1327
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1327
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtaa gcctattgtg agggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccatggt gtgtccacgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag cttgaggcgg cgcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1328
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1328

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg ggatattggt gattggttat attggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcgtttgg gcgtccgtgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgcgcag tgggggactc ctcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1329
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1329
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtaa tcgtattgag tatggtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctcgggg tcttcccgtt tgcaaagtgg ggtcccatca 180

cgtttcagta gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag cttgaggcgg cgcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1330
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1330
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg gaatattggg catttttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcttgggg gggtcctcgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag ttggtggagc ctcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1331
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1331
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagttc gagtatttat agtgatttat attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgatggg tggtccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag ctgcatcgtg ctcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1332
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1332
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag gtttattact gatcgtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggt gtttccgggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag agttcggagt tgccttggac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1333
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1333
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg taagattggt agtgagttat attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggtggt aggtcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag ttgtgggagc ctcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1334
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1334
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtag gaatattggt aatggtttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggggag gggtcccgtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag ctttggcata ctcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1335
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1335
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg gaatatttat ggttggttat cgtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcggtggg tggtccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgcgcag gattatacgt tgcctggtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1336
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1336
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattaag gattggttac attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatttt gcgtccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattctg ctacgtacta ctgtcaacag cattatagta cgccttatac gtccggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1337
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1337
gacatccaga tgacccagtc tccaccctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gttgatttct tctcatttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct ggtctatgat gcttccgagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag catcgcagtc tgccttttac gttcggccaa 300

gggaccaagg tagaaatcaa acgg 324

<210> 1338
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1338
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtggattggt ggggcgttag cgtggtacca gcagaaacca 120

gggaaagccc ctaggctcct tatctatcag atttccgttt tgcaaagtgg gatcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag tatattcggt ctccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1339
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1339
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gagtattggg gcggcgttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt ctgtcctctt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagattttg ctacgtacta ctgtcaacag ctgtttaggc ttcctttgac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1340
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1340
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gcctattggg ggtcgtttag tgtggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatctatggg tcttccattt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tatgctgagg ctcctattac gttcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1341
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1341
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gaatattggg tctagtttaa tttggtacca gcagaaacca      120

gggaaagccc ctacgctcct gatctattat tcgtccaagt tgcaaagtgg ggtcccatca      180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtcaacag tctttgtcga gtccttatac ggtcggccaa      300

gggaccaagg tggaaatcaa acgg                                             324


<210> 1342
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1342
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gggcaagtca gtggattggg agtgagttag cgtggtatca gcagaaacca      120
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gggaaagccc ctaagctcct gatctattgg acgtccaatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag attctggaga ctcctttgac gtttggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1343
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1343
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gaagatttgg gatgctttat attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcgt gggtccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag ttttatcggt ggcctcatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1344
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1344
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gcatattgag gattctttac ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattat ggttccgtgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag atgtataagt ttcctattac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1345
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1345

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gacatccaga cgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gcggattaat tcttctttac tgtggtacca gcagaaacca       120

gggaaagccc ctaagctcct gatctatgat acttccactt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtagatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagatttcg ctacgtacta ctgtcaacag atttggggtt cgcctcctac gttcggccag       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1346
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1346
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gtcgattcct gttggtttaa attggtacca gcagaaacca       120

gggaaagccc ctaggctcct gatctattct gggtccactt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag gattggtatt atcctaatac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1347
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1347
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gcctatttat ggttggttaa attggtatca gcagaaacca       120

gggaaagccc ctaagctcct gatctatttg acgtccgggt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag attcatagtt ctccttttac gttcggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1348
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1348
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtttattgat acgtcgttag agtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gggtcccatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttag ctacgtacta ctgtcaacag tattgggttc ttcctctgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1349
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1349
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattggg gatgctttat tttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctattat tcttccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcggtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag cggcatagta ctcctgctac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1350
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1350
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgat gagtctttaa tgtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctatggg gtgtcctatt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg ctacgtacta ctgtcaacag cggtggaagg ctccttttac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1351
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1351
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgttacc 60

atcacttgcc gggcaagtca ggagattgtg gaggatttat attggtatca gcagaaacca 120

gggaaagccg ctaagctcct gatctatggt gcgtcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acgcgtaggc gtccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1352
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1352
gacatccaga tgacccagtc tccagcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggatattgat cctatgttaa ggtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgcg ggttccattt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag acgctggtga ctccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1353
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1353
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtcgatttcg gatgcgttat tttggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattat ggttccgttt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag cgttttcagg agcctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

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<210> 1354
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 1354
gacatccaga tgacccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc        60

atcacttgcc gggcaagtca gcagattagt gatgagttaa attggtatca gcagaaacca       120

gggaaagccc ctaagctcct gatctatgct gtgtccattt tgcaaagtgg ggtcccatca       180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct       240

gaagattttg ctacgtacta ctgtcaacag tggttgagtt ttccttcgac gtttggccaa       300

gggaccaagg tggaaatcaa acgg                                              324


<210> 1355
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1355
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Glu
            20                  25                  30


Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys
        115                 120                 125
```

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Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser
    130                 135                 140

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
145                 150                 155                 160

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
                165                 170                 175

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
            180                 185                 190

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
        195                 200                 205

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
    210                 215                 220

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
225                 230                 235                 240

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                245                 250                 255

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
            260                 265                 270

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
        275                 280                 285

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
    290                 295                 300

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
305                 310                 315                 320

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                325                 330                 335

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            340                 345                 350

Lys


<210> 1356
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      peptide"

<400> 1356
Ala Ser Thr His Thr Cys Pro Pro Cys Pro
1               5                   10


<210> 1357
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1357
Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
1               5                   10                  15


Ser Pro



<210> 1358
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1358
Ala Ser Thr His Thr Ser Pro Pro Ser Pro
1               5                   10


<210> 1359
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1359
Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
1               5                   10                  15


Ser Pro



<210> 1360
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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      peptide"

<400> 1360
Ala Ser Thr His Thr Ser Pro Pro Ser Pro
1               5                   10


<210> 1361
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1361
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1               5                   10                  15


Ala Glu Val Gln Leu Leu Glu Ser
            20


<210> 1362
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1362
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1               5                   10                  15


Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            20                  25                  30


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
        35                  40                  45


Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    50                  55                  60


Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
65                  70                  75                  80


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                85                  90                  95


Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            100                 105                 110


Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
        115                 120                 125
```

```
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp
    130                 135                 140

Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly
145                 150                 155                 160

Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                165                 170                 175

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            180                 185                 190

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        195                 200                 205

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    210                 215                 220

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
225                 230                 235                 240

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                245                 250                 255

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            260                 265                 270

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        275                 280                 285

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    290                 295                 300

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
305                 310                 315                 320

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                325                 330                 335

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            340                 345                 350

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        355                 360                 365

Gly Lys
    370


<210> 1363
<211> 362
<212> PRT
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```
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1363
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1               5                   10                  15


Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            20                  25                  30


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
        35                  40                  45


Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    50                  55                  60


Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
65                  70                  75                  80


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                85                  90                  95


Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            100                 105                 110


Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
        115                 120                 125


Thr Leu Val Thr Val Ser Ser Ala Ser Thr His Thr Ser Pro Pro Ser
    130                 135                 140


Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro
145                 150                 155                 160


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                165                 170                 175


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            180                 185                 190


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        195                 200                 205


Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    210                 215                 220


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
225                 230                 235                 240
```

```
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                245                 250                 255


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            260                 265                 270


Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        275                 280                 285


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    290                 295                 300


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
305                 310                 315                 320


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                325                 330                 335


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            340                 345                 350


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        355                 360


<210> 1364
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1364
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1               5                   10                  15


Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            20                  25                  30


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
        35                  40                  45


Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    50                  55                  60


Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
65                  70                  75                  80


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                85                  90                  95


Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
```

```
            100                 105                 110

Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
        115                 120                 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp
    130                 135                 140

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
145                 150                 155                 160

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                165                 170                 175

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            180                 185                 190

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        195                 200                 205

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg
    210                 215                 220

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
225                 230                 235                 240

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                245                 250                 255

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            260                 265                 270

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        275                 280                 285

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    290                 295                 300

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
305                 310                 315                 320

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                325                 330                 335

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            340                 345                 350

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        355                 360                 365

Gly Lys
```

```
    370


<210> 1365
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1365
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1               5                   10                  15


Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            20                  25                  30


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
        35                  40                  45


Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    50                  55                  60


Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
65                  70                  75                  80


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                85                  90                  95


Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            100                 105                 110


Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
        115                 120                 125


Thr Leu Val Thr Val Ser Ser Ala Ser Thr His Thr Cys Pro Pro Cys
    130                 135                 140


Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
145                 150                 155                 160


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                165                 170                 175


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            180                 185                 190


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        195                 200                 205


Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    210                 215                 220
```

```
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
225                 230                 235                 240

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                245                 250                 255

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            260                 265                 270

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        275                 280                 285

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    290                 295                 300

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
305                 310                 315                 320

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                325                 330                 335

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            340                 345                 350

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        355                 360
```