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ABSTRACT

Libraries of nucleic acids encoding chimeric binding polypeptides based on plant scaffold polypeptide sequences. Also described are methods for generating the libraries.

PLANT CHIMERIC BINDING POLYPEPTIDES FOR UNIVERSAL MOLECULAR RECOGNITION

This is a divisional of Australian Patent Application No. 2007215062, the entire contents of which are incorporated herein by reference.

BACKGROUND

The binding specificity and affinity of a protein for a target are determined primarily by the protein's amino acid sequence within one or more binding regions. Accordingly, varying the amino acid sequence of the relevant regions reconfigures the protein's binding properties.

In nature, combinatorial changes in protein binding are best illustrated by the vast array of immunoglobulins produced by the immune system. Each immunoglobulin includes a set of short, virtually unique, amino acid sequences known as hypervariable regions (i.e., protein binding domains), and another set of longer, invariant sequences known as constant regions. The constant regions form β sheets that stabilize the three dimensional structure of the protein in spite of the enormous sequence diversity among hypervariable regions in the population of immunoglobulins. Each set of hypervariable regions confers binding specificity and affinity. The assembly of two heavy chain and two light chain immunoglobulins into a large protein complex (i.e., an antibody) further increases the number of combinations with diverse binding activities.

The binding diversity of antibodies has been successfully exploited in many biomedical and industrial applications. For example, libraries have been constructed that express immunoglobulins bearing artificially diversified hypervariable regions. Immunoglobulin expression libraries are very useful for identifying high affinity antibodies to a target molecule (e.g., a receptor or receptor ligand). A nucleic acid encoding the identified immunoglobulin can then be isolated and expressed in host cells or organisms.

However, despite the usefulness of immunoglobulins and antibodies in general, their expression in transgenic plants can be problematic. Immunoglobulins may not fold properly in plant cytoplasm because they require the formation of multiple disulfide bonds. Further, the large size of immunoglobulins prevents their effective uptake by some plant pests. Thus, immunoglobulins are frequently not useful as protein pesticides or pesticide targeting molecules. Finally, expressing mammalian proteins such as immunoglobulins (e.g., as so called "plantibodies") in edible plants

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also raises potential issues of consumer acceptance and is thus an impediment to commercialization. This may effectively prevent use of plantibodies for many input and output traits in transgenic plants.

The above-mentioned disadvantages of immunoglobulins can be circumvented by generating diverse libraries of binding proteins from other classes of structurally tolerant proteins, preferably plant-derived proteins. These libraries can be screened to identify individual proteins that bind with desired specificity and affinity to a target of interest. Afterwards, identified binding proteins can be efficiently expressed in transgenic plants.

SUMMARY

Diverse libraries of nucleic acids encoding plant chimeric binding polypeptides, as well as methods for generating them are described herein. The chimeric binding polypeptides are conceptually analogous to immunoglobulins in that they feature highly varied binding domains in the framework of unvarying sequences that encode a structurally robust protein. However, the chimeric binding polypeptides described herein have the considerable advantage of being derived from plant protein sequences thereby avoiding many of the problems associated with immunoglobulin expression in plants. The amino acid sequences of the encoded plant chimeric binding proteins are derived from a scaffold polypeptide sequence that includes subsequences to be varied. The varied subsequences correspond to putative binding domains of the plant chimeric binding polypeptides, and are highly heterogeneous in the library of encoded plant chimeric binding proteins. In contrast the sequence of the encoded chimeric binding proteins outside of the varied subsequences is essentially the same as the parent scaffold polypeptide sequence and highly homogeneous throughout the library of encoded plant chimeric binding proteins. Such libraries can serve as a universal molecular recognition platform to select proteins with high selectivity and affinity binding for expression in transgenic plants.

Accordingly, one aspect described herein is a library of nucleic acid molecules encoding at least ten (e.g., at least 1,000, 10^5, or 10^6) different chimeric binding polypeptides. The amino acid sequence of each polypeptide includes C_1-X_1-C_2-X_2-C_3-X_3.C_4, where C_1-C_4 are backbone subsequences selected from purple acid phosphatase (i.e., SEQ ID NOs: 1-30, 31-60, 61-90, and 91-120, respectively) that can include up to

30 (e.g., 20, 10, or 5) single amino acid substitutions, deletions, insertion, or additions to the selected purple acid phosphatase sequences. The C_1-C_4 subsequences are homogeneous across many of the polypeptides encoded in the library. In contrast to the C_1-C_4 backbone subsequences, the X_1-X_3 subsequences are independent variable subsequences consisting of 2-20 amino acids, and these subsequences are heterogeneous across many of the polypeptides in the library. For example, the library of chimeric polypeptides can have the amino acid sequence of any one of SEQ ID NOs:124-126 including one to ten single amino acid substitutions, deletions, insertions, or additions to amino acid positions corresponding to 23-39, 51-49, and 79-84 of SEQ ID NOs:124-126.

Another aspect described herein is a method for generating the just-described library. The method includes providing a parental nucleic acid encoding a plant scaffold polypeptide sequence containing C_1-X_1-C_2-X_2-C_3-X_3.C_4 as defined above. The method further includes replicating the parental nucleic acid (e.g., at least one of the X_1-X_3 subsequences is selected from SEQ ID NOs: 121-123) under conditions that introduce up to 10 single amino acid substitutions, deletions, insertions, or additions to the parental X_1, X_2, or X_3 subsequences, whereby a heterogeneous population of randomly varied subsequences encoding X_1, X_2, or X_3 is generated. The population varied subsequences is then substituted into a population of parental nucleic acids at the positions corresponding to those encoding X_1, X_2, or X_3. The amino acid substitutions, deletions, insertions or additions can be introduced into the parental nucleic acid subsequences by replication *in vitro* (e.g., using a purified mutagenic polymerase or nucleotide analogs) or *in vivo* (e.g., in a mutagenic strain of *E. coli*). The just-described library can be introduced into a biological replication system (e.g., *E. coli* or bacteriophage) and amplified.

A related aspect described herein is another method for generating the above-described library of nucleic acids. The method includes selecting an amino acid sequence containing C_1-X_1-C_2-X_2-C_3-X_3.C_4 as defined above. The method further includes providing a first and second set of oligonucleotides having overlapping complementary sequences. Oligonucleotides of the first set encode the C_1-C_4 subsequences and multiple heterogeneous X_1-X_3 subsequences. Oligonucleotides of the second set are complementary to nucleotide sequences encoding the C1-C4 subsequences and multiple heterogeneous X_1-X_3 subsequences. The two sets of

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oligonucleotides are combined to form a first mixture and incubated under conditions that allow hybridization of the overlapping complementary sequences. The resulting hybridized sequences are then extended to form a second mixture containing the above-described library.

Yet another aspect of the invention is a library of nucleic acids encoding chimeric binding polypeptides each of which include an amino acid sequence at least 70% (i.e., any percentage between 70% and 100%) identical to any of SEQ ID NOs: 127-129. The amino acid sequence of each of the encoded polypeptides includes amino acids that differ from those of SEQ ID NOs: 127-129 at positions 14, 15, 33, 35-36, 38, 47-48, 66, 68-69, 71, 80, 81, 99, 101-102, and 104, and the amino acid differences are heterogeneous across a plurality of the encoded polypeptides. The amino acid sequence of each of the encoded polypeptides outside of the above-listed positions is homogeneous across a plurality of the encoded chimeric polypeptides.

A related aspect described herein is a method for generating the just-described library. The method includes selecting an amino acid sequence corresponding to any of SEQ ID NOs: 127-129, in which the selected sequence differs from SEQ ID NOs:127-129 in at least one the above-mentioned positions. The method further includes providing a first and second set of oligonucleotides having overlapping complementary sequences. Oligonucleotides of the first set encode subsequences of the selected amino acid sequence, the subsequences being heterogeneous at the above-mentioned positions. Oligonucleotides of the second set are complementary to nucleotide sequences encoding subsequences of the selected amino acid sequence, the subsequences being heterogeneous at the above-mentioned positions. The two sets of oligonucleotides are combined to form a first mixture and incubated under conditions that allow hybridization of the overlapping complementary sequences. The resulting hybridized sequences are then extended to form a second mixture containing the above-described library.

Various implementations of the invention can include one or more of the following. For example, each nucleic acid in a library can include a vector sequence. Also featured is any nucleic acid isolated from one of the above-described libraries, as well as the chimeric binding polypeptide encoded by it, in pure form.

In one implementation, a population of cells (or individual cells selected from the population of cells) is provided which express chimeric binding polypeptides encoded by one of the libraries. Another implementation features a library of purified chimeric binding polypeptides encoded by one the nucleic acid libraries. Yet another implementation provides a population of filamentous phage displaying the chimeric binding polypeptides encoded by one of the nucleic acid libraries.

In various implementations of methods for generating the above described nucleic acid libraries by oligonucleotide assembly, one or more of the following can be included. For example, the method can further include, after the second mixture that contains the nucleic acid library is generated, performing a cycle of denaturing the population of nucleic acids followed by a hybridization and an elongation step. Optionally, this cycle can be repeated (e.g., up to 100 times). The nucleic acid libraries can be amplified by a polymerase chain reaction that includes a forward and a reverse primer that hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library. In one implementation, amino acids to be encoded in variable sequence positions are selected from a subset (e.g., only 4, 6, 8, 10, 12, 14 or 16) of alanine, arginine, asparagine, aspartate, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, cysteine and valine (the 20 naturally occurring amino acids). In other cases 19 of the 20 are used (excludes cysteine). In other cases all 20 are used. In another implementation, the subset of amino acids includes at least one aliphatic, one acidic, one neutral, and one aromatic amino acid (e.g., alanine, aspartate, serine, and tyrosine).

Described herein is library of nucleic acids encoding at least ten different polypeptides, the amino acid sequence of each polypeptide comprising:

C1-X1-C2-X2-C3-X3-C4, wherein: (i) subsequence C1 is selected from SEQ. ID NOs:1-30, subsequence C2 is selected from SEQ ID NOs:31-60, subsequence C3 is selected from SEQ. ID NOs:61-90; subsequence C4 is selected from SEQ. ID NOs:91-120, and each of C1-C4 comprise up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (ii) C1-C4 are homogeneous across a plurality of the encoded polypeptides; (iii) each of X1-X3 is an independently variable subsequence consisting of 2-20 amino acids; and each of X1-X3 are heterogeneous across a plurality of the encoded polypeptides.

Also described is a library of nucleic acids encoding at least ten different polypeptides, the amino acid sequence of each polypeptide comprising:

C1-X1-C2-X2-C3-X3-C4, wherein: (i) subsequence C1 is selected from FIG. 2 or FIG. 4, subsequence C2 is selected from FIG. 2 or FIG. 4, subsequence C3 is selected from FIG. 2 or FIG. 4; subsequence C4 is selected from FIG. 2 or FIG. 4, and each of C1-C4 comprise up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (ii) C1-C4 are homogeneous across a plurality of the encoded polypeptides

(iii) each of X1-X3 is an independently variable subsequence consisting of 2-20 amino acids; and each of X1-X3 are heterogeneous across a plurality of the encoded polypeptides.

Also described is a library of nucleic acids encoding at least ten different polypeptides, the amino acid sequence of each polypeptide comprising:

C1-X1-C2-X2-C3-X3-C4, wherein (i) subsequence C1 is selected from FIG. 3 or FIG. 5, subsequence C2 is selected from FIG. 3 or FIG. 5, subsequence C3 is selected from FIG. 3 or FIG. 5; subsequence C4 is selected from FIG. 3 XX, and each of C1-C4 comprise up to 30 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (ii) C1-C4 are homogeneous across a plurality of the encoded polypeptides (iii) each of X1-X3 is an independently variable subsequence consisting of 2-20 amino acids; and each of X1-X3 are heterogeneous across a plurality of the encoded polypeptides.

In various embodiments: at least 1,000 different polypeptides are encoded; at least 100,000 different polypeptides are encoded; at least 1,000,000 different polypeptides are encoded; each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; none of C1-C4 comprise amino acid substitutions, deletions, insertions, or additions to the selected subsequence; amino acids of X1-X3 are selected from fewer than 20 amino acids genetically encoded in plants; amino acids of X1-X3 are selected from all 20 amino acids genetically encoded in plants; the fewer than 20 genetically encoded amino acids include at least one aliphatic amino acid, at least one acidic amino acid, at least one neutral amino acid, and at least one aromatic amino acid; fewer than 20 genetically encoded amino acids comprise alanine, aspartate, serine, and tyrosine.

In some cases: the amino acid sequence of each polypeptide is selected from:

(a). a polypeptide comprising C1-X1-C2-X2-C3-X3-C4 wherein C1= SEQ. ID NO:1, C2= SEQ. ID NO: 31, C3= SEQ. ID NO: 61, and C4= SEQ. ID NO: 91;

(b). a polypeptide comprising C1-X1-C2-X2-C3-X3-C4 wherein C1= SEQ. ID NO:2, C2= SEQ. ID NO: 32, C3= SEQ. ID NO: 62, and C4= SEQ. ID NO: 92; and

(c). a polypeptide comprising C1-X1-C2-X2-C3-X3-C4 wherein C1= SEQ. ID NO:3, C2= SEQ. ID NO: 33, C3= SEQ. ID NO: 63, and C4= SEQ. ID NO: 93.

In some cases: each encoded polypeptide comprises C1-X1-C2-X2-C3-X3-C4, wherein C1= SEQ. ID NO: X1, C2= SEQ. ID NO: X2, C3= SEQ. ID NO: X3, and C4= SEQ. ID NO: X4; designated SEQ. ID NO: 130.

In some cases: each encoded polypeptide comprises C1-X1-C2-X2-C3-X3-C4, wherein C1= SEQ. ID NO: X1, C2= SEQ. ID NO: X2, C3= SEQ. ID NO: X3, and C4= SEQ. ID NO: X4; designated SEQ. ID NO: 130.

In some embodiments: wherein each of the nucleic acids comprises a vector sequence.

Also described: are an isolated nucleic acid selected from the library and a isolated cell expressing the nucleic acid as well as a purified library of purified polypeptides encoded by the library; and a population of filamentous phage displaying the polypeptides encoded by the library.

Described herein is a method of generating a library, comprising: (i) providing a parental nucleic acid encoding a parental polypeptide comprising the amino acid sequence: C1-X1-C2-X2-C3-X3-C4, wherein subsequence C1 is selected from SEQ ID NOs:1-30, subsequence C2 is selected from SEQ ID NOs:31-60, subsequence C3 is selected from SEQ ID NOs:61-90; subsequence C4 is selected from SEQ ID NOs:91 120; each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; and each of X1-X3 is an independent subsequence consisting of 2-20 amino acids; (ii) replicating the parental nucleic acid under conditions that introduce up to 10 single amino acid substitutions, deletions, insertions, or additions to the X1, X2, or X3 subsequences, whereby a population of randomly varied subsequences encoding X1', X2', or X3' is generated; and (iii) the population of randomly varied subsequences X1', X2', or X3'is substituted, into a population of parental nucleic acids at the positions corresponding to those that encode X1, X2, or X3.

In various instances: at least one of the X1-X3 subsequences is selected from SEQ ID NOs:121-123; each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; none of C1-C4 comprise amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the replicating generates a heterogeneous population of randomly varied subsequences by introducing up to 5 amino acid substitutions in each of X1, X2, or X3; the method further comprises amplifying the library by introducing it into a biological replication system and proliferating the biological replication system; the biological replication system is a plurality of E. coli cells; the biological replication system is a plurality of bacteriophage; the replicating occurs in vitro; the replicating is performed with a purified mutagenic polymerase; the replicating is performed in the presence of a nucleotide analog; the replicating occurs in vivo; the replicating in vivo occurs in a mutagenic species of E. coli.

Also described is a method of generating the library of claim 1, comprising:(i) selecting an amino acid sequence comprising the amino acid sequence C1-X1-C2-X2 C3 X3-C4 to be encoded, wherein: (a) subsequence C1 is selected from SEQ ID NOs:1-30, subsequence C2 is selected from SEQ ID NOs:31-60, subsequence C3 is selected from SEQ ID NOs:61 90, and subsequence C4 is selected from SEQ ID NOs:91-120; (b) each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (c) each of X1, X2, and X3 consists of an amino acid sequence 2-20 amino acids in length; (ii) providing a first plurality and a second plurality of oligonucleotides, wherein: (a) oligonucleotides of the first plurality encode the C1-C4 subsequences and multiple heterogeneous X1-X3 variant subsequences X1'-X3'; (b) oligonucleotides of the second plurality are complementary to nucleotide sequences encoding the C1-C4 subsequences and to nucleotide sequences encoding multiple heterogeneous X1' X3' subsequences; and (c) the oligonucleotides of the first and second pluralities have overlapping sequences

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complementary to one another; (iii) combining the population of oligonucleotides to form a first mixture; (iv) incubating the mixture under conditions effective for hybridizing the overlapping complementary sequences to form a plurality of hybridized complementary sequences; and (v) elongating the plurality of hybridized complementary sequences to form a second mixture containing the library.

In various instances: each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises from zero and up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the method further comprises performing a cycle of steps, the cycle of steps comprising denaturing the library by increasing the temperature of the second mixture to a temperature effective for denaturing double stranded DNA, followed by steps (iv) and (v); the method comprises repeating the cycle of steps up to 100 times; the method further comprises amplifying the library by a polymerase chain reaction consisting essentially of the library, a forward primer, and a reverse primer, wherein the forward and reverse primers can hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library; the amino acid to be encoded in each position of the X1, X2, or X3 subsequences, is selected from a subset of alanine, arginine, asparagine, aspartate, cysteine, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine; herein the amino acid selected for each single amino acid substitution is selected from a group of amino acids consisting of at least one aliphatic, at least one one acidic, at least one one neutral, and at least one one aromatic amino acid; and the group of amino acids consists of alanine, aspartate, serine, and tyrosine.

Also described herein is a method of generating a library, comprising: (i) providing a parental nucleic acid encoding a parental polypeptide comprising the amino acid sequence: C1-X1-C2-X2-C3-X3-C4, wherein subsequence C1 is selected from FIG. 2 or FIG 4, subsequence C2 is selected from FIG. 2 or FIG 4, subsequence C3 is selected from FIG.2 or FIG 4; subsequence C4 is selected from FIG.2 or FIG 4 each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; and each of X1-X3 is an independent

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subsequence consisting of 2-20 amino acids; (ii) replicating the parental nucleic acid under conditions that introduce up to 10 single amino acid substitutions, deletions, insertions, or additions to the X1, X2, or X3 subsequences, whereby a population of randomly varied subsequences encoding X1', X2', or X3' is generated; and (iii) the population of randomly varied subsequences X1', X2', or X3'is substituted, into a population of parental nucleic acids at the positions corresponding to those that encode X1, X2, or X3.

In various embodiments: at least one of the X1-X3 subsequences is selected from SEQ ID NOs:121-123; each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; none of C1-C4 comprise an amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the replicating generates a heterogeneous population of randomly varied subsequences by introducing up to 5 amino acid substitutions in each of X1, X2, or X3; the method further comprises amplifying the library by introducing it into a biological replication system and proliferating the biological replication system; the biological replication system is a plurality of E. coli cells; the biological replication system is a plurality of bacteriophage; the replicating occurs in vitro; the replicating is performed with a purified mutagenic polymerase the replicating is performed in the presence of a nucleotide analog; the replicating occurs in vivo; and the replicating in vivo occurs in a mutagenic species of E. coli.

Also described is a method of generating the library, comprising: (i) selecting an amino acid sequence comprising C1-X1-C2-X2 C3 X3-C4 to be encoded, wherein (a) subsequence C1 is selected from FIG. 2 or FIG 4, subsequence C2 is selected from FIG. 2 or FIG 4, subsequence C3 is selected from FIG. 2 or FIG 4, and subsequence C4 is selected from FIG. 2 or FIG 4; (b) each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (c) each of X1, X2, and X3 consists of an amino acid sequence 2-20 amino acids in length; (ii) providing a first plurality and a second plurality of oligonucleotides, wherein (a) oligonucleotides of the first plurality encode the C1-C4 subsequences and multiple

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heterogeneous X1-X3 variant subsequences X1'-X3'; (b) oligonucleotides of the second plurality are complementary to nucleotide sequences encoding the C1-C4 subsequences and to nucleotide sequences encoding multiple heterogeneous X1' X3' subsequences; and

(c) the oligonucleotides of the first and second pluralities have overlapping sequences complementary to one another; (iii) combining the population of oligonucleotides to form a first mixture; (iv) incubating the mixture under conditions effective for hybridizing the overlapping complementary sequences to form a plurality of hybridized complementary sequences; and (v) elongating the plurality of hybridized complementary sequences to form a second mixture containing the library.

In various cases: each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises from zero and up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the method further comprises performing a cycle of steps, the cycle of stepscomprising denaturing the library by increasing the temperature of the second mixture to a temperature effective for denaturing double stranded DNA, followed by steps (iv) and (v); the method further comprises repeating the cycle of steps up to 100 times; the method further comprises amplifying the library by a polymerase chain reaction consisting essentially of the library, a forward primer, and a reverse primer, wherein the forward and reverse primers can hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library; the amino acid to be encoded in each position of the X1, X2, or X3 subsequences, is selected from a subset of alanine, arginine, asparagine, aspartate, cysteine, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine; the amino acid selected for each single amino acid substitution is selected from a group of amino acids consisting of at least one aliphatic, at least one acidic, one at least one neutral, and at least one aromatic amino acid; and the group of amino acids consists of alanine, aspartate, serine, and tyrosine.

Also disclosed is a method of generating the library, comprising:. (i) providing a parental nucleic acid encoding a parental polypeptide comprising the amino acid sequence: C1-X1-C2-X2-C3-X3-C4, wherein subsequence C1 is selected from FIG. 3 or FIG 5, subsequence C2 is selected from FIG. 3 or FIG 5, subsequence C3 is selected from FIG. 3 or FIG 5; subsequence C4 is selected from FIG. 3 or FIG 5; each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; and each of X1-X3 is an independent subsequence consisting of 2-20 amino acids; (ii) replicating the parental nucleic acid under conditions that introduce up to 10 single amino acid substitutions, deletions, insertions, or additions to the X1, X2, or X3 subsequences, whereby a population of randomly varied subsequences encoding X1', X2', or X3' is generated; and (iii) the population of randomly varied subsequences X1', X2', or X3'is substituted, into a population of parental nucleic acids at the positions corresponding to those that encode X1, X2, or X3.

In various instances: at least one of the X1-X3 subsequences is selected from SEQ ID NOs:121-123; each of C1-C4 independently comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; none of C1-C4 comprise amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the replicating generates a heterogeneous population of randomly varied subsequences by introducing up to 5 amino acid substitutions in each of X1, X2, or X3; the method further comprises amplifying the library by introducing it into a biological replication system and proliferating the biological replication system; the biological replication system is a plurality of E. coli cells; the biological replication system is a plurality of bacteriophage; the replicating occurs in vitro; the replicating is performed with a purified mutagenic polymerase; the replicating is performed in the presence of a nucleotide analog; the replicating occurs in vivo; and the replicating in vivo occurs in a mutagenic species of E. coli.

Also described is a method of generating the library, comprising: (i) selecting an amino acid sequence comprising: C1-X1-C2-X2 C3 X3-C4 to be encoded, wherein (a) subsequence C1 is selected from FIG. 3 or FIG 5, subsequence C2 is selected from FIG. 3 or FIG 5, subsequence C3 is selected from FIG. 3 or FIG 5, and subsequence C4 is

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selected from FIG. 3 or FIG 5; (b) each of C1-C4 comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; (c) each of X1, X2, and X3 consists of an amino acid sequence 2-20 amino acids in length; (ii) providing a first plurality and a second plurality of oligonucleotides, wherein (a) oligonucleotides of the first plurality encode the C1-C4 subsequences and multiple heterogeneous X1-X3 variant subsequences X1'-X3'; (b) oligonucleotides of the second plurality are complementary to nucleotide sequences encoding the C1-C4 subsequences and to nucleotide sequences encoding multiple heterogeneous X1' X3' subsequences; and (c) the oligonucleotides of the first and second pluralities have overlapping sequences complementary to one another; (iii) combining the population of oligonucleotides to form a first mixture; (iv) incubating the mixture under conditions effective for hybridizing the overlapping complementary sequences to form a plurality of hybridized complementary sequences; and (v) elongating the plurality of hybridized complementary sequences to form a second mixture containing the library.

In various embodiments: each of C1-C4 comprises up to 20 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises up to 10 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; each of C1-C4 independently comprises from zero and up to 5 single amino acid substitutions, deletions, insertions, or additions to the selected subsequence; the method further comprises performing a cycle of steps, the cycle comprising denaturing the library by increasing the temperature of the second mixture to a temperature effective for denaturing double stranded DNA, followed by steps (iv) and (v); the method further comprises repeating the cycle up to 100 times; the method further comprises amplifying the library by a polymerase chain reaction consisting essentially of the library, a forward primer, and a reverse primer, wherein the forward and reverse primers can hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library; the amino acid to be encoded in each position of the X1, X2, or X3 subsequences, is selected from a subset of alanine, arginine, asparagine, aspartate, cysteine, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine the amino acid selected for each single amino acid substitution is selected from a group of amino acids consisting of at least

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one aliphatic, one acidic, one neutral, and one aromatic amino acid; and the group of amino acids consists of alanine, aspartate, serine, and tyrosine.

Also described is a library of nucleic acids encoding at least ten different polypeptides, wherein: (i) the amino acid sequence of each of the encoded polypeptides comprises an amino acid sequence at least 70% identical to any of SEQ ID NOs:127-129; (ii) the amino acid sequence of each of the encoded polypeptides includes amino acids that differ from those of SEQ ID NOs:127-129 at positions 14, 15, 33, 35-36, 38, 47-48, 66, 68-69, 71, 80, 81, 99, 101-102, and 104, and the amino acid differences are heterogeneous across a plurality of the encoded polypeptides; and (iii) the amino acid sequence of each of the encoded polypeptides outside of the residues corresponding to positions 14, 15, 33, 35-36, 38, 47-48, 66, 68-69, 71, 80, 81, 99, 101-102, and 104 of SEQ ID NOs: 127-129 is homogeneous across a plurality of the encoded polypeptides.

In various embodiments: the amino acid sequence of the polypeptides has at least 75% identity to any of SEQ ID NOs 127-129; the amino acid sequence of the polypeptides has at least 80% identity to any of SEQ ID NOs 127-129; and the amino acid sequence of the polypeptides has at least 85% identity to any of SEQ ID NOs 127-129 each of the nucleic acids comprises a vector sequence. Also disclosed: an isolated nucleic acid encoding a polypeptide, selected from the library; a purified polypeptide encoded by the nucleic acid; a population of cells expressing the polypeptides encoded by the library; .a cell selected from the population of cells; a purified library of polypeptides encoded by the library; a population of filamentous phage displaying the library of polypeptides encoded by the library.

Also disclosed is a method of generating the library, comprising: (i) selecting an amino acid sequence corresponding to any one of SEQ ID NOs: 127 129 to be encoded, wherein the selected sequence differs from those of SEQ ID NOs:127-129 in at least one of variable positions 14, 15, 33, 35-36, 38, 47-48, 66, 68-69, 71, 80, 81, 99, 101-102, and 104; (ii) chemically providing a first and a second plurality of oligonucleotides, wherein (a) oligonucleotides of the first plurality encode amino acid subsequences of the selected amino acid sequence; the subsequences being heterogeneous at the encoded variable positions; (b) oligonucleotides of the second plurality are complementary to nucleotide sequences encoding subsequences of the selected amino acid sequence, the subsequences being heterogeneous at the encoded variable positions; and (c) the first and second pluralities comprise

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oligonucleotides have overlapping sequences complementary to one another; (iii) combining the population of oligonucleotides to form a first mixture; (iv) incubating the mixture under conditions effective for hybridizing the overlapping complementary sequences to form a plurality of hybridized complementary sequences; and (v) elongating the plurality of hybridized complementary sequences to form a second mixture containing the library.

In various instances: the method further comprises performing a cycle of denaturing the library by increasing the temperature of the second mixture to a temperature effective for denaturing double stranded DNA, followed by steps (iv) and (v); the method further comprises repeating the cycle up to 100 times; the method further comprises amplifying the library by a polymerase chain reaction consisting essentially of the library, a forward primer, and a reverse primer, wherein the forward and reverse primers can hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library; the amino acids to be encoded for the variable positions, are selected from a subset of alanine, arginine, asparagine, aspartate, cysteine, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine the amino acids selected for the variable positions are selected from a group consisting of an aliphatic, an acidic, a neutral, and an aromatic amino acid; the group of amino acids consists of alanine, aspartate, serine, and tyrosine.

The details of one or more embodiments of the invention are set forth in the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

FIG. 1 is a schematic representation depicting the generation of a library of nucleic acids encoding chimeric binding polypeptides by diversifying subsequences within an encoded polypeptide scaffold sequence. Encoded scaffold polypeptide sequence is SEQ ID NO:124. Library of encoded chimeric binding polypeptides are SEQ ID NOs: 844, 845 and 846, respectively (i.e., from top to bottom).

FIG. 2 is an alignment of the sequences of a number of proteins that have regions which can be used as a scaffold. These proteins are homologous to oryzacystatin. The Cl, C2, C3 and C4 are boxed and labeled. The sequences shown are SEQ ID NO: 132 (i.e., homologous sequences Q2V8I6_CUCMA_1441/1-28 – Q2V8I4_CUCMO_734/1-28); SEQ ID NO: 133 (i.e., Q2V8H9_LAGLE_431/1-28); SEQ ID NO: 134 (i.e., Q6DKU9_CUCMA_1441/1-28 and Q6DLC8_CUCMA_1441/1-28); SEQ ID NO: 135 (i.e., 080389_CUCSA_795/1-89); SEQ ID NOs: 136 - 150 (i.e., QIRVW3_MEDTR_2578/1-54 – Q8GZV2_CHEMJ_340/1-38); SEQ ID NO:130 (i.e., Reference/1-102); and SEQ ID NOs: 151-198 and 200-330 (i.e., CYT1_ORYSA_1097/1-88 to end).

FIG. 3 is an alignment of the sequences of a number of proteins that have regions which can be used as a scaffold. These proteins are homologous to C2. The Cl, C2, C3 and C4 are boxed and labeled. Sheets 1-3 show SEQ ID NOs: 331-367 (i.e., Q9M366_ARATH_43120/1-78 – Q9FJG3_ARATH_325405/1-81); SEQ ID NO: 130 (i.e., Reference/1-156); and SEQ ID NOs: 368-384 (i.e., ERG1_ORYSA_795/1-89 – Q4JHI8_CUCMA_692/1-87). Sheets 4-6, 7-9, 10-12. 13-15, 16-18, 19-21, 22-24, and 25-27 show SEQ ID NOs: 385-827.FIG. 4 is an alignment of the sequences of a number of proteins that have regions which can be used as a scaffold. The sequences shown are SEQ ID NO:130 (i.e., oryza full) and SEQ ID NOs 828-838. These proteins are homologous to oryzacystatin. The Cl, C2, C3 and C4 are boxed and labeled.

FIG 5. is an alignment of the sequences of a number of proteins that have regions which can be used as a scaffold. The sequences shown are, from top to bottom, SEQ ID NO:131 and SEQ ID NOs 839-843. These proteins are homologous to C2. The Cl, C2, C3 and C4 are boxed and labeled.

DETAILED DESCRIPTION

Diverse libraries of nucleic acids (e.g., cDNA libraries) encoding plant chimeric binding polypeptides, as well as methods for generating them are described below. The amino acid sequences of the library of encoded plant chimeric binding proteins are derived from a scaffold polypeptide sequence that includes subsequences to be varied. The varied subsequences correspond to putative binding domains of the plant chimeric binding proteins, and are highly heterogeneous in the library of plant chimeric binding proteins. In contrast, the sequence of the encoded chimeric binding proteins outside of the varied subsequences is essentially the same as the parent scaffold polypeptide sequence and highly homogeneous throughout the library of encoded plant chimeric binding proteins. Thus, libraries of plant chimeric binding proteins can serve as a universal molecular recognition library platform for selection of specialized binding proteins for expression in transgenic plants. Libraries of plant chimeric binding proteins can be expressed by transfected cells (i.e., as expression libraries) and tested for interaction with a molecular

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I. Plant Scaffold Polypeptide Sequences

A plant scaffold polypeptide sequence is an amino acid sequence based on a plant protein that is structurally tolerant of extreme sequence variation within one or more regions. The regions to be varied within the scaffold polypeptide sequence are conceptually analogous to the hypervariable regions of immunoglobulins, and form putative binding domains in a chimeric binding polypeptide. Thus, a large library of nucleic acid sequences encoding diverse plant chimeric binding polypeptides is produced by diversifying specific sequences within a scaffold polypeptide sequence, as is described in detail below.

Plant scaffold polypeptide sequences are selected to have a number of properties, e.g., they: (i) are derived from sequences that are of plant origin; (ii) encode proteins that tolerate the introduction of sequence diversity structurally; (iii) only contain disulfide bonds that do not interfere with folding of the polypeptide when expressed in a plant; (iv) express at high levels in diverse plant tissues; and (v) can be targeted to different subcellular locations (e.g., cytoplasm, mitochondria, plastid) or secreted from the cell. Based on these properties, plant scaffold polypeptide sequences permit the generation of large libraries of chimeric binding polypeptides with highly diverse binding activities. Libraries of chimeric binding polypeptides can be screened for binding to a target molecule. Chimeric binding proteins having the desired binding activity can subsequently be expressed in plants to confer input traits (e.g., pest or pathogen resistance, drought tolerance) or output traits (e.g. modified lipid composition, heavy metal binding for phytoremediation, medicinal uses). Such binding proteins can also be used in various affinity-based applications, e.g., diagnostic detection of an antigen using a sandwich ELISA; histochemical detection of antigens; generation of protein biochips; and affinity purification of antigens.

It is helpful to select the scaffold polypeptide sequence based on the sequence of a plant protein or protein domain of known three dimensional structure (see, e.g., Nygren *et al.* (2004) "Binding Proteins from Alternative Scaffolds," *J. of Immun. Methods* 290:3-28). However, even without experimentally determined structural data for a potential scaffold polypeptide sequence, valuable inferences can be gleaned from computational structural analysis of a candidate amino acid sequence. Useful programs for structure prediction from an amino acid sequence include, e.g., the "SCRATCH Protein Predictor" suite of programs available to the public on the world wide web at

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ics.uci.edu/~baldig/scratch/index. It is important that introduction of sequence variation not destabilize the known or predicted secondary structure of the scaffold polypeptide sequence. Accordingly, the known or predicted secondary structure of the scaffold polypeptide sequence informs the selection of amino acid subsequences that can be varied within a scaffold polypeptide sequence to form putative binding domains. The structural adequacy of a particular scaffold polypeptide sequence can be readily tested, e.g., by phage display expression analysis methods that are commonly known in the art. For example, a scaffold polypeptide sequence containing 0, 1, 2, 3, or more disulfide bonds can be tested for its ability to fold into a stable protein. Since proteins that do not fold properly will not be incorporated into a phage coat, they will not be displayed. Thus, without undue effort, many candidate scaffold polypeptide sequences can be rapidly screened for their ability to fold into stable proteins once expressed.

The plant scaffold polypeptide sequences can be based on the accessory domain from purple acid phosphatases (PAPs). The crystal structure of the PAP accessory domain of kidney bean, *Phaseolus vulgaris*, has been determined (Strater *et al.* (1995), *Science* 268(5216):1489-1492). Three exposed loops within the protein are reminiscent of the hypervariable domains found in immunoglobulins. The loops are brought together by the rigid anti-parallel β-sheet framework of the protein. The subsequences that form each loop form the putative binding domains of a chimeric binding protein derived from a PAP. These subsequences are diversified by substituting, deleting, inserting, or adding up to 10 (e.g., up to 3, 4, 6, 8) amino acids. The loops that form the putative binding domains are particularly well suited to binding target molecules containing pockets or clefts.

PAP-based scaffold polypeptide sequences take the general form:

$$\mathbf{C_1\text{-}X_1\text{-}C_2\text{-}X_2\text{-}C_3\text{-}X_3\text{-}C_4}$$

where C_1, C_2, C_3, and C_4 correspond to "backbone" subsequences which can include some introduced variation, but are not highly diversified. On the other hand, X_1, X_2, and X_3 correspond to highly varied subsequences that form the putative binding domains of each PAP-based chimeric binding protein. Table 1 shows a list of suitable C_1-C_4 backbone subequences derived from the amino acid sequences of 30 PAPs.

C_1, C_2, C_3, and C_4 correspond to SEQ ID NOs: 1-30, 31-60, 61-90, and 91-120, respectively, in Table 1.

X_1, X_2, and X_3 can be based on naturally occurring variants of corresponding PAP sequences, e.g., those shown in Table 2 as SEQ ID NOs: 121-123. Table 2 shows the range variation at each amino acid position in subsequences corresponding, respectively, to X_1, X_2, and X_3, within 30 naturally occurring PAP sequences. Alternatively, the parent variable subsequences, X_1,-X_3, can be arbitrary sequences 2-20 amino acids in length.

In some implementations, C_1, C_2, C_3, and C_4 of a scaffold polypeptide sequence can be selected from multiple PAP-based scaffold polypeptide sequence sequences listed in Table 1, in any combination, e.g., $C_{1(\text{SEQ ID NO:5})}$, $C_{2(\text{SEQ ID NO:12})}$, $C_{3(\text{SEQ ID NO:7})}$, and $C_{4(\text{SEQ ID NO:19})}$; $C_{1(\text{SEQ ID NO:5})}$, $C_{2(\text{SEQ ID NO:12})}$, $C_{3(\text{SEQ ID NO:5})}$, and $C_{4(\text{SEQ ID NO:12})}$; $C_{4(\text{SEQ ID NO:22})}$; $C_{1(\text{SEQ ID NO:17})}$, $C_{2(\text{SEQ ID NO:17})}$, $C_{3(\text{SEQ ID NO:19})}$, and $C_{4(\text{SEQ ID NO:1})}$, and so forth.

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Table 1: SPSs Based on the Accessory Domain of PAPs			
Seq ID	C_1	Seq ID	C_2
1	PQQVHITQGDHVGKAVIVSWVT	31	VVVYWSENSKYKKSAEGTVTT
2	PQQVHITQGDLVGKAVIVSWVT	32	EVHYWSENSDKKKIAEGKLVT
3	PQQVHITQGDLVGRAMIISWVT	33	AVRYWSEKNGRKRIAKGKMST
4	PQQVHITQGDLVGKAVIVSWVT	34	EVHYWSENSDKKKIAEGKLVT
5	PQQVHITQGDHVGKAVIVSWVT	35	AVRYWSKNSKQKRLAKGKIVT
6	PQQVHITQGDHVGKAMIVSWVT	36	KVVYWSENSQHKKVAKGNIRT
7	PQQVHITQGDHVGKAMIVSWVT	37	KVVYWSENSQHKKVARGNIRT
8	PQQVHITQGDHEGKTVIVSWVT	38	TVLYWSEKSKQKNTAKGKVTT
9	PQQVHITQGDLVGQAMIISWVT	39	QVIYWSDSSLQNFTAEGEVFT
10	PQQVHITQGDLVGQAMIISWVT	40	QVIYWSDSSLQNFTAEGEVFT
11	PQQVHITQGDHVGKAMIVSWVT	41	TVLYWSNNSKQKNKATGAVTT
12	PQQVHITQGDLEGEAMIISWVR	42	KVLYWIDGSNQKHSANGKITK
13	PQQVHITQGDHVGKAVIVSWVT	43	TVVYWSEKSKLKNKANGKVTT
14	PQQVHITQGDHVGQAMIISWVT	44	EVIYWSNSSLQNFTAEGEVFT
15	PQQVYITQGDHEGKGVIASWTT	45	SVLYWAENSNVKSSAEGFVVS
16	PQQVHITQGDYEGKGVIISWVT	46	TVVYWAENSSVKRRADGVVVT
17	PQQVHITQGDLVGRAMIISWVT	47	AVRYWSEKNGRKRIAKGKMST
18	PQQVHLTQGDHVGKGVIVSWVT	48	KVLYWEFNSKIKQIAKGTVST
19	PQQVHITQGDVEGKAVIVSWVT	49	KVIYWKENSTKKHKAHGKTNT
20	PQQVHVTQGNHEGNGVIISWVT	50	TVRYWCENKKSRKQAEATVNT
21	PQQVHVTQGNHEGNGVIISWVT	51	TVQYWCENEKSRKQAEATVNT
22	PQQVHITQGDYDGKAVIVSWVT	52	KVQFGTSENKFQTSAEGTVSN
23	PQQVHITQGDHEGRSIIVSWIT	53	TVFYGTSENKLDQHAEGTVTM
24	PQQVHITLGDQTGTAMTVSWVT	54	TVRYGSSPEKLDRAAEGSHTR
25	PQQVHITQGDYDGKAVIVSWVT	55	EVVYGTSPNSYDHSAQGKTTN
26	PQQVHITQGDYDGKAVIISWVT	56	HIQYGTSENKFQTSEEGTVTN
27	PQQVHITQGDYDGEAVIISWVT	57	EVRYGLSEGKYDVTVEGTLNN
28	PQQVHITQGDYDGKAVIISWVT	58	QVHYGAVQGKYEFVAQGTYHN
29	PQQVHITQGDYDGKAVIISWVT	59	QVHYGAVQGKYEFVAQGTYHN
30	PQQVHITQGDYNGKAVIVSWVT	60	EVLYGKNEHQYDQRVEGTVTN

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Table 1 continued

Seq ID	C_3	Seq ID	C_4
61	YIHHCYIKGLEYDTKYYYV	91	SREFWFR
62	FIHHTTIRNLEYKTKYYYE	92	TRQFWFV
63	FIHHTTIRKLKYNTKYYYE	93	TRRFSFI
64	FIHHTTIRNLEYKTKYYYE	94	TRQFWFV
65	FIHHTTIRNLEYNTKYYYE	95	TRQFWFV
66	YIHHCTIRNLEYNTKYYYE	96	TRSFWFT
67	YIHHCTIRNLEYNTKYYYE	97	TRSFWFT
68	YIHHSTIRHLEFNTKYYYK	98	ARTFWFV
69	FIHHTTITNLEFDTTYYYE	99	TRQFWFI
70	FIHHTTITNLEFDTTYYYE	100	TRQFWFI
71	YIHHCIIKHLKFNTKYYYE	101	PRTFWFV
72	FIHHCTIRRLKHNTKYHYE	102	VRSFWFM
73	YIHHCNIKNLKFDTKYYYK	103	ARTFWFT
74	FIHHTNITNLEFNTTYFYV	104	TRQFWFI
75	YIHHCTIKDLEFDTKYYYE	105	TRKFWFV
76	YIHHCTIKDLEYDTKYYYE	106	KRQFWFV
77	YIHHCTIKNLEYNTKYFYE	107	TRQFWFT
78	YIHHCTIQNLKYNTKYYYM	108	RRTFWFV
79	FIHHCPIRNLEYDTKYYYV	109	ERKFWFF
80	YIHHCLIDDLEFDTKYYYE	110	SRRFWFF
81	YIHHCLIDDLEFDTKYYYE	111	SRRFWFF
82	YVHHCLIEGLEYKTKYYYR	112	SREFWFE
83	YIHHCVLTDLKYDRKYFYK	113	ARLFWFK
84	FIHHCTLTGLTHATKYYYA	114	VRTFSFT
85	YIHHCLLDKLEYDTKYYYK	115	AREFWFH
86	YIHHCLIEGLEYETKYYYR	116	SREFWFK
87	YIHQCLVTGLQYDTKYYYE	117	ARKFWFE
88	FIHHCLVSDLEHDTKYYYK	118	SREFWFV
89	FIHHCLVSDLEHDTKYYYK	119	SREFWFV
90	YIHHCLVDGLEYNTKYYYK	120	AREFWFE

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Table 2: Naturally Occurring Residue Variation in PAP Subsequences Corresponding to X_1, X_2, and X_3 (SEQ ID NOs:121-123)

X_1 (SEQ ID NO: 121)							X_2 (SEQ ID NO: 122)									X_3 (SEQ ID NO: 123)					
Position							Position									Position					
a	b	c	d	e	f	g	a	b	c	d	e	f	g	h	i	a	b	c	d	e	f
M	D	E	P	G	S	S	Y	K	Y	Y	N	Y	T	S	G	V	G	L	R	N	T
V	E	A	K		P	N		R	F	F	T		S		P	I	E	I	G	H	
E	N	K	L		K	K		T		H	K		N			L		V	E	D	
P	V	D				T		F			D		K			M		E	D	Q	
Q	S				H						E		E					T		K	
T	I				T													S		S	
A	A																	E		E	
F																		F			
																		K			

After diversification of the above-listed subsequences of the scaffold polypeptide sequence, the diversified X_1', X_2', and X_3' subsequences are highly heterogeneous within the library of encoded plant chimeric binding polypeptides, and can each contain up to 10 (e.g., 8, 6, 4, 3) single amino acid substitutions, deletions, insertions, or additions with respect to SEQ ID NOs: 121-123 listed in Tables 1, respectively (see, e.g., Fig. 1). For example, the length of the amino acid sequences corresponding to regions X_1, X_2, or X_3 can be unaltered, shortened, or lengthened relative to SEQ ID NOs: 121-123.

The regions outside of the putative binding domains are referred to as "backbone" regions (i.e., C_1, C_2, C_3, and C_4). Unlike the amino acid sequences for X_1, X_2, and X_3, the amino acid sequences of the backbone regions are generally not substantially diversified within the library of encoded chimeric binding proteins, although some sequence variation in these regions within the library is permissible. The backbone regions of a plant scaffold polypeptide sequence can be at least 70% (i.e., 80, 85, 90, 95, 98, or 100%) identical to any of SEQ ID NOs: 1-120. Alternatively, the backbone regions can contain up to 30 (i.e., 28, 26, 24, 22, 20, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1) single amino acid substitutions, deletions, insertions or additions. For example, C_1, C_2, C_3, and C_4 can each include 0, 1, 2, 3, 4, or 5 or more single amino acid changes. If amino acid substitutions are to be introduced into the backbone regions, it is preferable to make conservative substitutions. A conservative substitution is one that preserves the substitutes an amino acid with one that has similar chemical properties (e.g., substitution of a polar amino acid such as serine with another polar amino acid such as threonine).

In one embodiment, the plant scaffold polypeptide sequence is one of SEQ ID NOs: 124-126 shown below. Sequences corresponding to X_1, X_2, and X_3 are in bold and underlined.

SEQ ID NO: 124

PQQVHITQGDHVGKAVIVSWVT**MDEPGSS**VVVYWSENSKYKKSAEGTVTT**YRFYNYTSG**YIHHCYIKGLEYDTKYYYV**VGIGNT**SREFWFR

SEQ ID NO: 125

PQQVHITQGDLVGKAVIVSWVT**VDEPGSS**EVHYWSENSDKKKIAEGKLVT**YRFFNYSSG**FIHHTTIRNLEYKTKYYYE**VGLGNT**TRQFWFV

SEQ ID NO: 126

PQQVHITQGDLVGRAMIISWVT**MDEPGSS**AVRYWSEKNGRKRIAKGKMST**YRFFNYSSG**FIHHTTIRKLKYNTKYYYE**VGLRNT**TRRFSFI

In other embodiments, a plant scaffold polypeptide sequence is based on the amino acid sequence of plant proteins that have ankyrin-like repeats. Ankryin-like repeats are small turn-helix-helix (THH) repeats consisting of approximately 33 amino acids. The number of THH repeats within a scaffold polypeptide sequence can vary from 2 to 20. The putative binding sites within the THH repeats are typically non-contiguous, but clustered on the same side of the protein of which they are a part.

A plant THH repeat-containing scaffold polypeptide sequence can have an amino acid sequence that is based on any of SEQ ID NOs: 127-129 listed below. High levels of amino acid sequence variation are introduced at the bolded/underlined residues. The plant THH repeat-containing scaffold polypeptide sequences can contain substitutions of up to 3 amino acids or a deletion in the place of the amino acids

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corresponding to residues 12-13, 33, 35-36, 38, 46-47, 66, 68-69, 71, 79-80, 99, 101-102, 104, and 112-113 (residues in bold and underlined) of SEQ ID NOs:127-129.

SEQ ID NO: 127

GDDLGKKLHLAA**SR**GHLEIVRVLVEAGADVNA**L**D**KF**G**R**TALHIAA**SR**GHLEV
VKLLLEAGADVNA**L**D**KF**G**R**TALHLAA**SR**GHLEVVKLLLEAGADVNA**L**D**KF**G
DTALHVSI**DN**GNEDIAEILQ

SEQ ID NO: 128

GDDLGKKLHLAA**SR**GHLEIVRVLVEAGADVNA**L**D**KF**G**R**TPLHIAA**SK**GNEQV
VKLLLEAGADPNA**L**D**KF**G**R**TPLHIAA**SK**GNEQVVKLLLEAGADPNA**Q**D**KF**G**D**
TALHVSI**DN**GNEDIAEILQ

SEQ ID NO: 129

GSDLGKKLLEAA**RA**GQDDEVRILMANGADVNA**L**D**KF**G**R**TPLHIAA**SK**GNEQ
VVKLLLEAGADPNA**L**D**KF**G**R**TPLHIAA**SK**GNEQVVKLLLEAGADPNA**Q**D**KF**G
KTAFDISI**DN**GNED**L**AEILQ

The sequence of the scaffold polypeptide sequences can be at least 70% (i.e., 80, 85, 90, 95, 98, or 100%) identical to the sequence outside of the foregoing amino acid positions (in bold) of SEQ ID NOS: 127-129. Alternatively, the sequence of the scaffold polypeptide sequences outside of the foregoing amino acid positions (in bold) of SEQ ID NOS:127-129 can contain up to 30 (i.e., 28, 26, 24, 22, 20, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1) single amino acid substitutions, deletions, insertions or additions. In some cases it can be desirable to include additional repeating units. SEQ ID NOs: 127-129 have an amino-terminal cap, two internal repeats and a carboxy-terminal cap. It might be desirable to have 1-6 internal repeats. The amino-terminal cap sequence is aa 1-33. The first internal repeat is 34-66 and the second internal repeat is 67- 99. The carboxy-terminal cap sequence is aa 100-123. The first or the second internal repeats or both can be independently repeated 1, 2, 3, 4, 5 or 6 times.

The putative binding sites are formed by amino acid side chains protruding from the rigid secondary structure formed by the scaffold polypeptide sequence. These proteins may typically form a larger, flatter binding surface and are particularly useful for binding to targets that do not have deep clefts or pockets.

Another suitable scaffold can be based on oryzacystatin (*J Biol Chem* 262:16793 (1987); *Biochemistry* 39:14753 (2000)), a member of the cystatin/Papain

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Family (Pfam Identifier PF00031) that is identified as a cysteine proteinase inhibitor of rice. The sequence of oryzacystatin is depicted below. A scaffold having the amino acid sequence C1-X1-C2-X2-C3-X3-C4 where each of Xl, X2, X3 and X4 is a variable region and Cl, C2, C3 and C4 are the backbone regions can be created based on oryzacystatin.

MSSVGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLEFEKLV SVKQQVVAGTLYYFTLEVKEGDAKKLYEAKVWEKPWMDFKELQEFKPVDAS ANA (SEQ ID NO: 130)

Cl-MSS (aa 1-3 of SEQ ID NO: 130)

Xl-VGGP (aa 4-7 of SEQ ID NO: 130)

C2- VLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLEFEKLVSV (aa-8-50 of SEQ ID NO: 130)

X2-KQQ VVAGT (aa 51-58 of SEQ ID NO: 130)

C3-LYYFTLEVKEGD AKKLYEAKVWE (aa 59-81 of SEQ ID NO: 130)

X3-KPWM (aa 82-85 of SEQ ID NO: 130)

C4-DFKELQEFKPVDASANA (aa 86-102 of SEQ ID NO: 130)

FIG. 2 depicts the sequences of a large number of plant proteins aligned with oryzacystatin. Examples of suitable C1-C4 regions are indicated. FIG. 4 depicts the sequences of a small number of plant proteins aligned with oryzacystatin. Examples of suitable C1-C4 regions are indicated. In general, Xl can be a sequence of 2-20 random amino acids (e.g., 3 amino acids). X2 can be a sequence of 2-20 random amino acids (e.g., 4 amino acids). X3 can be a sequence of 2-20 random amino acids (e.g., 4 amino acids).

Yet another suitable can be based on the C2 protein of rice (*Biochemistry* 42:11625 (2003)), a member of the C2 domain family (Pfam Identifier PF00168) that is thought to be involved in plant defense signaling systems. The sequence of rice C2 is depicted below. A scaffold having the amino acid sequence Cl-Xl -C2-X2-C3-X3-C4 where each of Xl , X2, X3 and X4 is a variable region and Cl, C2, C3 and C4 are the backbone regions can be created based on rice C2.

MAGSGVLEVHLVDAKGLTGNDFLGKIDPYVVVQYRSQERKSSVARDQ GKNPSWNEVFKFQINSTAATGQHKLFLRLMDHDTFSRDDFLGEATINVTDLISL

GMEHGTWEMSESKHRVVLADKTYHGEIRVSLTFTASAKAQDHAEQVGGWAH SFRQ (SEQ ID NO: 131)

C1 -MAGSGVLEVHLVDAKG (aa 1-16 of SEQ ID NO: 131)
X1 -LTGNDFLGKID (aa 17-27 of SEQ ID NO: 131)
C2-PYVVVQYRSQERK (aa 28-40 of SEQ ID NO: 131)
X2-SSVARDQGKNP (aa 41-51 of SEQ ID NO: 131)
C3-SWNEVFKFQINSTAATGQHKLFLRL (aa 52-76 of SEQ ID NO: 131)
X3- MDHDTFSRDDFL (aa 77-88 of SEQ ID NO: 131)
C4-
GEATINVTDLISLGMEHGTWEMSESKHRVVLADKTYHGEIRVSLTFTASAKAQ DHAEQVGGWAHSFRQ (aa 89-156 of SEQ ID NO: 131)

FIG. 3 depicts the sequences of a large number of plant proteins aligned with rice C2. Examples of suitable C1-C4 regions are indicated. FIG. 4 depicts the sequences of a small number of plant proteins aligned with oryzacystatin. Examples of suitable C1-C4 regions are indicated. In general, X1 can be a sequence of 2-20 random amino acids (e.g., 11 amino acids). X2 can be a sequence of 2-20 random amino acids (e.g., 11 amino acids). X3 can be a sequence of 2-20 random amino acids (e.g., 12 amino acids).

The following sections disclose methods for generating libraries of nucleic acids encoding chimeric binding proteins based on plant scaffold polypeptide sequences.

II. Generation of Nucleic Acid Libraries based on a Plant scaffold polypeptide sequence

A large library of nucleic acid sequence variants encoding the plant scaffold polypeptide sequence is created based on one or more plant scaffold polypeptide sequences. The library of nucleic acids encodes at least 5 (e.g., 1,000, 10^5, 10^6, 10^7, 10^9, 10^{12}, 10^{15} or more) different chimeric binding protein sequences. It is recognized that not every member of a library generated by the methods described herein will encode a unique amino acid sequence. Nevertheless, it is desirable that at least 10%

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(e.g., 25%, 30%, 40%, 50%, 60%, 70%, 75%, or 90%) of the encoded chimeric binding proteins represented in the library be unique.

Prior to diversifying a plant scaffold polypeptide sequence, it may be useful to estimate computationally the expected sequence diversity to be generated with a given set of sequence variation parameters. A method for estimating sequence diversity is described, e.g., in Volles *et al.* (2005), 33(11): 3667-3677. For example, the number of different sequences expected in a library of nucleic acids generated by PCR can be estimated based on the mutation frequency of the mutagenic polymerase used for the amplification. Useful algorithms for estimating sequence diversity in randomized protein-encoding libraries can also be found on the world wide web, e.g., at guinevere.otago.ac.nz/mlrgd/STATS/index.

Libraries of nucleic acids encoding plant chimeric binding proteins can be generated by a number of known methodologies. Sequence diversity is introduced into a plant scaffold polypeptide sequence by substitution, deletion, insertion, or addition of amino acids at the highly variable positions of a scaffold polypeptide sequence as described above. Since the set of 20 amino acids that are genetically encoded in plants have somewhat redundant chemical and structural properties, a subset of amino acids (e.g., a subset of 4 types of amino acids) that encompasses this structural diversity can be adopted for substitutions. For example, amino acids to be used for substitution or insertion can be selected to include an acidic amino acid, a neutral amino acid, an aliphatic amino acid, and an aromatic amino acid (see Table 3). For example, the amino acids used for substitution could be limited to aspartate, serine, alanine, and tyrosine. Limiting the redundancy of amino acid substitutions will increase the overall structural and binding diversity of the library of chimeric binding proteins.

Table 3 Chemical Properties of Amino Acids Genetically Encoded in Plants

Acidic	Neutral	Aliphatic	Aromatic	Basic
Aspartate, Glutamate,	Asparagine, Cysteine Glutamine, Methionine, Proline, Serine, Threonine,	Alanine, Glycine, Isoleucine, Leucine, Valine	Histidine, Phenylalanine, Tryptophan, Tyrosine	Arginine, Lysine

The library of nucleic acids can be generated *in vitro* by assembly of sets of oligonucleotides with overlapping complementary sequences. First, a scaffold polypeptide sequence sequence is selected that is to be encoded by sets of assembled oligonucleotides. The sequences to be encoded in the variable regions of a given scaffold polypeptide sequence will include a multitude of heterogeneous sequences containing substitutions, insertions, deletions in additions in accordance with the library of chimeric binding polypeptides to be generated as described above. The scaffold polypeptide sequences to be encoded can include the C_1-C_4 subequences corresponding to any of SEQ ID NOs:1-30, 31-60, 61-90, and 91-120, respectively.

One set of oligonucleotides encodes regions of the plant scaffold polypeptide sequence where diversity is to be introduced (e.g., at X_1, X_2, and X_3). In contrast, regions of the scaffold polypeptide sequence in which little or no variation is to be introduced (e.g., in backbone domains of PAP scaffold polypeptide sequences) are encoded by a set of oligonucleotides encoding amino acid sequences with no less than 70% (i.e., 75%, 80%, 85%, 90%, 95%, or 100%) identity to any one of the above-mentioned scaffold polypeptide sequences. The details of this method are described, e.g., in U.S. patent No. 6,521,453, hereby incorporated by reference.

Sequence-varied oligonucleotides used to generate libraries of nucleic acids are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers (1981), Tetrahedron Letts., 22(20):1859-1862, e.g., using an automated synthesizer, as described in Needham-VanDevanter *et al.* (1984) Nucleic Acids Res., 12:6159-6168. A wide variety of equipment is commercially available for automated oligonucleotide synthesis. Multi-nucleotide synthesis approaches (e.g., tri-nucleotide synthesis), as discussed, supra, are also useful.

Nucleic acids can be custom ordered from a variety of commercial sources, such as Sigma-Genosys (at sigma-genosys.com/oligo.asp); The Midland Certified Reagent Company (mcrc@oligos.com), The Great American Gene Company (at genco.com), ExpressGen Inc. (at expressgen.com), Operon Technologies Inc. (Alameda, Calif.) and many others.

The oligonucleotides can have a codon use optimized for expression in a particular cell type (e.g., in a plant cell, a mammalian cell, a yeast cell, or a bacterial cell). Codon usage frequency tables are publicly available, e.g., on the world wide web at kazusa.or.jp/codon. Codon biasing can be used to optimize expression in a cell or

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on the surface of a cell in which binding of a plant chimeric binding protein is to be assessed, and can also be used to optimize expression of the chimeric binding protein in a transgenic organism of commercial interest (e.g., a transgenic plant). In general, codons with a usage frequency of less than 10% are not used. Before synthesis oligonucleotide sequences are checked for potentially problematic sequences, e.g, restriction sites useful for subcloning, potential plant splice acceptor or donor sites (see, e.g., cbs.dtu.dk/services/FeatureExtract/), potential mRNA destabilization sequences (e.g., "ATTTA"), and stretches of more than four occurrences of the same nucleotide. Potentially problematic sequences are changed accordingly.

Populations of oligonucleotides are synthesized that encode amino acid variations in the putative binding regions of the selected scaffold polypeptide sequence (e.g., in regions X_1, X_2, and X_3 of a PAP scaffold polypeptide sequence).

Preferably, all of the oligonucleotides of a selected length (e.g., about 10, 12, 15, 20, 30, 40, 50, 60, 70, 80, 90, or 100 or more nucleotides) that correspond to regions where sequence diversity is to be introduced in the scaffold polypeptide sequence encode all possible amino acid variations from a diverse set of amino acids as described above. This includes N oligonucleotides per N sequence variations, where N is the number of different sequences at a locus. The N oligonucleotides are identical in sequence, except for the nucleotide(s) encoding the variant amino acid(s). In generating the sequence-varied oligonucleotides, it can be advantageous to utilize parallel or pooled synthesis strategies in which a single synthesis reaction or set of reagents is used to make common portions of each oligonucleotide. This can be performed e.g., by well-known solid-phase nucleic acid synthesis techniques, or, e.g., utilizing array-based oligonucleotide synthetic methods (see e.g., Fodor *et al.* (1991) Science, 251: 767-777; Fodor (1997) "Genes, Chips and the Human Genome" FASEB Journal. 11:121-121; Fodor (1997) "Massively Parallel Genomics" Science. 277:393-395; and Chee *et al.* (1996) "Accessing Genetic Information with High-Density DNA Arrays" Science 274:610-614).

In typical synthesis strategies the oligonucleotides have at least about 10 bases of sequence identity to either side of a region of variance to ensure reasonably efficient recombination. However, flanking regions with identical bases can have fewer identical bases (e.g., 4, 5, 6, 7, 8, or 9) and can, of course, have larger regions of identity (e.g., 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 50, or more).

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The oligonucleotides to be assembled together are incubated to allow hybridization between oligonucleotides containing overlapping complementary sequences. Each set of hybridizing overlapping oligonucleotides thereby forms a contiguous nucleic acid interrupted by small gaps. These small gaps can be filled to form full length sequences using any of a variety of polymerase-mediated reassembly methods, e.g.,·as described herein and as known to one of skill. The greatest sequence diversity is introduced in oligonucleotides encoding the plant scaffold polypeptide sequence putative binding regions and residues. However, oligonucleotides encoding specific sequence variations can be "spiked" in the recombination mixture at any selected concentration, thus causing preferential incorporation of desirable modifications into the encoded plant chimeric binding proteins in regions outside of the putative binding domains.

For example, during oligonucleotide elongation, hybridized oligonucleotides are incubated in the presence of a nucleic acid polymerase, e.g., Taq, Klenow, or the like, and dNTP's (i.e., dATP, dCTP, dGTP and dTTP). If regions of sequence identity are large, Taq or other high-temperature polymerase can be used with a hybridization temperature of between about room temperature (i.e., about 25 °C) and, e.g., about 65 °C. If the areas of identity are small, Klenow, Taq or polymerases can be used with a hybridization temperature of below room temperature. The polymerase can be added to the assembly reaction prior to, simultaneously with, or after hybridization of the oligonucleotides. Afterwards, the resulting elongated double-stranded nucleic acid sequences are denatured, hybridized, and elongated again. This cycle can be repeated for any desired number of times. The cycle is repeated e.g., from about 2 to about 100 times.

Optionally, after multiple cycles of combinatorial nucleic acid assembly, the resulting products can be amplified, e.g., by standard polymerase chain reaction (PCR). A portion of the volume of the above-described assembly reaction is incubated with unique forward and reverse primers that hybridize universally to the ends of the nucleic acids, as well as dNTPs and a suitable polymerase (e.g., *pfu* polymerase). The PCR reaction is then carried out for about 10 to 40 cycles.

To determine the extent of oligonucleotide incorporation any approach which distinguishes similar nucleic acids can be used. For example, the nucleic acids can be cloned and sequenced, or amplified (*in vitro* or by cloning, e.g., into a standard cloning

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or expression vector) and cleaved with a restriction enzyme which specifically recognizes a particular oligonucleotide sequence variant.

It is useful to include rare restriction sites (e.g., Not I) in the 5' ends of the 5' and 3' most primers used either in the assembly or PCR reactions. Inclusion of restriction sites in these primers facilitates subcloning of the nucleic acids into a vector by restriction digestion and subsequent ligation. Alternatively, the assembly reaction or PCR products can also be subcloned, without being restriction digested, using standard methods, e.g.,"TA" cloning.

Other methods for introducing diversity into a plant scaffold polypeptide sequence can also be used. For example, a scaffold polypeptide sequence can be encoded in a nucleic acid template, e.g., a plasmid contruct. Alternatively, a PCR product, mRNA or genomic DNA from an appropriate plant species such as soybean may also serve as a template encoding a plant scaffold polypeptide sequence. One or more scaffold polypeptide sequence subsequences to be diversified (e.g., the X_2 region of a PAP scaffold polypeptide sequence) can be diversified during or after amplification from the scaffold polypeptide sequence nucleic acid template by any of a number of error-prone PCR methods. Error-prone PCR methods can be divided into (a) methods that reduce the fidelity of the polymerase by unbalancing nucleotides concentrations and/or adding of chemical compounds such as manganese chloride (see, e.g., Lin-Goerke *et al.* (1997) *Biotechniques*, 23, 409–412), (b) methods that employ nucleotide analogs (see, e.g., U.S. Patent No. 6,153,745), (c) methods that utilize 'mutagenic' polymerases (see, e.g., Cline, J. and Hogrefe,H.H. (2000) *Strategies* (Stratagene Newsletter), 13, 157–161 and (d) combined methods (see, e.g., Xu, H., Petersen, E.I., Petersen, S.B. and el-Gewely, M.R. (1999) *Biotechniques*, 27, 1102–1108. Other PCR-based mutagenesis methods include those, e.g., described by Osuna J, Yanez J, Soberon X, and Gaytan P. (2004), *Nucleic Acids Res.* 2004, 32(17):e136 and Wong TS, Tee KL, Hauer B, and Schwaneberg, Nucleic Acids Res. 2004 Feb 10;32(3):e26), and others known in the art.

After generating a population of sequence variants, these can be substituted into the appropriate region of a chosen plant scaffold polypeptide sequence nucleic acid (e.g., a plasmid containing a scaffold polypeptide sequence) by subcloning which thereby effectively acts as a vector for the library of diversified sequences.

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Yet another approach to mutagenizing specific plant scaffold polypeptide sequence regions is the use of a mutagenic *E. coli* strain (see, e.g., Wu *et al.* (1999), *Plant Mol. Biol.*, 39(2):381-386). A nucleic acid vector containing a target sequence to be mutated is introduced into the mutator strain, which is then propagated. Error-prone DNA replication in the mutator *E. coli* strain introduces mutations into the introduced target sequence. The population of altered target sequences is then recovered and subcloned into the appropriate position of a nucleic acid encoding the selected plant scaffold polypeptide sequence to generate a diverse library of nucleic acids encoding plant chimeric binding proteins.

III. Expression and Screening of Plant chimeric binding proteins

The library of nucleic acids based on a plant scaffold polypeptide sequence and encoding plant chimeric binding polypeptides are subcloned into an expression vector and introduced into a biological replication system to generate an expression library. The expression library can be propagated and screened to identify plant chimeric binding proteins that bind a target molecule (TM) of interest (e.g., a nematode, insect, fungal, viral or plant protein).

The biological replication system on which screening of plant chimeric binding proteins will be practiced should be capable of growth in a suitable environment, after selection for binding to a target. Alternatively, the nucleic acid encoding the selected plant chimeric binding protein can be isolated by in vitro amplification. During at least part of the growth of the biological replication system, the increase in number is preferably approximately exponential with respect to time. The frequency of library members that exhibits the desired binding properties may be quite low, for example, one in 10^6 or less.

Biological replication systems can be bacterial DNA viruses, vegetative bacterial cells, bacterial spores. Eukaryotic cells (e.g., yeast cells) can also be used as a biological replication system.

In a particularly useful embodiment, a chimeric binding protein-phage coat protein fusion is encoded in a phagemid construct. The phagemid constructs are transformed into host bacteria, which are subsequently infected with a helper phage that expresses wild type coat proteins. The resulting phage progeny have protein coats that include both fusion protein and wild-type coat proteins. This approach has the

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advantage that phage viability is greater compared to viability of phage that have exclusively chimeric binding protein-coat fusion proteins. Phagemid-based display library construction and screening kits are commercially available, e.g., the EZnet™ Phage Display cDNA Library Construction Kit and Screening Kit (Maxim Biotech, Inc., San Francisco, CA).

Nonetheless, a strain of any living cell or virus is potentially useful if the strain can be: 1) genetically altered with reasonable facility to encode a plant chimeric binding protein, 2) maintained and amplified in culture, 3) manipulated to display the potential binding protein domain where it can interact with the target material, and 4) selected while retaining the genetic information encoding the expressed plant chimeric binding protein in recoverable form. Preferably, the biological replication system remains viable after affinity-based selection.

When the biological replication system is a bacterial cell or a phage which is assembled in the periplasm, the expression vector for display of the plant chimeric binding protein encodes the chimeric binding protein itself fused to two additional components. The first component is a secretion signal which directs the initial expression product to the inner membrane of the cell (a host cell when the package is a phage). This secretion signal is cleaved off by a signal peptidase to yield a processed, mature, plant chimeric binding protein. The second component is an outer surface transport signal which directs the biological replication system to assemble the processed protein into its outer surface. This outer surface transport signal can be derived from a surface protein native to the biological replication system (e.g., the M13 phage coat protein gIII).

For example, the expression vector comprises a DNA encoding a plant chimeric binding protein operably linked to a signal sequence (e.g., the signal sequences of the bacterial phoA or bla genes or the signal sequence of M13 phage gene III) and to DNA encoding a coat protein (e.g., the M13 gene III or gene VIII proteins) of a filamentous phage (e.g., M13). The expression product is transported to the inner membrane (lipid bilayer) of the host cell, whereupon the signal peptide is cleaved off to leave a processed hybrid protein. The C-terminus of the coat protein-like component of this hybrid protein is trapped in the lipid bilayer, so that the hybrid protein does not escape into the periplasmic space. As the single-stranded DNA of the nascent phage particle passes into the periplasmic space, it collects both wild-type coat protein and the hybrid protein from the lipid bilayer. The hybrid protein is thus packaged into the surface sheath of the filamentous phage, leaving the plant chimeric binding protein exposed on its outer surface. Thus, the filamentous phage, not the host bacterial cell, is the biological replication system in this embodiment. If a secretion signal is necessary for the display of the plant chimeric binding protein, a "secretion-permissive" bacterial strain can be used for growth of the filamentous phage biological replication system.

It is unnecessary to use an inner membrane secretion signal when the biological replication system is a bacterial spore, or a phage whose coat is assembled intracellularly. In these cases, the display means is merely the outer surface transport signal, typically a derivative of a spore or phage coat protein.

Filamentous phage in general are attractive as biological replication systems for display of plant chimeric binding proteins, and M13 in particular, is especially attractive because: 1) the 3D structure of the virion is known; 2) the processing of the coat protein is well understood; 3) the genome is expandable; 4) the genome is small; 5) the sequence of the genome is known; 6) the virion is physically resistant to shear, heat, cold, urea, guanidinium Cl, low pH, and high salt; 7) the phage is a sequencing vector so that sequencing is especially easy; 8) antibiotic-resistance genes have been cloned into the genome; 9) It is easily cultured and stored, with no unusual or expensive media requirements for the infected cells, 10) it has a high burst size, each infected cell yielding 100 to 1000 M13 progeny after infection; and 11) it is easily harvested and concentrated by standard methods.

For example, when the biological replication system is M13 the gene III or the gene VIII proteins can be used as an outer surface targeting signal. Alternatively, the proteins from genes VI, VII, and IX may also be used.

The encoded plant chimeric binding protein can be fused to the surface targeting signal (e.g., the M13 gene III coat protein) at its carboxy or amino terminal. The fusion boundary between the plant chimeric binding protein and the targeting signal can also include a short linker sequence (e.g., up to 20 amino acids long) to avoid undesirable interactions between the chimeric binding protein and the fused targeting signal. In some embodiments it is advantageous to include within the linker sequence a specific proteolytic cleavage site. In addition, the amino terminal or carboxy terminal of the fused protein can include a short epitope tag (e.g., a hemaglutinin tag). Inclusion of a proteolytic cleavage site or a short epitope tag is particularly useful for purification of a

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library of chimeric binding proteins from a population of cells expressing the library. Epitope-tagged chimeric binding proteins can be conveniently purified by proteolytic cleavage of linker sequence followed by affinity chromatography utilizing an antibody or other binding agent that recognizes the epitope tag.

Many methods exist for screening phage display libraries (see, e.g., Willats (2002), *Plant Mol. Biol.*, 50:837-854). As commonly practiced, the target molecule of interest is adsorbed to a support and then exposed to solutions of phage displaying plant chimeric binding proteins. The target molecule can be immobilized by passive adsorption on a support medium, e.g, tubes, plates, columns, or magnetic beads. Generally, the adsorptive support medium is pre-blocked, e.g., with bovine serum albumin, milk, or gelatin, to reduce non-specific binding of the phage during screening. Alternatively, the target molecule can be biotinylated, so interaction between chimeric binding protein-bearing phage and the target molecule can be carried out in solution. Phage that bind to the target can then be selected using avidin or streptavidin bound to a solid substrate (e.g., beads or a column).

After phage are allowed to interact with the target molecule, non-interacting phage are removed by washing. The remaining, specifically binding phage are then eluted by one of any number of treatments including, e.g., lowering or increasing pH, application of reducing agents, or use of detergents. In one embodiment, a specific proteolytic cleavage site is introduced between the plant chimeric binding protein sequence and the phage coat protein sequence. Thus, phage elution can be accomplished simply by addition of the appropriate protease.

Eluted phage are then amplified by infection of host cells and can subsequently be re-screened by the method just outlined to reduce the number of false positive binders. During each round of phage screening, care should be taken to include growth of the phage on a solid medium rather than exclusively in a liquid medium as this minimizes loss of phage clones that grow sub-optimally.

Plant chimeric binding proteins can also be expressed and screened for binding solely *in vitro* using ribosomal display. An exclusively *in vitro* approach circumvents the requirement to introduce the library of nucleic acids encoding plant chimeric binding proteins into a biological replication system. Methods for screening polypeptides *in vitro* by ribosomal protein display are described in detail, e.g., in U.S. Patent No. 6,589,741. The nucleic acids described in the section above are modified by

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adding a phage promoter sequence (e.g., a T7 promoter) enabling *in vitro* transcription, a ribosome binding sequence upstream to the start of translation of the encoded plant chimeric binding protein, and a transcription termination sequence (e.g., from phage T3). The modified library of nucleic acids is then transcribed *in vitro* to generate a corresponding mRNA population encoding plant chimeric binding proteins. Plant chimeric binding proteins are then expressed *in vitro* by translating the population of mRNA molecules devoid of stop codons in the correct reading frame in an in vitro translation system, under conditions that allow the formation of polysomes. The polysomes so formed are then brought into contact with a target molecule under conditions that allow the interaction of plant chimeric binding proteins with the target molecule. Polysomes displaying chimeric binding proteins that interact with the target molecule are then separated from non-interacting polysomes displaying no such (poly)peptides; and the mRNA associated with the interacting polysome is then amplified (e.g., by PCR) and sequenced.

Interaction of a plant chimeric binding protein with a target protein can also be detected in a genetic screen. In the screen, the target protein functions as a "bait protein" and each plant chimeric binding protein functions as a potential "prey" protein in a binding assay that utilizes a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J. Biol. Chem. 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; Hubsman *et al.* (2001) Nuc. Acids Res. Feb 15;29(4):E18; and Brent WO94/10300).

A two-hybrid assay can be carried out using a target polypeptide as the bait protein. In sum, the target polypeptide is fused to the LexA DNA binding domain and used as bait. The prey is plant chimeric binding protein library cloned into the active site loop of TrxA as a fusion protein with an N-terminal nuclear localization signal, a LexA activation domain, and an epitope tag (Colas *et al.* 1996 Nature 380:548; and Gyuris *et al.* Cell 1993 75:791). Yeast cells are transformed with bait and prey genes. When the target fusion protein binds to a plant chimeric binding protein fusion protein, the LexA activation domain is brought into proximity with the LexA DNA binding domain and expression of reporter genes or selectable marker genes having an appropriately positioned LexA binding site increases. Suitable reporter genes include fluorescent proteins (e.g., EGFP), enzymes (e.g., luciferase, β-galactosidase, alkaline phosphatase, etc.) Suitable selectable marker genes include, for example, the yeast LEU2 gene.

After identification of one or more target-binding chimeric binding proteins, the isolated nucleic acids encoding the chimeric binding proteins can be mutagenized by the methods described herein, to generate small expression libraries expressing variant chimeric binding proteins. The chimeric binding protein-variant expression libraries can be screened to identify chimeric binding protein variants with improved target binding properties (e.g., increased affinity or specificity).

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The following specific examples are to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. Without further elaboration, it is believed that one skilled in the art can, based on the description herein, utilize the present invention to its fullest extent. All publications cited herein are hereby incorporated by reference in their entirety.

EXAMPLES

Example 1 Design and Expression of Plant Scaffold Polypeptide Sequences

Several protein domain families were analyzed for their potential use as scaffolds. A search of PFAM domains (pfam.wustl.edu; see Bateman et al. (2004)), restricting the output to *Viridiplantae*, was conducted to limit domains only to those present in green plants. Four protein domain families were selected to develop plant universal molecular recognition libraries; the accessory domain of purple acid phosphatase (PAP), plant

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cystatins, plant C2 domains and the turn-helix-helix (THH) motif found in ankyrin repeat proteins.

Three purple acid phosphatase scaffolds were designed having the sequence of SEQ ID NOs:34-36. The amino acid sequence of the accessory domain from kidney bean PAP was used as a query sequence to BLAST the NCBI database. When the output was restricted to proteins found in Viridiplantae, 62 unique sequences were identified. From an alignment of these sequences, a consensus plant PAP sequence was generated (SEQ ID NO:34) by selecting the most frequent amino acid at each position in the alignment. The kidney bean (*Phaseolus vulgaris*) PAP was selected as a parental scaffold (SEQ ID NO:35), because of its known structure. A PAP from soybean,

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Glycine max, was also chosen (SEQ ID NO:36), as this species represents a common crop species in which transgenic products are generated.

A set of scaffold polypeptide sequences which contain plant ankyrin-like repeats was also designed. Ankyrin-like repeats are small turn-helix-helix (THH) motifs consisting of approximately 33 amino acids. They are common elements of proteins from all organisms and are often found in tandem arrays of 2 to 20 repeats within a protein.

Three THH scaffolds were generated. These proteins are similar in structure to GA binding protein (GABP-β). This protein consists of THH like amino and carboxy terminal caps with 3 THH internal repeats. In this protein, it is thought that the caps help stabilize the protein by shielding hydrophobic residues found in the internal repeats.

Three hundred and twelve Viridiplantae ankyrin repeats proteins found in PFAM were aligned to aid in designing plant-specific THH scaffolds. A plant consensus THH sequence was generated by selecting the most frequently occurring amino acid at each position. This sequence was termed the plant consensus internal repeat sequence. This sequence was used to search the NCBI databases by BLAST alignment to find the closest natural THH sequence found in plants. A sequence from wheat (*Triticum aestivum*) was found. The designed repeat based on *T. aestivum* contains a substitution of valine for the single cysteine occurring in the *T. aestivum* sequence. Two sets of N and C terminal caps were generated. One set consists of sequences derived from GABP-β and the second set was derived from the plant THH consensus sequence and optimized to resemble the structure of GABP-β. In particular, the N terminal cap has an extended alpha-helical structure, while the C terminal cap has a truncated helix compared to the typical THH repeat.

Three THH scaffolds were designed, one consists of plant consensus N and C caps and two plant consensus internal THH repeats (SEQ ID NO:37). Another consists of plant consensus N and C caps and two wheat internal repeats (SEQ ID NO:38) and the third consists of ankyrin like N and C caps with two wheat internal repeats (SEQ ID NO:39).

The genes encoding the plant scaffold polypeptide sequences were designed for expression testing in plants, bacteria, and on the surface of phage. Codons were selected for plant expression using a publicly available *Glycine max* codon usage table

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(at kazusa.or.jp/codon, codon usage tabulated from the international DNA sequence databases: status for the year 2000. Nakamura, Y, Gojobori, T and Ikemura, T (2000) *Nucl. Acids Res.* 28:292.). Codon selection was done manually with the aim for the final codon frequency to roughly reflect the natural frequency for *Glycine max*. Rarely used codons (<10% frequency) were not used. Final sequences were checked for potential problematic sequences, including removal of restriction sites needed for cloning, potential plant splice acceptor or donor sites (see website at cbs.dtu.dk/services/NetPgene/), potential mRNA destabilization sequences (ATTTA) and stretches of more than 4 occurrences of the same nucleotide. Any potential problematic sequences were altered in the genes by modifying codon usage. Since the THH sequences have 4 similar repeat sequences within each protein, steps were taken to reduce nucleotide similarity within repeats; the average repeat identity was reduced 10-15% by these means.

Seven constructs were produced using synthetic gene assembly, (three based on THH scaffold polypeptide sequences, two based on PAP scaffold polypeptide sequences, one plant cystatin and one plant C2 domain protein). The three THH scaffold polypeptide sequences were placed into a phagemid vector as fusion sequences with the gene III coat protein (gIII) at its carboxy terminus (Phage 3.2, Maxim Biotech, Inc., South San Francisco, CA). A 6-His tag was included at the 5' end of the gene as well as a c-Myc tag between the scaffold gene and the encoded amino terminus of gIII. The phagemid constructs were then packaged into phage particles and the phage were tested for expression and surface display of the THH scaffold. A phage ELISA using either anti-His and anti-Myc indicated that the THH scaffold proteins were expressed on the surface of phage in phage ELISAs, suggesting that all 3 THH scaffold polypeptide sequence constructs are folding and expressing well on the phage surface. The selected scaffold polypeptide sequences were then used to generate expression vectors to evaluate their expression in transgenic plants by immunoblotting.

Tobacco leaves were injected with *agrobacterium*, LB4404 transformed with THH containing plant expression vectors. Two days later, sections of leaves injected with agrobacterium were harvested, frozen on dry ice, then ground into a fine powder with a pestle. PBS containing 0.2% Tween-20 was added to the fine powder at a 1:1 weight to volume ratio and additional grinding was done. Insoluble material was removed by centrifugation and 10 ul of the remaining supernatant was loaded onto a 4-

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12% acrylamide SDS page gel (NuPage, Intvitrogen). Proteins were transferred to PVDF membranes. Proteins were detected using a rat anti-HA antibody (Roche) and an anti-rat HRP conjugated secondary antibody (Chemicon). HRP was detected using Amerham Lumigen reagents.

All three THH scaffold were found to be expressed, with the relative level of expression of the three scaffolds being TA-THH > CC-THH >. TC-THH.

OTHER EMBODIMENTS

All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose. Thus, unless expressly stated otherwise, each feature disclosed is only an example of a generic series of equivalent or similar features.

From the above description, one skilled in the art can easily ascertain the essential characteristics of the present invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Thus, other embodiments are also within the scope of the following claims.

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A library of nucleic acids encoding at least ten different polypeptides, wherein

(i) the amino acid sequence of each of the encoded polypeptides comprises an amino acid sequence at least 70% identical to any of SEQ ID NOs:127-129;

(ii) the amino acid sequence of each of the encoded polypeptides includes amino acids that differ from those of SEQ ID NOs:127-129 at positions 13, 14, 33, 35-36, 38, 46-47, 66, 68-69, 71, 79, 80, 99,101-102, 104, and 112-113 and the amino acid differences are heterogeneous across a plurality of the encoded polypeptides; and

(iii) the amino acid sequence of each of the encoded polypeptides outside of the residues corresponding to positions 13, 14, 33, 35-36, 38, 46-47, 66, 68-69, 71, 79, 80, 99,101-102, 104, and 112-113 of SEQ ID NOs: 127-129 is homogeneous across a plurality of the encoded polypeptides.

2. The library of claim 1, wherein the amino acid sequence of the polypeptides has at least 75% identity to any of SEQ ID NOs 127-129.

3. The library of claim 1, wherein the amino acid sequence of the polypeptides has at least 80% identity to any of SEQ ID NOs 127-129.

4. The library of claim 1, wherein the amino acid sequence of the polypeptides has at least 85% identity to any of SEQ ID NOs 127-129.

5. The library of claim 1, wherein each of the nucleic acids comprises a vector sequence.

6. A population of cells expressing the polypeptides encoded by the library of claim 1.

7. A cell selected from the population of cells of claim 6.

8. A purified library of polypeptides encoded by the library of claim 1.

9. A population of filamentous phage displaying the library of polypeptides encoded by the library of claim 1.

10. A method of generating the library of claim 1, comprising:

(i) selecting an amino acid sequence corresponding to any one of SEQ ID NOs: 127-129 to be encoded, wherein the selected sequence differs from those of SEQ ID NOs:127-129 in at least one of variable positions 13, 14, 33, 35-36, 38, 46-47, 66, 68-69, 71, 79, 80, 99,101-102, 104, and 112-113;

(ii) chemically providing a first and a second plurality of oligonucleotides, wherein

(a) oligonucleotides of the first plurality encode amino acid subsequences of the selected amino acid sequence; the subsequences being heterogeneous at the encoded variable positions;

(b) oligonucleotides of the second plurality are complementary to nucleotide sequences encoding subsequences of the selected amino acid sequence, the subsequences being heterogeneous at the encoded variable positions; and

(c) the first and second pluralities comprise oligonucleotides have overlapping sequences complementary to one another;

(iii) combining the population of oligonucleotides to form a first mixture;

(iv) incubating the mixture under conditions effective for hybridizing the overlapping complementary sequences to form a plurality of hybridized complementary sequences; and

(v) elongating the plurality of hybridized complementary sequences to form a second mixture containing the library.

11. The method of claim 10, further comprising performing a cycle of denaturing the library by increasing the temperature of the second mixture to a temperature effective for denaturing double stranded DNA, followed by steps (iv) and (v).

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12. The method of claim 11, comprising repeating the cycle up to 100 times.

13. The method of claim 12, further comprising amplifying the library by a polymerase chain reaction consisting essentially of the library, a forward primer, and a reverse primer, wherein the forward and reverse primers can hybridize to the 5' and 3' end sequences, respectively, of all nucleic acids in the library.

14. The method of claim 10, wherein amino acids to be encoded for the variable positions, are selected from a subset of alanine, arginine, asparagine, aspartate, cysteine, glutamine, glutamate, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine.

15. The method of claim 14, wherein the amino acids selected for the variable positions are selected from a group consisting of an aliphatic, an acidic, a neutral, and an aromatic amino acid.

16. The method of claim 15, wherein the group of amino acids consists of alanine, aspartate, serine, and tyrosine.

17. The library of claim 1 or the method of claim 10, substantially as herein described and with reference to any of the Examples and/or Figures.

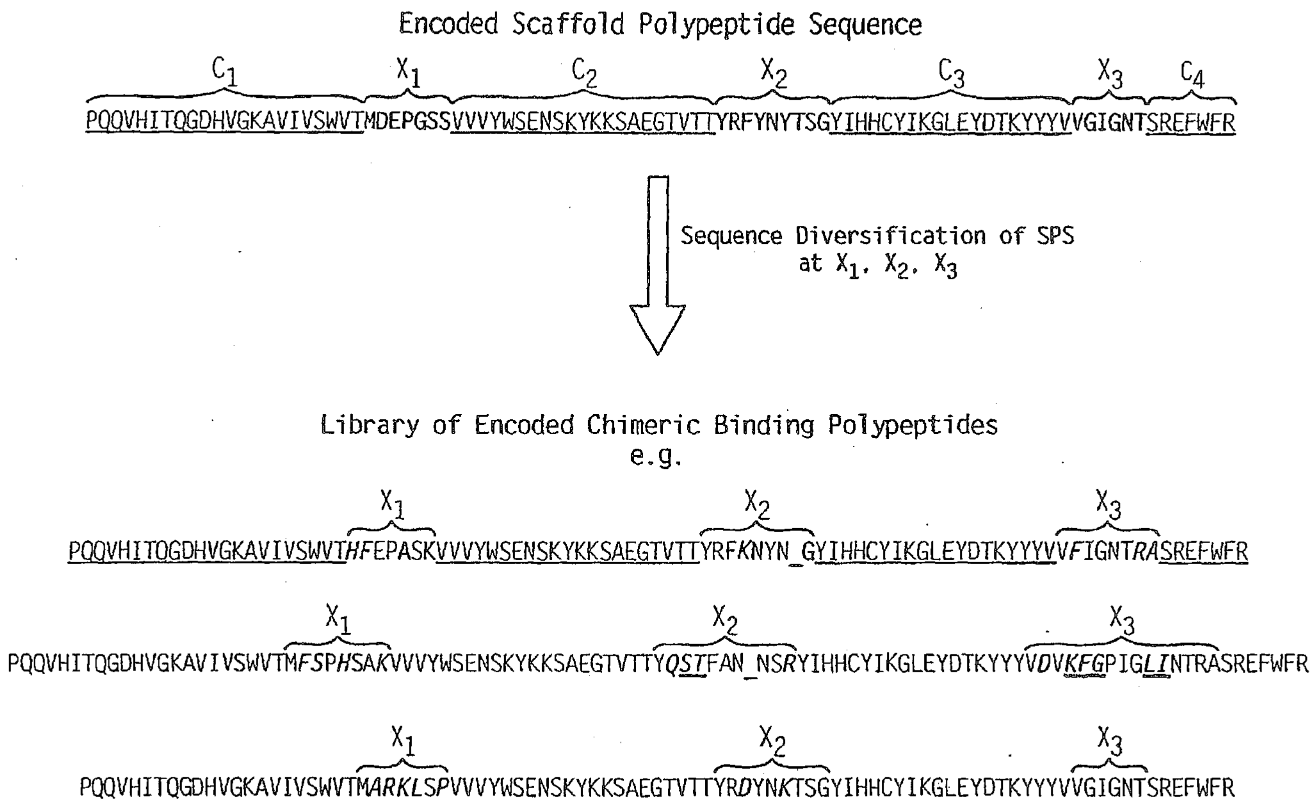
Encoded Scaffold Polypeptide Sequence
C1
X1
C2
X2
C3
X3
C4
PQQVHITQGDHVGKAVIVSWVTMDEPGSSVVVYWSENSKYKKSAEGTVTTYRFYNYTSGYIHHCYIKGLEYDTKYYYVVGIGNTSREFWFR
Sequence Diversification of SPS at X1, X2, X3
Library of Encoded Chimeric Binding Polypeptides e.g.
X1
X2
X3
PQQVHITQGDHVGKAVIVSWVTHFEPASKVVVYWSENSKYKKSAEGTVTTYRFKNYN_GYIHHCYIKGLEYDTKYYYVVFIGNTRASREFWFR
X1
X2
X3
PQQVHITQGDHVGKAVIVSWVTMFSPHSAKVVVYWSENSKYKKSAEGTVTTYQSTFAN_NSRYIHHCYIKGLEYDTKYYYVDVKFGPIGLINTRASREFWFR
X1
X2
X3
PQQVHITQGDHVGKAVIVSWVTMARKLSPVVVYWSENSKYKKSAEGTVTTYRDYNKTSGYIHHCYIKGLEYDTKYYYVVGIGNTSREFWFR

FIG. 1

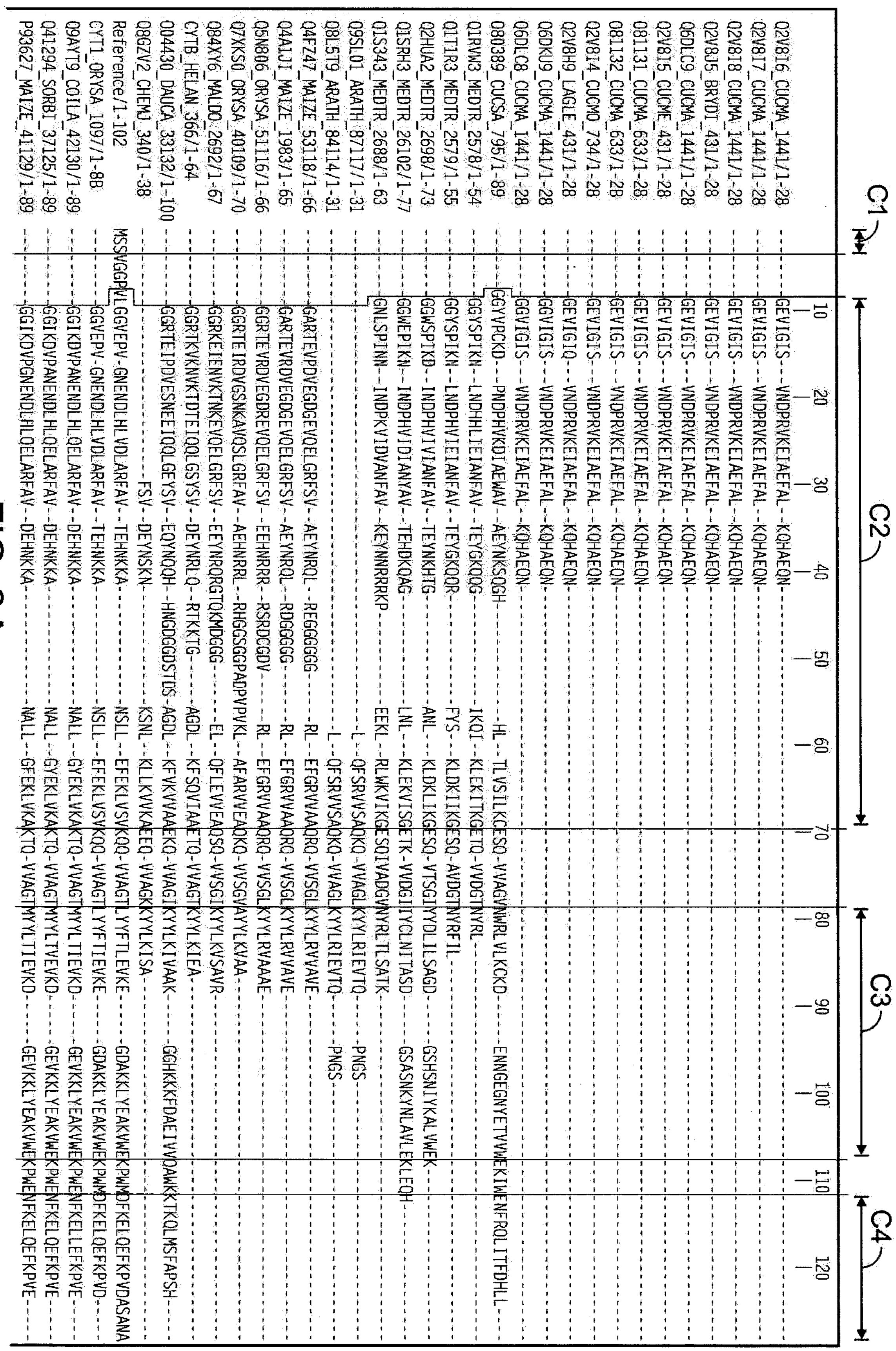
C1
C2
C3
C4
10
20
30
40
50
60
70
80
90
100
110
120
Q2V8I6_CUCMA_1441/1-28
Q2V8I7_CUCMA_1441/1-28
Q2V8I8_CUCMA_1441/1-28
Q2V8J5_BRYDI_431/1-28
Q6DLC9_CUCMA_1441/1-28
Q2V8I5_CUCME_431/1-28
O81131_CUCMA_633/1-28
O81132_CUCMA_633/1-28
Q2V8I4_CUCMO_734/1-28
Q2V8H9_LAGLE_431/1-28
Q6DKU9_CUCMA_1441/1-28
Q6DLC8_CUCMA_1441/1-28
O80389_CUCSA_795/1-89
Q1RVW3_MEDTR_2578/1-54
Q1T1R3_MEDTR_2579/1-55
Q2HUA2_MEDTR_2698/1-73
Q1SRH3_MEDTR_26102/1-77
Q1S343_MEDTR_2688/1-63
Q9SL01_ARATH_87117/1-31
Q8L5T9_ARATH_84114/1-31
Q4FZ47_MAIZE_53118/1-66
Q4A1J1_MAIZE_1983/1-65
Q5N806_ORYSA_51116/1-66
Q7XKS0_ORYSA_40109/1-70
Q8X4Y6_MALDO_2692/1-67
CYTB_HELAN_366/1-64
O04430_DAUCA_33132/1-100
Q8GZV2_CHEMJ_340/1-38
Reference/1-102
CYT1_ORYSA_1097/1-88
Q9AYT9_COILA_42130/1-89
Q41294_SORBI_37125/1-89
P93627_MAIZE_41129/1-89

FIG. 2A

```
                                      C2                                                                             C3                              C4
Q30KW0_ZEAMP_41129/1-89  --------GGIKDVPGNENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENFKELQEFKPVE-----
Q41897_MAIZE_41129/1-89  --------GGIKDVPGNENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENFKELQEFKPVD-----
Q30KV8_ZEAMP_41129/1-89  --------GGIQDVPGSENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKVKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENLKGLQEFKPVE-----
Q30KW7_ZEAMP_41129/1-89  --------GGIQDVPGSENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENLKGLQEFKPVE-----
Q30KV7_ZEAMP_41129/1-89  --------GGIKDVPGNENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENLKGLQEFKPVE-----
Q30KW6_ZEAMP_41129/1-89  --------GGIQDVPGSENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENFKELQEFKPVE-----
Q41825_MAIZE_41129/1-89  --------GGIQDVPENENDLHLQELARFAV--DEHNKKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWEKFKELQEFKPVE-----
Q4A1K0_MAIZE_42130/1-89  --------GGIKDVPANENDLQLQELARFAV--NEHNQKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVNKLYEAKVWEKPWENFKQLQEFKPVE-----
CYT1_MAIZE_42130/1-89    --------GGIKDVPANENDLQLQELARFAV--NEHNQKA-------------NALL--GFEKLVKAKTQ-VVAGTMYYLTIEVKD------GEVKKLYEAKVWEKPWENFKQLQEFKPVE-----
Q45KJ0_WHEAT_167/1-67    ---------------------------V--SEHKNKT-------------NALL--EFEKVVRLKQQ-VVAGMMYYITIQVNE------GGAKKMYEAKVWERPWMDFKKLMEFRPAE-----
Q9FS03_WHEAT_172/1-72    ----------------------LARFAV--SEHKNKT-------------NALL--EFEKVVRLKQQ-VVAGMTYYITIQVNE------GGAKKMYEAKVWERPWMDFKKLMEFRPAE-----
Q2XNE8_WHEAT_48136/1-89  --------GGIVDS-LRRENDPYIVDLARFAV--SEHNKEG-------------NTQL--ELEKVVKVKEQ-AVAGRLYYITIQVDE------GGAKKLYEAKVLEQLWLDVKKLVEFKPAE-----
Q9FS05_WHEAT_48136/1-89  --------GGIVDS-LGRENDPYIVDLARFAV--SEHNKEG-------------NTQL--ELEKVVKVKEQ-AVAGRLYYITIQVDE------GGAKKLYEAKVLEQLWLDVKKLVEFKPAE-----
Q9FS07_WHEAT_391/1-89    --------GGIVDS-PGRENDPYIVDLARFAV--SQHNKEA-------------NTQL--ELEKVVKVKEQ-AIAGRLYYITIQVDE------GGAKKLYKAKVLEQLWLDVKKLLEFKPAE-----
Q2XNF0_WHEAT_48137/1-90  --------GGISDSPMGQENDLDVIALARFAV--SEHNNKA-------------NALL--EFENVVKVKKQ-TVAGTMHYITIRVTE------GGAKKLYEAKVWEKPWENFKKLEEFKLVE-----
Q9FS06_WHEAT_48137/1-90  --------GGISDSPMGQENDLDVIALARFAV--SEHNNKA-------------NALL--EFENVVKVKKQ-TVAGTMHYITIRVTE------GGAKKLYEAKVWEKPWENFKKLEEFKLVE-----
Q9FS04_WHEAT_31120/1-90  --------GGIKDSPMGQENDLDVIALARFAV--SEHNNKA-------------NALL--EFENVVKLKKQ-TVAGTMHYITIRVTE------GGAKKLYEAKVWEKPWENFKQLQEFKPVE-----
Q4A1J8_MAIZE_1395/1-83   --------GDVRDAPVGRENDLEAIELARFAV--AEHNSKT-------------NAML--EFERLVKVRHQ-VVAGTLHHFTVEVKEAG----GGEKKLYEAKVWEKAWENFK-------------
Q4FZ53_MAIZE_14105/1-92  --------GDVRDAPVGRENDLEAIELARFAV--AEHNSKT-------------NAML--EFERLVKVRHQ-VVAGTLHHFTVEVKEAG----GGEKKLYEAKVWEKAWENFKQLQSFELVG-----
Q7Y0Q9_SACOF_24104/1-81  -------------------ENDLEAIELARFAV--AEHNSKT-------------NAML--EFERLVKVRHQ-VVAGTMHHFTVQVKEAG----GG-KKLYEAKVWEKVWENFKQLQSFQPVG-----
Q9LEI7_HORVU_18107/1-90  --------GGVQDAPAGRENDLETIELARFAV--AEHNAKA-------------NALL--EFEKLVKVRQQ-VVAGCMHYFTIEVKE------GGAKKLYEAKVWEKAWENFKQLQEFKPAA-----
Q4W4C8_HORVU_18107/1-90  --------GGVQDAPAGRENDLETIELARFAV--AEHNAKA-------------NALL--EFERLVKVRQQ-VVAGCMHYFTIEVKE------GGAKKLYEAKVWEKAWENFKQLQEFKPAA-----
CYT2_ORYSA_14104/1-91    --------GGIHDAPAGRENDLTTVELARFAV--AEHNSKA-------------NAML--ELERVVKVRQQ-VVGGFMHYLTVEVKEP-----GGANKLYEAKVWERAWENFKQLQDFKPLD-----
Q687J0_ANACO_44133/1-90  --------GGIYDAPLNNENGFDKEDLARFAV--REYNNKN-------------NALL--EFVRVVKAKEQ-VVSGMMHYLTVEVND------AGKKKLYEAKVWEQVWMNFRQLQEFTYLG-----
Q42380_BRACM_189/1-89    ---------GTSRDVDPNANDLQVESLARFAV--DEHNKKE-------------NVSL--EYRRLIGAKTQ-VVAGTMHHLTVEVAD------GETKKVYEAKVLEKAWENLKKLEDFTHLR-----
Q71QE1_BRARP_1199/1-89   ---------GGVRDVDPNANDLQVESLARFAV--DEHNKKE-------------NVSL--EYRRLIGAKTQ-VVAGTMHHLTVEVAD------GETKKVYEAKVLEKAWENLKKLEDFTHLR-----
O48589_ARATH_1199/1-89   ---------GGVRDIDANANDLQVESLARFAV--DEHNKNE-------------NLTL--EYKRLLGAKTQ-VVAGTMHHLTVEVAD------GETNKVYEAKVLEKAWENLKQLESFNHLH-----
Q945Q1_ARATH_1199/1-89   ---------GGVRDIDANANDLQVESLARFAV--DEHNKNE-------------NLTL--EYKRLLGAKTQ-VVAGTMHHLTVEVAD------GETNKVYEAKVLEKAWENLKQLESFNHHH-----
Q5ZFX6_POPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS-----
Q5ZFV4_POPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS-----
Q5ZFU9_POPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWAKPWLNFKELHEFKDAS-----
Q5ZFX8_POPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------VGKKKLYEAKAWVKPWLNFKELHEFKDAS-----
Q5ZFW6_PDPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------VGKKKLYEAKVWVKPWLNFKELHEFKDAS-----
Q5ZFY0_PDPTN_40128/1-89  --------GGVQDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVRVKPWLNFKELHEFKDAS-----
Q5ZFV2_POPTN_40128/1-89  --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKPKDQ-VFAGPMHHLTIEAIE------AGKKKLNEAKVWVNPWLNFKELHEFKDAG-----
```

FIG. 2B

C2 C3 C4

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Q5ZFV8_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKPKEQ-VFAGPMHHLTIEAIE------AGKKKLYEAKVWVNPWLNFKELHEFKDAG----
Q5ZFX4_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKPKEQ-VFAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFX1_PDPTN_40128/1-89 --------GGVQDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VFAGPMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKESHEFKDAG----
Q5ZFU7_PDPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VFAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFU3_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VFAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFV6_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VFAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS----
Q5ZFX9_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARLVKAKDQ-VFAGTMHHLTIEAIE------AGKKKLYEAKVWVNPWLNFKELHEFKDAS----
Q5ZFV7_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARLVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFW5_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGPMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS----
Q5ZFW3_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGPMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFW9_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFT9_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFW8_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFU0_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARLAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKRLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFX2_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAI--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q4U123_9ROSI_40128/1-89 --------GGVHDS-QSSQNSAEIDSLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAG----
Q5ZFT8_POPTN_40128/1-89 --------GGVHDS-QTSQNSAEIDGLARFAV--DEHNKKE-------------NAIL--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS----
Q5ZFW0_POPTN_40128/1-89 --------GGVHDS-QSSQNSAEIDGLARFAV--DEHNKKE-------------NAML--EFARVVKAKEQ-VVAGTMHHLTIEAIE------AGKKKLYEAKVWVKPWLNFKELHEFKDAS----
Q43635_RICCO_695/1-90   --------GGVHDSPQGTANNAEIDGIARFAV--DEHNKKE-------------NAMV--EFGRVLKAKEQ-VVAGTLHHLTIEAIE------AGKKKIYEAKVWVKPWLNFKELQEFKHAT----
Q84LB7_MALDO_48136/1-89 --------GGVHES-HGAQNSAEVEDLARFAV--QEHNNKE-------------NALL--EFVSVVKAKEQ-VVAGTLHHLTIEAIE------AGKKKLYQAKVWVKPWMGFKEVQEFKHAD----
Q8L5J8_COLES_593/1-89   --------GGIVDV-EGAQNSAEVEELARFAV--DEHNKKE-------------NALL--QFSRLVKAKQQ-VVSGIMHHLTVEVIE------GGKKKVYEAKVWVQAWLNSKKLHEFSPIG----
Q8H0X6_ARATH_593/1-89   --------GGVGDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTLHHLTLEILE------AGQKKLYEAKVWVKPWLNFKELQEFKPAS----
Q8VZA2_ARATH_593/1-89   --------GGVGDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTLHHLTLEILE------AGQKKLYEAKVWVKPWLNFKELQEFKPAS----
Q9LHF9_ARATH_38126/1-89 --------GGVGDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTLHHLTLEILE------AGQKKLYEAKVWVKPWLNFKELQEFKPAS----
Q9FUB0_ARATH_13101/1-89 --------GGVGDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTLHHLTLEILE------AGQKKLYEAKVWVKPWLNFKELQEFTPAS----
Q1L0Q7_BOEDR_38126/1-89 --------GGVRDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTLHHLTLEILE------AGEKKLYEAKVWVKPWLNFKELQEFKPAS----
Q39268_BRACM_592/1-88   --------GGVRDV-PANQNSGEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTMHHLTLEIIE------AG-KKLYEAKVWVKPWLNFKELQEFKPAS----
Q39270_BRACM_593/1-89   --------GGVRDV-PSNENSVEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTMHHLTLEIIE------AGKKKLYEAKVWVKPWLNFKELQEFKPST----
Q8VYX5_BRAOL_593/1-89   --------GGVRDL-PANENSVEVESLARFAV--DEHNKKE-------------NALL--EFARVVKAKEQ-VVAGTMHHLTLEIIE------AGKKKLYEAKVWVKPWLNFKELQEFKPAS----
O22202_ARATH_36124/1-89 --------GGVHDL-RGNQNSGEIESLARFAI--QEHNKQQ-------------NKIL--EFKKIVKAREQ-VVAGTMYHLTLEAKE------GDQTKNFEAKVWVKPWMNFKQLQEFKESS----
Q41906_ARATH_35123/1-89 --------GGVHDL-RGNQNSGEIESLARFAI--QEHNKQQ-------------NKIL--EFKKIVKAREQ-VVAGTMYHLTLEAKE------GDQTKNFEAKVWVKPWMNFKQLQEFKESS----
Q8RXS7_ARATH_27115/1-89 --------GGVHDL-RGNQNSGEIESLARFAI--QEHNKQQ-------------NKIL--EFKKIVKAREQ-VVAGTMYHLTLEAKE------GDQTKNFEAKVWVKPWMNFKQLQEFKESS----
Q9FXN6_ARATH_391/1-89   --------GGVHDL-RGNQNSGEIESLARFAI--QEHNKQQ-------------NKIL--EFKKIVKAREQ-VVAGTMYHLTLEAKE------GDQTKNFEAKVWVKPWMNFKQLQEFKESS----
Q1SNM2_MEDTR_43131/1-89 --------GGIQDS-PSSENSLEIESLARFAV--DQHNAKQ-------------NSLL--EFARVVKAREQ-VVAGTLHHLTLEAID------AGEKKIYEAKVWVKPWMNFKELTEFKHAG----
Q1S5M8_MEDTR_43131/1-89 --------GGIQDS-PSSENSLEIESLARFAV--DQHNAKQ-------------NSLL--EFARVVKAREQ-VVAGTLHHLTLEAID------AGEKKIYEAKVWVKPWMNFKELTEFKHAG----
```

FIG. 2C

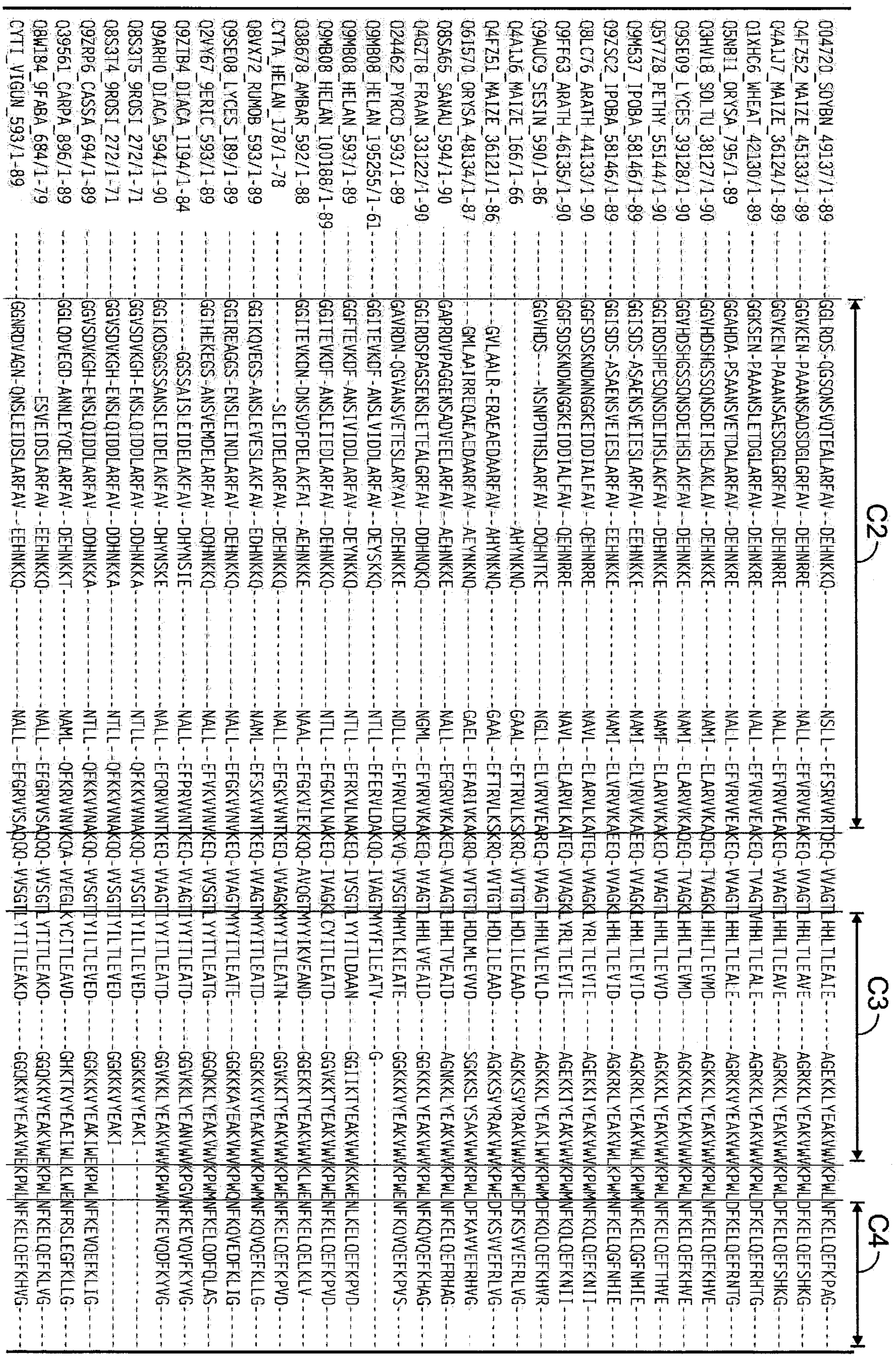

FIG. 2D

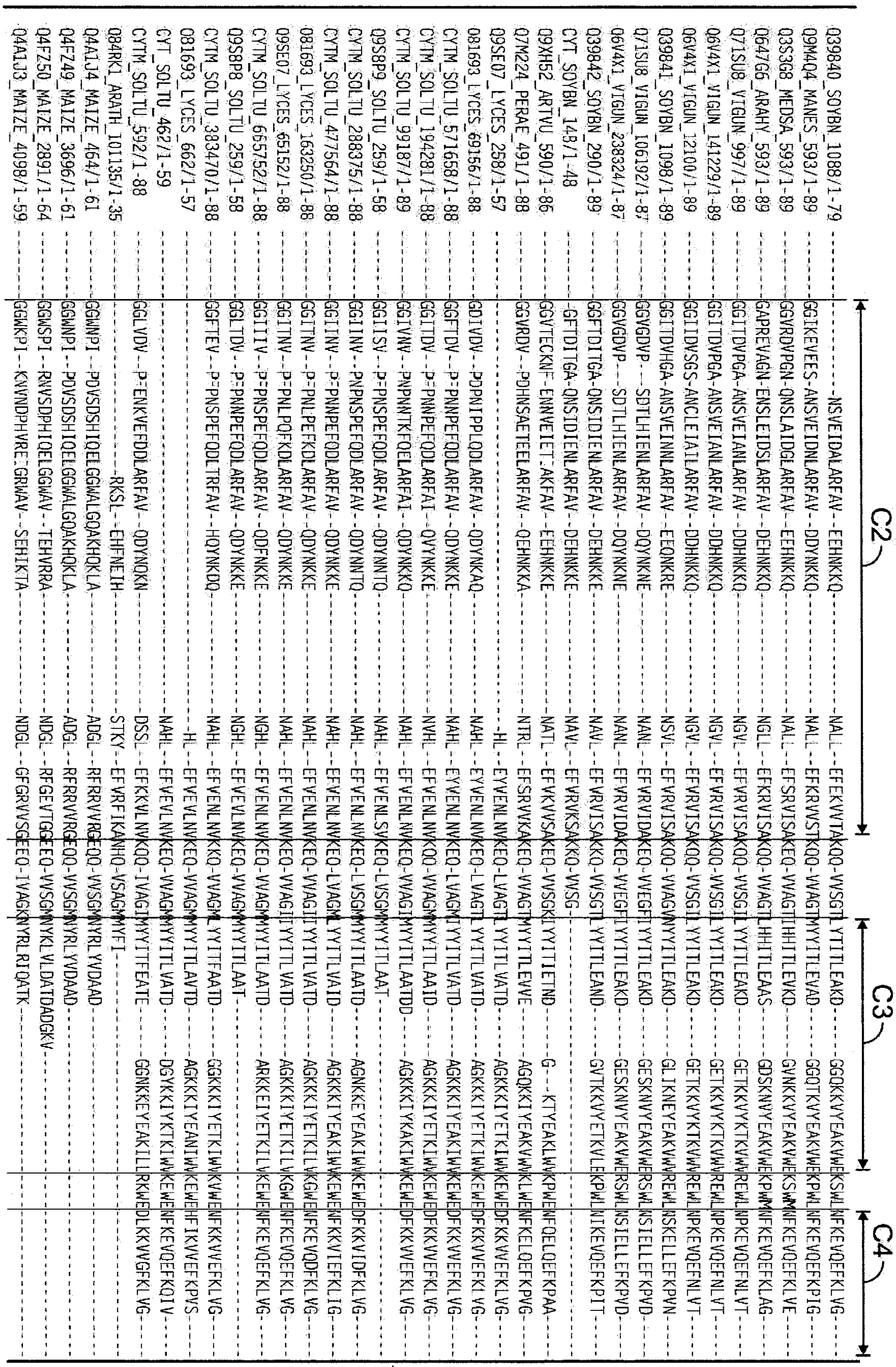

FIG. 2E

```
                                   C2                                                      C3                  C4
Q4FZ46_MAIZE_4098/1-59  --------GGWKPI--KNVNDPHVQEIGRWAV--SEHIKTA-------------NDGL--GFGRVVSGEEQ-IVAGKNYRLRIQATK-------------------------------------
Q8W252_WHEAT_4198/1-58  ---------GWEPI--GNINDQHIQELGRWAV--LEFGKHV-------------NCVL--KFNKVVSGRQQ-LVSGMNYELIIEASD-------------------------------------
Q2A9P9_BRAOL_2790/1-64  --------GGWSPI--SDAKDPHVVEIGVFAV--SEYDKQS-------------KSGL--KFVTVVSGESQ-VAAGTNYRLIVTV-DG--SIGVA-----------------------------
Q2A9Y7_BRAOL_24115/1-92 --------GRWSPI--SNVKDPHVVEVGKFAV--SEYDMES-------------KSEL--KFVVVVSGESK-VVAGTNYRLIVAVNDG--VAGPGASKNYEAIVWEKQWLKSMNLTSFKPVV-----
Q2A9T6_BRAOL_27120/1-94 --------GGWRPL--SDVNDPHVVEIGKFSV--SEYNKQS-------------KAGL--KFVAVVSGESQ-VVAGMNYRLIVAVNDGVETAGAGASKNYEAIVWERAWLKSMNLTSFKPAI-----
Q8LBN6_ARATH_29117/1-89 --------GGWSPI--SNVTDPQVVEIGEFAV--SEYNKRS-------------ESGL--KFETVVSGETQ-VVSGTNYRLKVAANDG----DGVSKNYLAIVWDKPWMKFRNLTSFEPAN-----
Q9FGK2_ARATH_29117/1-89 --------GGWSPI--SNVTDPQVVEIGEFAV--SEYNKRS-------------ESGL--KFETVVSGETQ-VVSGTNYRIKVAANDG----DGVSKNYLAIVWDKPWMKFRNLTSFEPAN-----
Q41916_ARATH_29117/1-89 --------GGWSPI--SNVTDPQVVEIGEFAV--SEYNKRS-------------ESGL--KFETVVSGETQ-VVSGTNYRLKVAANDG----DGVSKNYLAIVWVKPWMKFRNLTSFEPAN-----
Q9FQ13_CITPA_30117/1-88 --------GGWKPI--EDPKEKHVMEIGQFAV--TEYNKQS-------------KSAL--KFESVEKGETQ-VVSGTNYRLILVVKDG------PSTKKFEAVVWEKPWEHFKSLTSFKPMV-----
Q84WT8_ARATH_30115/1-86 --------GSRKPI--KNVSDPDVVAVAKYAI--EEHNKES-------------KENL--VFVKVVEGTTQ-VVSGTKYDLKIAAKDG----GGKIKNYEAVVVEKLWLHSKSLESFK--------
O23494_ARATH_30115/1-86 --------GSRKPI--KNVSDPDVVAVAKYAI--EEHNKES-------------KEKL--VFVKVVEGTTQ-VVSGTKYDLKIAAKDG----GGKIKNYEAVVVEKLWLHSKSLESFK--------
Q4FZ48_MAIZE_88143/1-56 --------GQYVKI--ENVKDPYVQGVGEWAV--KEHNRQT-------------GESL--QFAEVVSGMEQ-VVAGTNYKLNLA-----------------------------------------
Q6TPK4_ACTDE_3089/1-60  --------GGWRPI--ESLNSAEVQDVAQFAV--SEHNKQA-------------NDEL--QYQSVVRGYTQ-VVAGTNYRLVIAAKDG-------------------------------------
Q6TPK2_9ERIC_2988/1-60  --------GGWRPI--ENLNSAEVQDVAQFAV--SEHNKQA-------------NDEL--QYQSVVRGYTQ-VVSGTNYRLVIAAKDG-------------------------------------
Q6TPK3_ACTDE_2988/1-60  --------GGWRPI--KDLNSAEVQDVAQFAV--SEHNKQA-------------NDKL--QYQRVVRGYSQ-VVAGTNYRLVIAAKDG-------------------------------------
Q1SNM2_MEDTR_152194/1-43 -------PGWQSVP---AHDPQVQDAANHAI--KTIQQRS-------------NSLVPYELHEVTDAK-------------------------------------------------------
Q1S5M8_MEDTR_152194/1-43 -------PGWQSVP---AHDPQVQDAANHAI--KTIQQRS-------------NSLVPYELHEVTDAK-------------------------------------------------------
Q84LB7_MALDO_157199/1-43 -------PGWQSVP---PHDPQVQDAANHAV--KSLQQRS-------------NSLLPYELQEVVHAQ-------------------------------------------------------
Q4GZT8_FRAAN_147192/1-46 -------PGWQDVH---PQDPQVQDAANHAV--KSLQQKS-------------NSLFPYELQEVVHAKSEV----------------------------------------------------
Q1XHC6_WHEAT_149195/1-47 -------PGWRDVP--VHDPVVKDAASHAV--KSIQQRS-------------NSLLPYELVEIVRAKAEVV---------------------------------------------------
Q5NBI1_ORYSA_114160/1-47 -------PGWRDVP--VHDPVVKDAADHAV--KSIQQRS-------------NSLFPYELLEIVRAKAEVV---------------------------------------------------
Q4A1J7_MAIZE_143189/1-47 -------PGWREVP---VEDPVVKDAAHHAV--KSIQERS-------------NSLFPYELLEILRAHAQVV---------------------------------------------------
Q4FZ52_MAIZE_152198/1-47 -------PGWREVP---VEDPVVKDAAHHAV--KSIQERS-------------NSLFPYELLEILRAHAQVV---------------------------------------------------
Q9FUB0_ARATH_120208/1-89 -------SGWREVP---GDDPEVKHVAEQAV--KTIQQRS-------------NSLFPYELLEVVHAKAEVTGEAAKYNMLLKLKR------GEKEEKFKVEVHKNHEGALHVNHAEQHH------
Q8VZA2_ARATH_112182/1-71 -------SGWREVP---GDDPEVKHVAEQAV--KTIQQRS-------------NSLFPYELLEVVHAKAEVTGEAAKYNMLLKLKR------GEKEEKFKVE--------------------------
Q9LHF9_ARATH_145215/1-71 -------SGWREVP---GDDPEVKHVAEQAV--KTIQQRS-------------NSLFPYELLEVVHAKAEVTGEAAKYNMLLKLKR------GEKEEKFKVE--------------------------
Q8H0X6_ARATH_112182/1-71 -------SGWREVP---GDDPEVKHAAEQAV--KTIQQRS-------------NSLFPYELLEVVHAKAEVTGEAAKYNMLLKLKR------GEKEEKFKVE--------------------------
Q39270_BRACM_109197/1-89 -------SGWREVP---GDDPEVQHVADHAV--KSIQQRS-------------NSLFPYELQEVVHANAEVTGEAAKYNMVLKLKR------GEKEEKFKVEVHKNHEGVLHLNHMEQQH------
Q39268_BRACM_115203/1-89 -------SGWREVP---GDDPEVQHVADHAV--KTIQQRS-------------NSLFPYELQEVVHANAEVTGEAAKYNMVLKLKR------GEKEEKFKVEVHKNHEGVLHLNHMEQQH------
Q8VYX5_BRAOL_118206/1-89 -------SGWREVP---GDDPEVQHVADHAV--KTIQQRS-------------NSLFPYELQEVVHANAEVTGEAAKYNMVLKLKR------GEKEEKFKVEVHKNHEGVLHLNHMEQHH------
Q1L0Q7_BOEDR_142230/1-89 -------SGWREVP---GDDPEVQHVAEHAV--KTIQQRS-------------NSLFPYELQEVVHANAEVTGETAKFNMLLKLKR------GEKEEKFKVEVHKNHEGALHLNHMEQHH------
Q9AUC9_SESIN_109155/1-47 -------SGWRPVP---VHDPVVQDAAHHAI--KTIQERS-------------NSLFPYELSEVVHANAEVV---------------------------------------------------
Q43635_RICCO_121167/1-47 -------AEWKEVA---AHDPVVQDAATHAV--NTIQQRS-------------NSLFPYQLQEIVHAKAQVV---------------------------------------------------
Q8LC76_ARATH_150212/1-63 -------FDWRSVS---TNNPEVQEAAKHAM--KSLQQKS-------------NSLFPYKLIDIILARAKVVEERVKFELLLKLER------GN---------------------------------
Q9FF63_ARATH_152214/1-63 -------FDWRSVS---TNNPEVQEAAKHAM--KSLQQKS-------------NSLFPYKLIDIILARAKVVEERVKFELLLKLER------GN---------------------------------
```

FIG. 2F

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C1

```
                              10        20        30        40        50        60        70
                               |         |         |         |         |         |         |
Q9M366_ARATH_43120/1-78       ------LYVQVIQAINNSVVNPSAR------------------------------------------ICC
Q9LZE5_ARATH_42107/1-66       ------LYVDVIRAIKNSDVDPGP--------------------------------------------CD
Q6K6B6_ORYSA_263333/1-71      ------LYVRVVRARGVAAVG------------------------------------------------E
O64492_ARATH_281355/1-75      ------LYVNIVKAKDLSVLG------------------------------------------------E
Q6EUH5_ORYSA_49126/1-78       ------LYVRVVKARGLKWS----------------------------------------------GEFD
Q7XR21_ORYSA_51139/1-89       ------LYVRVVRARGLTAAASTVAGG---------------------------------------GGCN
Q84TJ7_ARATH_280360/1-81      ------LYVRVVKARELPIMDIT-------------------------------------------GSVD
Q9T0C8_ARATH_126206/1-81      ------LYVRVVKARELPIMDIT-------------------------------------------GSVD
Q259Q9_ORYSA_276356/1-81      ------LFVRVVKARDLPDMDVT-------------------------------------------GSLD
Q7XPV3_ORYSA_276356/1-81      ------LFVRVVKARDLPDMDVT-------------------------------------------GSLD
Q8H2Q5_ORYSA_277357/1-81      ------LFVRVVKARDLPHMDIT-------------------------------------------GSLD
O65279_ARATH_84164/1-81       ------LYVRVVKARDLPNKDLT-------------------------------------------GSLD
Q8RXU9_ARATH_270350/1-81      ------LYVRVVKARDLPNKDLT-------------------------------------------GSLD
Q2HRE0_MEDTR_283363/1-81      ------LFIRVVKARDLPRMDLT-------------------------------------------GSLD
Q9SKA3_ARATH_296377/1-82      ------LYVSVVKARDLPVMDVS-------------------------------------------GSLD
O80558_ARATH_50131/1-82       ------LYVSVVKARDLPVMDVS-------------------------------------------GSLD
Q7XKA3_ORYSA_291371/1-81      ------LYVSVVKARDLPNMDIT-------------------------------------------GALD
Q9M2D4_ARATH_251331/1-81      ------LFIKIVKARNLPSMDLT-------------------------------------------GSLD
Q1RSQ4_MEDTR_457538/1-82      ------LYVRVVKAKDLPPGTIT-------------------------------------------SSCD
Q1S9Y9_MEDTR_80161/1-82       ------LYVRVVKAKNLTLNSLT-------------------------------------------STCD
Q9FL59_ARATH_56137/1-82       ------LYVRVVKAKDLPPNPVT-------------------------------------------SNCD
Q9FI32_ARATH_296378/1-83      ------LYVRVVKAKELPPGSIT-------------------------------------------GGCD
Q94JQ8_ARATH_41121/1-81       ------LYVRVVKAKELPGKDMT-------------------------------------------GSCD
Q9M2R0_ARATH_41121/1-81       ------LYVRVVKAKELPGKDMT-------------------------------------------GSCD
Q9C8H3_ARATH_41121/1-81       ------LYVRVVKAKELPGKDLT-------------------------------------------GSCD
Q9LXU2_ARATH_42122/1-81       ------LYVRVVKAKELPGKDVT-------------------------------------------GSCD
Q60EW9_ORYSA_42122/1-81       ------LYVRVVKAKDLPSKDIT-------------------------------------------GSCD
Q5TKJ0_ORYSA_73154/1-82       ------LYVHVVKAKDLPAVSAA-------------------------------------------GTID
Q9FIZ1_ARATH_40112/1-73       ------LYIRIVKARALPSN-------------------------------------------------D
O48584_ARATH_40112/1-73       ------LYIRIVKARALPSN-------------------------------------------------D
O49435_ARATH_48124/1-77       ------LYARIVRARALPVN-------------------------------------------------D
Q2QWP5_ORYSA_200283/1-84      ------LFVRVIKARKLPDMDAN-------------------------------------------GSLD
Q9CA47_ARATH_337419/1-83      ------LFVRIVKARGLPPNE------------------------------------------------S
Q9SSF7_ARATH_337419/1-83      ------LFVRIVKARGLPPNE------------------------------------------------S
Q8S1F8_ORYSA_344423/1-80      ------LFVRVVKVRGIRACE------------------------------------------------G
Q7XID7_ORYSA_66152/1-87       ------LFVRVVRARGLPAGA------------------------------------------------H
Q9FJG3_ARATH_325405/1-81      ------VFIRVVKARSLPTSG------------------------------------------------S
Reference/1-156               MAGSGVLEVHLVDAKGLT--------------GNDFL-----------------------------GKID
ERG1_ORYSA_795/1-89           ------LEVHLVDAKGLT--------------GNDFLGEI--------------------------GKID
Q259F2_ORYSA_163/1-63         ----------------------------------------------------------------------MD
Q7XPW6_ORYSA_687/1-82         ------LEVLLVCAKGLE--------------DTDFLN-----------------------------DMD
O24582_MAIZE_686/1-81         ------LEVLLVSAKGLE--------------DTDFLN-----------------------------NMD
Q9SWH6_MAIZE_686/1-81         ------LEVLLVSAKGLE--------------DTDFLN-----------------------------NMD
Y1322_ARATH_687/1-82          ------LEVVLVSAKGLE--------------DADFLN-----------------------------NMD
ERG3_ORYSA_687/1-82           ------LEVLLVGAKGLE--------------NTDYLC-----------------------------NMD
Q25AG5_ORYSA_687/1-82         ------LEVLLVGAKGLE--------------NTDYLC-----------------------------NMD
Q6H7E3_ORYSA_687/1-82         ------LEVLLVGAKGLE--------------NTDYLC-----------------------------NMD
Q9ZRV6_CICAR_687/1-82         ------LEVVLISAKGLE--------------DNDFLS-----------------------------SID
PP16A_CUCMA_591/1-87          ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
Q4JHI7_9ROSI_692/1-87         ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
Q4JHJ0_CUCMA_692/1-87         ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
Q4JHI5_9ROSI_692/1-87         ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
Q4JHI9_CUCMA_692/1-87         ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
PP16B_CUCMA_591/1-87          ------MEVHLISGKGLQ--------------AHDPLN----------------------------KPID
Q4JHI8_CUCMA_692/1-87         ------MEVHLISGKGLQ--------------ALDPLN----------------------------KPID
```

FIG. 3A

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```
           C2                              C3
       80        90        100       110       120       130       140       150
PVVEITL------------GNY-KSSTKNL---PMGPN-----MDWNQ----VFAFD----KSKGD-------VLSVTL
PVVEITL------------GNY-KSSTKDL---PVGPN-----MDWNQ----VFAFD----KTKGD-------VLSVTL
TVAEVKL------------GNY-RGVTPAT---AAH--------HWDQ----VFAFS--KETIQSS-------FVEVFV
VVSEVKL------------GNY-RGVTKKV---SSNSSN----PEWNQ----VFVFS--KERIQSS-------VVELFV
PFAELRL------------GGY-SQITRHV---EKTAS-----PEWDD----VFAFS--RERIHAP-------FLDVLV
PYVEVRL------------GNY-RGTTRHH---ERKAA-----PEWNQ----VFAFS--RERVQAS-------VLEVFV
PFVEVRV------------GNY-KGITRHF---EKRQH-----PEWNQ----VFAFA--KERMQAS-------VLEVVV
PFVEVRV------------GNY-KGITRHF---EKRQH-----PEWNQ----VFAFA--KERMQAS-------VLEVVV
PYVEVRV------------GNY-RGITRHF---EKQKN-----PEWNA----VFAFS--RDRMQAT-------ILEVVV
PYVEVRV------------GNY-RGITRHF---EKQKN-----PEWNA----VFAFS--RDRMQAT-------ILEVVV
PYVEVHL------------GNY-KMKTRHF---EKNQR-----PCWDE----VFAFP--REVMQST-------SLEVIV
PYVVVKI------------GNF-KGVTTHF---NKNTD-----PEWNQ----VFAFA--KDNLQSN-------FLEVMV
PYVVVKI------------GNF-KGVTTHF---NKNTD-----PEWNQ----VFAFA--KDNLQSN-------FLEVMV
PYVIVKV------------GNF-KGTTNHF---EKNNS-----PEWNL----VFAFA--KENQQAT-------TLEVVI
PYVEVKL------------GNY-KGLTKHL---EKNSN-----PIWKQ----IFAFS--KERLQSN-------LLEVTV
PYVEVKL------------GNY-KGLTKHL---EKNSN-----PIWKQ----IFAFS--KERLQSN-------LLEVTV
PYVEVRL------------GNF-KGVTRHL---EKNPN-----PVWRQ----VFAFS--RDHLQSS-------QLEVVV
PYIEVKL------------GNY-TGKTKHF---EKNQN-----PVWNE----VFAFS--KSNQQSN-------VLEVIV
PYVEVKL------------GNY-RGRTKHL---EKKLN-----PEWNQ----VFAFS--KDRIQSS-------VLEVFV
PYVEVRL------------GNY-KGRTKHL---DKRSN-----PEWNQ----VYAFS--KDQIQSS-------ILEVIV
PYVEVKI------------GNY-KGKTKHF---EKRTN-----PEWNQ----VFAFS--KDKVQSS-------TVEVFV
PYVEVKL------------GNY-KGRTKIF---DRKTTI----PEWNQ----VFAFT--KERIQSS-------VLEVFV
PYVEVKL------------GNY-KGTTRHF---EKKSN-----PEWNQ----VFAFS--KDRIQAS-------FLEATV
PYVEVKL------------GNY-KGTTRHF---EKKSN-----PEWNQ----VFAFS--KDRIQAS-------FLEATV
PYVEVKL------------GNY-RGTTRHF---EKKSN-----PEWNQ----VFAFS--KDRVQAS-------YLEATV
PYVEVKL------------GNY-RGMTKHF---EKRSN-----PEWKQ----VFAFS--KERIQAS-------ILEVVV
PYVEVKL------------GNY-KGTTRHF---EKKTN-----PEWNQ----VFAFS--KERIQSS-------VVEIIV
PFVEVKL------------GNF-KGTTPVL---GGNHN-----PSWKQ----VFAFS--ATHLQAH-------VLEVAV
LFVEVTI------------GRY-KGRTKRS---TNPYPN----LEFDE----VFAFN--SDRLQGN-------MLEVMK
LFVEVTI------------GRY-KGRTKRS---TNPYPN----LEFDE----VFAFN--SDRLQGN-------MLEVMK
SFVAVKI------------GSY-KGRTKQI---LNSNPN----PEFHE----TFAFT--KTRLQGD-------ILEVVV
PYVEVKF------------GAYNRGVTRCF---KRNKN-----PEWNE----TFAFSFQHDKIPSP-------TVDIVV
AYVKVRT------------SNHFVRSKPAVNRPGESVDS----PEWNQ----VFALGHNRSDSAVTG-----ATLEISA
AYVKVRT------------SNHFVRSKPAVNRPGESVDS----PEWNQ----VFALGHNRSDSAVTG-----ATLEISA
PYVKIQA------------GPHTLRSRPGRDVSG--TGN----PEWNQ----VFAINHAKPE----------PTLEISV
PHVRVAA------------GGRHASTREAR-----RGAF----FEWDQ----TFAFVRDPGATDSPG-----PTLEVSV
PVTKISL------------SGTMIQSKPAR-----KTSC----FEWDQ----TFAFLRDSPDLSSS------PILEISV
PYVVVQY------------RSQERKSSVARD--QGKN------PSWNE----VFKFQINSTAATGQ------HKLFLRL
PYVVVQY------------RSQERKSSVARD--QGKN------PSWNE----VFKFQINSTAATGQ------HKLFLRL
PYVILTC------------RTQEQKSSVAKG--AGSE------PEWNE----TFVFTVSDDVP---------QLNVKI
PYVILTC------------RTQEQKSSVAKG--AGSE------PEWNE----TFVFTVSDDVP---------QLNVKI
PFVILTC------------RTQEQKSSVANG--AGSE------PEWNE----TFVFTVSDDTP---------QLHLKI
PFVILTC------------RTQEQKSSVANG--AGSE------PEWNE----TFVFTVSDDTP---------QLHLKI
PYVQLTC------------RTQDQKSNVAEG--MGTT------PEWNE----TFIFTVSEGTT---------ELKAKI
PYAVLKC------------RSQEQKSSVASG--KGSD------PEWNE----TFMFSVTHNAT---------ELIIKL
PYAVLKC------------RSQEQKSSVASG--KGSD------PEWNE----TFMFSVTHNAT---------ELIIKL
PYAILKC------------RSQEQRSSIASG--KGSN------PEWNE----NFVFTVSDKAT---------ELLIKL
PYVILSY------------RAQEHKSTVQEG--AGSN------PQWNE----TFLFTVSDSAS---------ELNLRI
PYAEINF------------KGQERMSKVAKN--AGPN------PLWDE----KFKFLAEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPN------PLWDE----KFKFLAEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPN------PLWDE----KFKFLAEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPD------PIWNE----KFKFLVEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPD------PIWNE----KFKFLVEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPD------PIWNE----KFKFLVEYPGSGGD------FHILFKV
PYAEINF------------KGQERMSKVAKN--AGPD------PIWNE----KFKFLVEYPGSGGD------FHILFKV
```

FIG. 3B

C4

```
          160       170       180       190       200       210       220       230       240
            |         |         |         |         |         |         |         |         |
KDG-------P-------------------TNTVINKRN----------------------------------------------------------------
KDR--------------------------------------------------------------------------------------------------
RAR-------G-------------------SDDHVGRVW----------------------------------------------------------------
KEG-------N-------------------KDEYTGRVL----------------------------------------------------------------
RGR-----GFA-------------------KDDYVGSTR----------------------------------------------------------------
RDKDA-VAAVA-------------------RDGYVGRVA----------------------------------------------------------------
KDK----DLL--------------------KDDYVGFVR----------------------------------------------------------------
KDK----DLL--------------------KDDYVGFVR----------------------------------------------------------------
KDK----DLL--------------------KDDFVGLVR----------------------------------------------------------------
KDK----DLL--------------------KDDFVGLVR----------------------------------------------------------------
KDK----DFI--------------------RDDYVGRVS----------------------------------------------------------------
KDK----DIL--------------------LDDFVGIVK----------------------------------------------------------------
KDK----DIL--------------------LDDFVGIVK----------------------------------------------------------------
KDK----DTI--------------------HDDFVGTVR----------------------------------------------------------------
KDK----DLLT-------------------KDDFVGRVH----------------------------------------------------------------
KDK----DLLT-------------------KDDFVGRVH----------------------------------------------------------------
KDK----DVL--------------------KDDFVGRVV----------------------------------------------------------------
MDK----DMV--------------------KDDFVGLIR----------------------------------------------------------------
KDK----EMVG-------------------RDDYLGRVI----------------------------------------------------------------
KDK----ETVG-------------------RDDYIGRVA----------------------------------------------------------------
RDK----EMVT-------------------RDEYIGKVV----------------------------------------------------------------
KDK----ETLG-------------------RDDILGKVV----------------------------------------------------------------
KDK----DFV--------------------KDDLIGRVV----------------------------------------------------------------
KDK----DFV--------------------KDDLIGRVV----------------------------------------------------------------
KDK----DLV--------------------KDDLIGRVV----------------------------------------------------------------
KDK----DVV--------------------LDDLIGRIM----------------------------------------------------------------
KDK----DFV--------------------KDDFIGRVL----------------------------------------------------------------
KAK----DLAG-------------------GDDLIGRVG----------------------------------------------------------------
K--------MN-------------------EEEIIGQCR----------------------------------------------------------------
K--------MN-------------------EEEIIGQCR----------------------------------------------------------------
RNR----DNPN-------------------EDDIVGKCK----------------------------------------------------------------
NDK-----DLV-------------------RDDFVGKLH----------------------------------------------------------------
WD-----ASS---------------------ESFLGGVC----------------------------------------------------------------
WD-----ASS---------------------ESFLGGVC----------------------------------------------------------------
WDG---GAPSPI-------------------EAFLGGVC----------------------------------------------------------------
WDLPP-DADVSDAD----------------DRHFLGGLC----------------------------------------------------------------
WDSST-GIETS---------------------QFLGGIC----------------------------------------------------------------
MDHDT-----------------------FSRDDFLGEATINVTDLISLGMEHGTWEMSESKHRVVLADKTYHGEIRVSLTFTASAKAQDHAEQVGGWAHSFRQ
MDHDT-----------------------FSRDDFLGEAT----------------------------------------------------------------
MDSDA-----------------------FSADDFVGEAN----------------------------------------------------------------
MDSDA-----------------------FSADDFVGEAN----------------------------------------------------------------
MDSD------------------------LTNDDFVGERT----------------------------------------------------------------
MDSD------------------------LTNDDFVGEAT----------------------------------------------------------------
FDKDV-----------------------GTEDDAVGEAT----------------------------------------------------------------
MDSDS-----------------------GTDDDFVGEAT----------------------------------------------------------------
MDSDS-----------------------GTDDDFVGEAT----------------------------------------------------------------
LDSDT-----------------------GSADDFVGEAT----------------------------------------------------------------
MEKDN-----------------------FNNDDNLGEAI----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVK----------------------------------------------------------------
MDHDA-----------------------IDGDDYIGDVI----------------------------------------------------------------
```

FIG. 3C

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```
                                   C1
                              |<-------------->|
                                       10         20         30         40         50         60         70
                                        |          |          |          |          |          |          |
Q4JHJ3_CUCMO_692/1-87        ------LEVHLISGKGLQ-------------AHDPLN-----------------------------KPID
Q4JHI6_9ROSI_692/1-87        ------LEVHLISGKGLQ-------------AHDPLN-----------------------------KPID
Q4JHJ2_CUCMO_692/1-87        ------LEVHLISGKGLQ-------------AHDPLN-----------------------------KPID
Q4JHI4_9ROSI_692/1-87        ------LEVHLISGKGLQ-------------AHDPLN-----------------------------KPID
Q4JHJ1_CUCMO_692/1-87        ------LEVHLISGKGLR-------------AHDPLN-----------------------------KPID
Q9M2T2_ARATH_692/1-87        ------LEVSLISGKGLK-------------RSDFLG-----------------------------K-ID
O49490_ARATH_39115/1-77      -----------VGCQKLK-------------DTEWFS------------------------------RQD
Q945K9_ARATH_1293/1-82       ------LEVTVVGCQKLK-------------DTEWFS------------------------------RQD
Q9SDM4_DUNTE_485/1-82        ------VDCTLVSARGIK-------------DVEIVG------------------------------KQS
Q67UD3_ORYSA_502605/1-104    ------LRASVIEAHDLRVP-----------APSPGLPF------------------------------D
Q8S1F8_ORYSA_499586/1-88     ------LRASVIEAQDLRVP-----------APPPGLPF------------------------------D
Q9CA47_ARATH_499585/1-87     ------LRVTVLEAQDLHIA-----------PNLPPLTAP-----------------------------E
Q9SSF7_ARATH_499585/1-87     ------LRVTVLEAQDLHIA-----------PNLPPLTAP-----------------------------E
O49435_ARATH_205287/1-83     ------LRVNVIEAQDLVLL-----------H--PNRINP-----------------------------E
Q7XZZ4_ORYSA_473566/1-94     ------LRLSVIQAQDLRLP-----------APPDAKAKP----------------------M-GPAFPE
Q9SS68_ARATH_441533/1-93     ------LRLTVIQTQDLQLG-----------LGSEAKSK--------------------------IPTTE
Q9FJG3_ARATH_479562/1-84     ------LRATVIEAQDLLPP-----------QLTAFKEA------------------------------S
Q7XR21_ORYSA_228303/1-7      ------LRISVLEAQDVVPG-----------AVAGAGGDK-----------------------GRHGEAF
O64492_ARATH_436531/1-96     ------LRISVIEAQDV--------------AIMDKGSSL-----------------------MRFPE--
Q8H2Q5_ORYSA_438519/1-82     ------VRVNVIGAQD--I-------------FPMEN---------------------------HIPD--
Q9M2D4_ARATH_406486/1-81     ------LRVNVIEAQDLVI-------------VPDRT---------------------------RLPN--
Q2HRE0_MEDTR_448519/1-72     ------LRVKVIEAHDLVS-------------HDNKS---------------------------RAPD--
Q1S9Y9_MEDTR_243325/1-83     ------LRVNVIEAQDVI--------------SSDRN---------------------------RVPE--
Q1RSQ4_MEDTR_620702/1-83     ------LRVNVIEAQDVI--------------PSDRN---------------------------RLPE--
Q9FI32_ARATH_461543/1-83     ------LRVNVIEAQDMI--------------PSDRN---------------------------RLPD--
Q93ZA2_ARATH_94176/1-83      ------LRVNVIEAQDVE--------------PSDRS---------------------------QPPQ--
Q9FL59_ARATH_219301/1-83     ------LRVNVIEAQDVE--------------PSDRS---------------------------QPPQ--
Q69T22_ORYSA_46128/1-83      ------LRVNVIEAQDVQ--------------PQARG---------------------------RAPE--
Q7XPV3_ORYSA_438520/1-83     ------LRVNIIEAQDIA--------------ITDKT---------------------------RYPD--
Q259Q9_ORYSA_438520/1-83     ------LRVNIIEAQDIA--------------ITDKT---------------------------RYPD--
Q94JQ8_ARATH_203285/1-83     ------LRVNVIEAQDLI--------------PTDKQ---------------------------RYPE--
Q9M2R0_ARATH_203285/1-83     ------LRVNVIEAQDLI--------------PTDKQ---------------------------RYPE--
Q9C8H3_ARATH_203285/1-83     ------LRVNVIEAQDLI--------------PSDKG---------------------------RYPE--
Q9LXU2_ARATH_203285/1-83     ------VRVNVIEAQDLI--------------PHDKT---------------------------KFPE--
Q60EW9_ORYSA_203285/1-83     ------LRVNVIEAQDLI--------------PNDRT---------------------------RFPD--
Q9T0C8_ARATH_290372/1-83     ------VRVNVIEAQDLI--------------PTDKT---------------------------RFPD--
Q84TJ7_ARATH_444526/1-83     ------VRVNVIEAQDLI--------------PTDKT---------------------------RFPD--
Q6K6B6_ORYSA_415506/1-92     ------LRVSVIEAQDLI--------------PMDKGPMA----------------------IGRYPE--
O65279_ARATH_209276/1-68     ----------------------------------DKS---------------------------RVPE--
Q8RXU9_ARATH_434516/1-83     ------LRVQILEAQDVII-------------VSDKS---------------------------RVPE--
Q9SKA3_ARATH_459541/1-83     ------LRIHVMEAQDLV--------------PSDKG---------------------------RVPD--
O80558_ARATH_213295/1-83     ------LRIHVMEAQDLV--------------PSDKG---------------------------RVPD--
Q7XKA3_ORYSA_453534/1-82     ------LKVVAIAAQDLI--------------PAEKG--------------------------RPLAP--
Q5TKJ0_ORYSA_236319/1-84     ------LRVAAIGAQDLV--------------PLDAS--------------------------RP-AN--
Q9LZE5_ARATH_195276/1-82     ------VRVTIVSGHDLI--------------STDRN---------------------------RTPS--
Q9M366_ARATH_201281/1-81     ------VRVTIVSGHDLI--------------SKDKN---------------------------KTPS--
Q93ZM0_ARATH_483561/1-79     ------IIVTVLAGKNL--------------VSKDKSGKC------------------------DAS---
Q9LS53_ARATH_453531/1-79     ------IIVTVLAGKNL--------------VSKDKSGKC------------------------DAS---
Q93ZM0_ARATH_293392/1-100    ------IYVTVVSGNNLNRRILRGSPSKSSEIGEGSSGNS------------------------SSKPVQ
Q9LS53_ARATH_263362/1-100    ------IYVTVVSGNNLNRRILRGSPSKSSEIGEGSSGNS------------------------SSKPVQ
Q5NA77_ORYSA_287368/1-82     ------VKLEILEGSDMKP-------------SDMNG------------------------------LSD
Q6Z6R6_ORYSA_287368/1-82     ------AKVEILEGADMKP-------------SDPNG------------------------------LAD
Q9LUD5_ARATH_208289/1-82     ------ALVEVVEACDVKP-------------SDLNG------------------------------LAD
Q67XP8_ARATH_240321/1-82     ------ALVEVVEACDVKP-------------SDLNG------------------------------LAD
Q93XX4_ARATH_284365/1-82     ------VLVEVFEASDLKP-------------SDLNG------------------------------LAD
Q9C8L5_ARATH_239320/1-82     ------VLVEVFEASDLKP-------------SDLNG------------------------------LAD
```

FIG. 3D

```
   C2                               C3
|<--------------->|           |<------------------------>|
      80      90     100      110     120     130     140     150
PYVEINY------------KGQERMSKVAKN--AGPD------PLWDE----KFKFLAEYPGSGGD------FHVLFKV
PYVEINY------------KGQERMSKVAKN--AGPD------PLWDE----KFKFLAEYPGSGGD------FHILFKV
PYAEINY------------KGQERMSKVAKN--AGPD------PLWDE----KFKFLAEYPGSGGD------FHIFFKV
PYVEINY------------KGQERMSKVAKN--AGPD------PVWNE----KFKFLAEYPGSGGD------FLILFKV
PYVEINY------------KGQERMSKVAKN--AGPD------PVWNE----KFKFLAEYPGSGGD------FLILFKV
PYVEIQY------------KGQTRKSSVAKED-GGRN------PTWND----KLKWRAEFPGSGAD------YKLIVKV
PYVVLEY------------GGRSHRTRTCTD--GGKN------AVFQE----KFIFTLIEGLR----------DLKVAV
PYVVLEY------------GGRSHRTRTCTD--GGKN------AVFQE----KFIFTLIEGLR----------DLKVAV
PYAVLTV------------GPKTFKSGTANG--GGSD------PVWNQ----TFSFTNVTPDS----------SVKLEI
VRVKIKI------------GFQSARTQR---SVASTSSGSAFAWEWEE----DLMFVVSEPLDES---------LIVLV
VRVKIQV------------GFQSARTRR---SVASRSSGSAFA--WEE----DLMFVVSEPLDES---------LVVLV
IRVKAQL------------GFQSARTRR---GSMNNHSGSFH---WHE----DMIFVAGEPLEDC---------LVLMV
IRVKAQL------------GFQSARTRR---GSMNNHSGSFH---WHE----DMIFVAGEPLEDC---------LVLMV
ILIKGFL------------GNVVVRSRI---SQTKSVSPV-----WNE----DMMFVAVEPFDDS---------LILSV
LYVKAQL------------GAQVFKTCRVALGSAAT--GTSNP-SWNE----DLLFVAAEPFDPF---------LTVVV
LYVKAQL------------GPQVFKTARTSIGPSASSSGSGNP-TWNE----DLVFVASEPFEPF---------LIVTV
FQLKAQL------------GSQVQKTK-----SAVT--RNGAP-SWNE----DLLFVAAEPFSDQ---------LVFTL
VVVKVQV------------GGVTLRTKPC----CR-PTS----PSWNE----ELVFVVAEPFDEP---------AVLVI
LSAKLQV------------GSQILRTAIA----SAIPTKSFSNPYWNE----DLMFVVAEPFEDC---------VTVVV
VFVKVRL------------GHQMLKTRPA----RSPT----RNFMWNE----EMMFVAAEPFEED---------LIIQI
PYVKIRL------------NNQVVRTKPS----HS------LNPRWNE----EFTLVAAEPFED----------LIISI
AFVKVQH------------GNQIFKTKPV----QSRI----NNPRWDQ----GTLFVAAEPFEEP---------LIITV
VFIKAQM------------GSQVLRTKVC----PTRS----TTQIWNE----DLVFVAAEPFEEQ---------LTITV
VSVKAHL------------GCQVLKTKIC----STRT----TSPLWNE----DLVFVAAEPFEEQ---------LTITV
VFVKASV------------GMQTLKTSIC----SIKT----TNPLWKE----DLVFVVAEPFEEQ---------LVISV
AFVKVQV------------GNQILKTKLC----PNKT----TNPMWNE----DLVFVAAEPFEEQ---------FFLTV
AFVKVQV------------GNQILKTKLC----PNKT----TNPMWNE----DLVFVAAEPFEEQ---------FFLTV
VFVKAQV------------GNQILKTSVV----AAPT----LNPRWNE----DLVFVVAEPFEEQ---------LLLTV
VFVRAQV------------GHQHGRTKPV----QARN----FNPFWNE----DLMFVAAEPFEDH---------LILSL
VFVRAQV------------GHQHGRTKPV----QARN----FNPFWNE----DLMFVAAEPFEDH---------LILSL
VYVKAIV------------GNQALRTRVS----QSRT----INPMWNE----DLMFVAAEPFEEP---------LILSV
VYVKAIV------------GNQALRTRVS----QSRT----INPMWNE----DLMFVAAEPFEEP---------LILSV
VFVKVIM------------GNQALRTRVS----QSRS----INPMWNE----DLMFVVAEPFEEP---------LILSV
VYVKAML------------GNQTLRTRIS----QTKT----LNPMWNE----DLMFVVAEPFEEA---------LILAV
VYVKAML------------GNQALRTRVS----PSRT----LNPMWNE----DLMFVAAEPFEEH---------LILSV
VYVKAQL------------GNQVMKTRPC----QART----LGAVWNE----DFLFVVAEPFEDH---------LVLTV
VYVKAQL------------GNQVMKTRPC----QART----LGAVWNE----DFLFVVAEPFEDH---------LVLTV
LFVRAQV------------GSQMLRTRPA----PVAANRGPSSPFWNE----DLMFVVAEPFEEF---------LVLSL
VFVRVKV------------GNQMLRTKFP----QRSN-----NPKWGD----EFTFVVAEPFEDN---------LVLSV
VFVRVKV------------GNQMLRTKFP----QRSN-----NPKWGD----EFTFVVAEPFEDN---------LVLSV
AIVKIQA------------GNQMRATRTP----QMRT----MNPQWHE----ELMFVVSEPFEDM---------VIVSV
AIVKIQA------------GNQMRATRTP----QMRT----MNPQWHE----ELMFVVSEPFEDM---------VIVSV
SIVKIQL------------GGQTRRTRS-------QG---SANPMWNE----EFLFVAAEPFDEP---------LVVTV
FCVKLQL------------AGQVRRTRPG----APPG---TLNPIWNE----EFMFVVSEPFDEP---------LFVTV
VYVTATL------------GQVTLKTEVS----SGTN------PSWNK----DLIFVASEPLEGT---------VYIRL
VYVTATL------------GKVALKTKVS----SGTN------PSWNQ----DLIFVASEPLEGT---------VYIRL
--VKLQY------------GKIIQKTKIV----NAAE------CVWNQ----KFEFEELAGEEYL---------KVKCY
--VKLQY------------GKIIQKTKIV----NAAE------CVWNQ----KFEFEELAGEEYL---------KVKCY
TFVEVEL------------EQLSRRTEMK----SGPN------PAYQS----TFNMILHDNTGTL---------KFNLY
TFVEVEL------------EQLSRRTEMK----SGPN------PAYQS----TFNMILHDNTGTL---------KFNLY
PYVKGRL------------GPFKFQTQIQK---KTLS------PKWFE----EFKIPITSWESL---------NELAME
PYVKGHL------------GPYRFQTKIHK---KTLN------PKWME----EFKIPVTSWAAL---------NLLSLQ
PYVKGQL------------GAYRFKTKILW---KTLA------PKWQE----EFKIPICTWDSA---------NILNIE
PYVKGQL------------GAYRFKTKILW---KTLA------PKWQE----EFKIPICTWDSA---------NILNIE
PYVKGKL------------GAYRFKTKIQK---KTLS------PKWHE----EFKIPIFTWDSP---------SILNIE
PYVKGKL------------GAYRFKTKIQK---KTLS------PKWHE----EFKIPIFTWDSP---------SILNIE
```

FIG. 3E

C4

```
                 160        170        180    |   190        200        210        220        230        240
MDHDA---------------------IDGDDYI|GDVK------------------------------------------------------------
MDHDA---------------------IDGDDYI|GDVK------------------------------------------------------------
MDHDA---------------------IDDDDLI|GEVK------------------------------------------------------------
MDHDV---------------------IDGDDYI|GDVS------------------------------------------------------------
MDHDV---------------------IDGDDYI|GDVS------------------------------------------------------------
MDHDT---------------------FSSDDFI|GEAT------------------------------------------------------------
WNSNT---------------------LSTDDFI|GNAT------------------------------------------------------------
WNSNT---------------------LSTDDFI|GNAT------------------------------------------------------------
FNSNV---------------------VLRDVAI|GGCK------------------------------------------------------------
KDRT---------------------MIKEPARR|GARPTSALLPAKEAAHVC----------------------------------------------
EDRS---------------------MIKEPALL|GHAT------------------------------------------------------------
EDR----------------------TTKEATLL|GHAM------------------------------------------------------------
EDR----------------------TTKEATLL|GHAM------------------------------------------------------------
EDKV---------------------GPRE-ECL|GRCE------------------------------------------------------------
EDIF---------------------S-G--QPV|GQAR------------------------------------------------------------
EDIT---------------------N-G--QSI|GQTK------------------------------------------------------------
EYRT---------------------SKGP-VTV|GMAR------------------------------------------------------------
E--------------------------------|----------------------------------------------------------------
EDRLNG---------------GAIGGQNDVAV|GRVQ------------------------------------------------------------
EDRV---------------------AQNKDEVI|GETM------------------------------------------------------------
EDRV---------------------APNREETL|GEVH------------------------------------------------------------
ED---------------------------KD--|----------------------------------------------------------------
EDRV---------------------HGSKDEVL|GKIM------------------------------------------------------------
EDHV---------------------QPSKDEVL|GRIS------------------------------------------------------------
EDRV---------------------HTSKDEVI|GKIT------------------------------------------------------------
ENKV---------------------TPAKDEVM|GRLI------------------------------------------------------------
ENKV---------------------TPAKDEVM|GRLI------------------------------------------------------------
EDRV---------------------TPRKDDLL|GRAA------------------------------------------------------------
EDRV---------------------APNKDEVL|GRVI------------------------------------------------------------
EDRV---------------------APNKDEVL|GRVI------------------------------------------------------------
EDRV---------------------APNKDEVL|GRCA------------------------------------------------------------
EDRV---------------------APNKDEVL|GRCA------------------------------------------------------------
EDRV---------------------APNKDEVL|GRCA------------------------------------------------------------
EDRV---------------------APNKDETL|GRCA------------------------------------------------------------
EDRI---------------------APGKDDVL|GRTI------------------------------------------------------------
EDRV---------------------APGKDEIV|GRTY------------------------------------------------------------
EDRV---------------------APGKDEIV|GRTY------------------------------------------------------------
EDHV---------------------SPGRDDVL|GRLV------------------------------------------------------------
EDHT---------------------APNRDEPV|GKAV------------------------------------------------------------
EDHT---------------------APNRDEPV|GKAV------------------------------------------------------------
DDRI---------------------GPGKDEIL|GRVF------------------------------------------------------------
DDRI---------------------GPGKDEIL|GRVF------------------------------------------------------------
EERV---------------------AAGRDEPV|GRVI------------------------------------------------------------
EDRV---------------------GPGRDEPL|GRIM------------------------------------------------------------
IDRVD--------------------DQHEERII|GKLE------------------------------------------------------------
IDRED--------------------EQHEG-CI|GTLK------------------------------------------------------------
REE----------------------MLGTDNI|GTAT------------------------------------------------------------
REE----------------------MLGTDNI|GTAT------------------------------------------------------------
ENNP---------------------GSVRYDSL|ASCE------------------------------------------------------------
ENNP---------------------GSVRYDSL|ASCE------------------------------------------------------------
VCD----KDHMF---------------DDSL|GTCT------------------------------------------------------------
VRD----KDPIF---------------DDTL|GDCS------------------------------------------------------------
VQD----KDRFS---------------DDSL|GDCS------------------------------------------------------------
VQD----KDRFS---------------DDSL|GDCS------------------------------------------------------------
VGD----KDRFV---------------DDTL|GECS------------------------------------------------------------
VGD----KDRFV---------------DDTL|GECS------------------------------------------------------------
```

FIG. 3F

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```
                                C1
                                10        20        30        40        50        60        70
                                 |         |         |         |         |         |         |
Q9LPH4_ARATH_284365/1-82    ------VLVEVFEASDLKP------------SDLNG---------------------------LAD
Q6Z7A3_ORYSA_23103/1-81     ------LCVHVLEARGLQA------------AYLTG---------------------------HSD
Q66VB0_ORYSA_24104/1-81     ------LQVRVVEARGLPA------------VRVDG---------------------------TSD
Q9ZVT9_ARATH_383/1-81       ------LQVRVVEARNLPA------------MDLNG---------------------------FSD
Q6Z8U1_ORYSA_383/1-81       ------LNVRVIEARNLRA------------MDSNG---------------------------FSD
Q5Z6I4_ORYSA_384/1-82       ------LLVQVSEARNLPA------------IDGGGG--------------------------LSD
Q6SR86_CHLRE_569/1-65       ------LCVSVIEARNVQA------------DDFAG---------------------------KNF
Q8W4D4_ARATH_83163/1-81     ------VKVELLAAKNLIG------------ANLNG---------------------------TSD
Q9M1A2_ARATH_83163/1-81     ------VKVELLAAKNLIG------------ANLNG---------------------------TSD
Q69MT7_ORYSA_91171/1-81     ------VKLELLAAKNLIA------------ANLNG---------------------------TSD
Q6K8R7_ORYSA_117207/1-91    ------IKLELLCAKYLIG------------ANLNG---------------------------SSD
Q6Y3R3_PTEVI_2858/1-31      ------LEVHLLEAHGLLD------------TDTFG---------------------------KSD
Q9LS53_ARATH_577655/1-79    ------IELVLVEARDLVA------------ADIRG---------------------------TSD
Q93ZM0_ARATH_607685/1-79    ------IELVLVEARDLVA------------ADIRG---------------------------TSD
Q1T680_MEDTR_420502/1-83    ------LVVIVHEAQDVEG------------KH------------------------------HTN
Q6ETC4_ORYSA_421503/1-83    ------LVVIVHEAQDVEG------------KH------------------------------HTN
Q9LNT5_ARATH_418499/1-82    ------LVVIVHEAEDLEG------------KY------------------------------HTN
Q1PF28_ARATH_1882/1-65      ------FVVIVHSAEDVEG------------KH------------------------------HTN
Q9SKQ7_ARATH_1882/1-65      ------FVVIVHSAEDVEG------------KH------------------------------HTN
Q9SKR0_ARATH_137201/1-65    ------LVVIVHSAEDVEG------------KH------------------------------HTN
Q5MD16_BRANA_158241/1-84    ------LAVIVHSAEDVEG------------KH------------------------------HTN
Q9SKR2_ARATH_422505/1-84    ------LVVIVHSAEDVEG------------KH------------------------------HTN
Q69JE2_ORYSA_421504/1-84    ------LYVVVHEAQDLEG------------KH------------------------------HTN
Q5QLZ9_ORYSA_398461/1-64    ------LYVVVHEAKELEG------------KC------------------------------NTN
Q7XA06_ARATH_422505/1-84    ------LSVAVQSAKDVEG------------KKK-----------------------------HSN
Q3E9M4_ARATH_200283/1-84    ------LSVAVQSAKDVEG------------KKK-----------------------------HSN
Q9FYD9_ARATH_465548/1-84    ------LSVAVQSAKDVEG------------KKK-----------------------------HSN
Q655F0_ORYSA_421505/1-85    ------LLVSVENAEDVEG------------KR------------------------------HTN
Q7XPV3_ORYSA_692/1-87       ------LGVEVASAHDLMP------------KDGQG---------------------------SAS
Q259Q9_ORYSA_692/1-87       ------LGVEVASAHDLMP------------KDGQG---------------------------SAS
Q9T0C9_ARATH_893/1-86       ------LGVDVIGAHNLFP------------KDGQG---------------------------TSN
Q84TJ7_ARATH_893/1-86       ------LGVDVIGAHNLFP------------KDGQG---------------------------TSN
Q8H2Q5_ORYSA_791/1-85       ------LGVEVTSAHDLLP------------KE-QG---------------------------TCN
Q2HRE0_MEDTR_1398/1-86      ------LCVEVVGAHDLVA------------KDGEG---------------------------SST
O65279_ARATH_664/1-59       ------LGVEVISAQGLLQ------------RDKHN---------------------------SCS
Q8RXU9_ARATH_691/1-86       ------LGVEVISAQGLLQ------------RDKHN---------------------------SCS
Q9M2D4_ARATH_790/1-84       ------LGVEVISAR-LKP------------REDYG---------------------------GVN
Q2QWP5_ORYSA_689/1-84       ------LVVEVISAD-IPS------------SSNTS---------------------------QTN
Q7XZZ4_ORYSA_10103/1-94     ------VVVEVCNARNLMP------------KDGQG---------------------------TAS
Q9SS68_ARATH_994/1-86       ------LIVEICSARNLMP------------KDGQG---------------------------TAS
Q9CA47_ARATH_19108/1-90     ------LVVEVVEARNILP------------KDGQG---------------------------SSS
Q9SSF7_ARATH_19108/1-90     ------LVVEVVEARNILP------------KDGQG---------------------------SSS
Q8S1F8_ORYSA_27121/1-95     ------LAVEVVDARDLVP------------KDGLG---------------------------TSS
Q1RSQ4_MEDTR_389/1-87       ------LIVEVINAHDLMP------------KDGEG---------------------------SAS
Q9FI32_ARATH_793/1-87       ------LVVHVVDAQYLMP------------RDGQG---------------------------SAS
Q6K6B6_ORYSA_8104/1-97      ------LVVEVVAAHNLMP------------KDGQG---------------------------SSS
O64492_ARATH_1398/1-86      ------LVVEIVGAHNLMP------------KDGED---------------------------SSS
Q9SKA3_ARATH_489/1-86       ------LVVEIVDASDLMP------------KDGQG---------------------------SAS
Q7XKA3_ORYSA_393/1-91       ------VGVEILDASELAP------------KDGAG---------------------------ACN
Q9FJG3_ARATH_796/1-90       ------LVVEVVDAKDLTP------------KDGHG---------------------------TSS
O04823_SPOST_1394/1-82      ------LNVRVVRGSNLA----------------ICDPL-----------------------THTSD
Q69RN2_ORYSA_1596/1-82      ------LNVRVVRGSNLI----------------IADPL-----------------------THTSD
Q6ZII7_ORYSA_889/1-82       ------LKVRVMRGLNLA----------------ICDPL-----------------------THSSD
Q7XIV3_ORYSA_887/1-80       ------LKIRVVRGINLA----------------YRD-------------------------TRGSD
Q7XIU9_ORYSA_887/1-80       ------LSVRVLRGVNLV----------------SRD-------------------------AGGSD
Q6YWF1_ORYSA_987/1-79       ------VKVRVVRGVNLA----------------VRD-------------------------LRSSD
```

FIG. 3G

```
                C2                              C3
         80        90        100       110       120       130       140       150
          |         |         |         |         |         |         |         |
PYVKGKL------------GAYRFKTKIQK---KTLS------PKWHE----EFKIPIFTWDSP---------SILNIE
PYVRLQM------------GRRRAKTTVVK---RCLS------PLWDE----EFGFAVGDAEE----------ELVVSV
PFVKLQL------------GKRRAKTAVAR---RTLA------PAWDE----EFSFLVGDIAE----------ELVVSV
PYVRLQL------------GKQRSRTKVVK---KNLN------PKWTE----DFSFGVDDLND----------ELVVSV
PYVKLQL------------GKQRFKTKVVK---KNLN------PAWDQ----EFSFSVGDVRD----------VLKLYV
PYAKLQL------------GRQRGKTRVAK---RTLS------PTWDE----EFAFRVVDLKD----------ELVVVV
FYVKLRV------------GSNEVKTDVVK---GSLA------PKFLK----DCRLAVPTPES----------DYLRIE
PYAIVNC------------GSEKRFSSMVP---GSRN------PMWGE----EFNFPTDELP----------AKINVTI
PYAIVNC------------GSEKRFSSMVP---GSRN------PMWGE----EFNFPTDELP----------AKINVTI
PYALITC------------GEEKRFSSMVP---GSRN------PMWGE----EFNFFVDSLP----------VKINVTI
PYAVISC------------GEQRRFSSMVP---SSRN------PLWGE----EFNFLVRELPVEFCTAPVNDSKVTITM
PYAIVYC------------QKE------------------------------------------------------
PYVRVQY------------GEKKQRTKVIY---KTLQ------PKWNQ----TMEFPDDGSS------------LELHV
PYVRVQY------------GEKKQRTKVIY---KTLQ------PKWNQ----TMEFPDDGSS------------LELHV
PQARLIF------------RGEEKKTKRIK---KNRD------PRWED----EFQFIAEEPPTN--------DKLHVEV
PYVRIVF------------RGEERKTKHIK---KNRD------PRWEQ----EFQFVCEEPPIN--------DKMQIEV
PSVRLLF------------RGEERKTKRVK---KNRE------PRWDE----DFQFPLDEPPIN--------DKLHVEV
PYVHIYF------------KGEERKTKHVK---KNKD------PKWNE----EFSFMLEEPPIH--------EKMHVKV
PYVHIYF------------KGEERKTKHVK---KNKD------PKWNE----EFSFMLEEPPIH--------EKMHVKV
PYVHIYF------------KGEERKTKNVK---KNKD------PKWNE----EFSFMLEEPPVH--------EKLHVEV
PYVRIYF------------KGEERKTKHVK---KNRD------PRWEE----EFTFMLEEPPVR--------XKLHVEV
PYVRIYF------------KGEERKTKHVK---KNRD------PRWNE----EFTFMLEEPPVR--------EKLHVEV
PYAKIIF------------KGEEKKTKVIK---KNRD------PRWED----EFEFVCEEPPVN--------DKLHIEV
PYVKLTF------------KGVEKKTKVVK---ENRN------PRWKE----EFEFECEETPAN--------DKLHVEV
PYAVVLF------------RGEKKKTKMLK---KTRD------PRWNE----EFQFTLEEPPVK--------ESIRVEV
PYAVVLF------------RGEKKKTKMLK---KTRD------PRWNE----EFQFTLEEPPVK--------ESIRVEV
PYAVVLF------------RGEKKKTKMLK---KTRD------PRWNE----EFQFTLEEPPVK--------ESIRVEV
PYAVVHF------------RGERKETKIIK---KTRD------PRWNE----EFQFMVDEAPVD--------DKIHIEV
ACVELTF------------DGQRFRTAIKD---KDLN------PVWNE----RFYFNVSD-PSNL----P-ELALEAYV
ACVELTF------------DGQRFRTAIKD---KDLN------PVWNE----RFYFNVSD-PSNL----P-ELALEAYV
AYVELYF------------DGQKHRTTIKD---RDLN------PVWNE----SFFFNISD-PSRL----H-YLNLEAQA
AYVELYF------------DGQKHRTTIKD---RDLN------PVWNE----SFFFNISD-PSRL----H-YLNLEAQA
PYVEIEF------------DDQKFRTAIKE---RDIN------PVWNE----QFYFNISD-PSRL----T-EKDLEAYV
TFVELEF------------DDQKFRTTTKD---KDLS------PYWNE----IFYFNITD-PSKL----S-NLNLEACI
PFVELKF------------DNQIFRATTKH---NDPN------PVWHE----CFYFVVSD-PSV---------------
PFVELKF------------DNQIFRATTKH---NDPN------PVWHE----CFYFVVSD-PSVL----S-TRTLEAHV
AYVELRF------------DDQKVITMTKI---DDSS------PVWNE----KFFFNISD-TEDL----S-NQFLDAYV
YSVELHF------------NSQSKSTTIKE---N--V------AVWNE----RFSFDMRQ-REDP----SGNLILEAAV
AYAVVDF------------DGQRRRTATRP---RDLN------PQWGE----RLEFLVHD-PDA-----MCAETLELNL
AYAIVDF------------DGQRRRTKTKF---RDLN------PQWDE----KLEFFVHD-VAT-----MGEEILEINL
AYVVVDF------------DAQKKRTSTKF---RDLN------PIWNE----MLDFAVSD-PKN-----MDYDELDIEV
AYVVVDF------------DAQKKRTSTKF---RDLN------PIWNE----MLDFAVSD-PKN-----MDYDELDIEV
AFAVVDF------------DGQRKRTRTVP---RDLS------PQWHE----RLEFAVHD-PAA-----MHAEALDVSL
TFVEVDF------------ENQLSRTRTVP---KNLN------PTWNQ----KLVFNLDT-TKP-----YHHKTIEVSV
PFVEVDF------------LNQLSKTRTVP---KSLN------PVWNQ----KLYFDYDQ-SVIN----QHNQHIEVSV
AYVEVEF------------EHQRRRTRARP---KELN------PVWNE----RLVFAVAD-PDD-----LPYRAIDVGV
PFVEVQF------------ENQRLRTKVKP---KDLN------PIWNE----KLVFHVID-VND-----LRHKALEINV
PFVEVEF------------DEQRQRTQTRF---KDLN------PQWNE----KLVFNVGD-LKR-----LNNKTVDVTV
AFVEVEF------------DGQKQRTPTKP---ADRS------PQWNH----TLVFDVRD-PSR-----LPSLPVDVSV
PYVVLDY------------YGQRRRTRTIV---RDLN------PVWNE----TLEFSLAKRPSHQ----LFTDVLELDM
PYVVLHY------------GAQKVKTSVQK---KNPN------PVWNE----VLQLSVTNP----------TKPVHLEV
PYVVLSY------------GPQKVKTSVQK---KNSN------PVWNE----VLQLAVTNP----------TKPVKLEV
PYVVLRH------------GSQKVKSSIRY---HSIN------PEWNE----ELTLSITNM----------MLPVKIEV
PYVVLRL------------GKQKVKTSVKK---KSVN------PIWHE----ELTLSIMNP----------IAPIKLGV
PYVVLHL------------DNQKLKTGVVK---KTTN------PVWNE----ELTLAVRNP----------ETPIQLEV
PYVIVRM------------GKQKLKTRVIK---KTTN------PEWND----ELTLSIEDP----------AVPVRLEV
```

FIG. 3H

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```
                                   |<----------------------------C4-------------------------------->|
          160       170       180       190       200       210       220       230       240
           |         |         |         |         |         |         |         |         |
VGD----KDRFV-------------------DDTLGFAP----------------------------------------------------------------
LNE----EGYFG-------------------GGFLGRVK----------------------------------------------------------------
LNE----DKYFS-------------------NDLLGKVR----------------------------------------------------------------
LDE----DKYFN-------------------DDFVGQVR----------------------------------------------------------------
YDE----DMIGI-------------------DDFLGQVK----------------------------------------------------------------
VDE----DRYFS-------------------DDFLGQVR----------------------------------------------------------------
L----------------------------------------------------------------------------------------------------
HDW----DIIWK-------------------STVLGSVT----------------------------------------------------------------
HDW----DIIWK-------------------STVLGSVT----------------------------------------------------------------
YDW----DIVWK-------------------STVLGSVI----------------------------------------------------------------
YDW----DTVCK-------------------CKVIGSVT----------------------------------------------------------------
-------------------------------------------------------------------------------------------------------
KDY----NTLLP-------------------TSSIGNCV----------------------------------------------------------------
KDY----NTLLP-------------------TSSIGNCV----------------------------------------------------------------
VSS----SSRT----------------LLHQKESLGYVD----------------------------------------------------------------
ISR----PPSI----------------GIHSKENLGYVV----------------------------------------------------------------
ISS----SSR-----------------LIHPKETLGYVV----------------------------------------------------------------
F----------------------------------------------------------------------------------------------------
F----------------------------------------------------------------------------------------------------
F----------------------------------------------------------------------------------------------------
LST----SSRI---------------GLLHPKETLGYVD----------------------------------------------------------------
LST----SSRI---------------GLLHPKETLGYVD----------------------------------------------------------------
LSK----ASKK---------------GLIHGKETLGYID----------------------------------------------------------------
-------------------------------------------------------------------------------------------------------
MSK----GTG----------------FHFRSKEELGHVD----------------------------------------------------------------
MSK----GTG----------------FHFRSKEELGHVD----------------------------------------------------------------
MSK----GTG----------------FHFRSKEELGHVD----------------------------------------------------------------
VSK----RRGLR--------------LPFRNKESLGHVD----------------------------------------------------------------
YNI----NRSID-----------------GSRSFLGKVR----------------------------------------------------------------
YNI----NRSVD-----------------GSRSFLGKVR----------------------------------------------------------------
YSH----NRSTN-----------------G-RSFLGKVS----------------------------------------------------------------
YSH----NRSTN-----------------G-RSFLGKVS----------------------------------------------------------------
YHA----NRASN-----------------S-KTCLGKVR----------------------------------------------------------------
NHY----NK-TN-----------------GSKIPLGKVK----------------------------------------------------------------
-------------------------------------------------------------------------------------------------------
YSY----QNEFD-----------------A-KPFLGKVR----------------------------------------------------------------
Y------NKTSS-----------------ITKSCLGKIR----------------------------------------------------------------
YCF----DQMSN-----------------S-KSLLGKVL----------------------------------------------------------------
YND----KKAI----------AATGGGGRRGGTFLGKVK----------------------------------------------------------------
CND----KK--------------TG---KRS-TFLGKVK----------------------------------------------------------------
YND----KRF--------------GNGGGRKNHFLGRVK----------------------------------------------------------------
YND----KRF--------------GNGGGRKNHFLGRVK----------------------------------------------------------------
YHD----RRFNP---------SGGGGGGGGKNHFLGRVR----------------------------------------------------------------
YND----RRQPN-----------------PGRNFLGRVR----------------------------------------------------------------
YHE----RR-PI-----------------PGRSFLGRVK----------------------------------------------------------------
YND----RAASGGV-------AGGGGAAPHGRNFLGKVR----------------------------------------------------------------
YNE----KRSS------------------NSRNFLGKVR----------------------------------------------------------------
YDD----RRDN------------------QPGKFLGRVK----------------------------------------------------------------
HHD----RSLTD-------------HHATRLHTFLGRVR----------------------------------------------------------------
YHD----KNFG----------------QTRRNNFLGRIR----------------------------------------------------------------
FDE----DKFT-------------------ADDSMGVAE----------------------------------------------------------------
FDE----DKFT-------------------ADDSMGVAE----------------------------------------------------------------
FDK----DTFT-------------------KDDSMGDAE----------------------------------------------------------------
FDK----DTFS-------------------RDDPMGDAE----------------------------------------------------------------
FDK----DTFS-------------------KDDQMGDAE----------------------------------------------------------------
YDK----DTF--------------------IDDAMGNAE----------------------------------------------------------------
```

FIG. 3I

C1 (positions 1–16, marked by arrow)

```
                                    10        20        30        40        50        60        70
                                     |         |         |         |         |         |         |
Q9C5M6_ARATH_887/1-80       ------LRIRVKRGINLA-------------------QRD-------------------------TLGSD
Q9SSL1_ARATH_887/1-80       ------LRIRVKRGINLA-------------------QRD-------------------------TLSSD
Q9CAC6_ARATH_839/1-32       ------LRIRVKRGINLA-------------------QRD-------------------------TLSSD
Q9S764_ARATH_1796/1-80      ------VRILVKRGIDLA-------------------RRD-------------------------ALSSD
O49303_ARATH_887/1-80       ------LRIRVKRGINLV-------------------SRD-------------------------SNTSD
Q9S7J9_ARATH_988/1-80       ------LRVHVKRGINLA-------------------IRD-------------------------ATTSD
Q9ZVF1_ARATH_988/1-80       ------LTIHVKRGINLA-------------------IRD-------------------------HRSSD
Q1S8S5_MEDTR_989/1-81       ------LKLRIKRGINLA-------------------IRD-------------------------SNSSD
Q9LVH4_ARATH_2099/1-80      ------LRIRIKRGVNLA-------------------VRD-------------------------ISSSD
Q9LP65_ARATH_44123/1-80     ------LRIRIKRGVNLA-------------------VRD-------------------------LNSSD
Q1SSA3_MEDTR_24103/1-80     ------LRIRIKRGVNLA-------------------VRD-------------------------VNTSD
Q9FHP6_ARATH_887/1-80       ------LRIHVKRGVNLA-------------------IRD-------------------------ISSSD
Q9C8Y2_ARATH_887/1-80       ------LRLHVIRGVNLA-------------------IRD-------------------------SQSSD
Q9C6B7_ARATH_1190/1-80      ------LRVRVQRGVNLA-------------------VRD-------------------------VSSSD
Q8LFN9_ARATH_182261/1-80    ------LKVTIKKGTNLA-------------------IRD-------------------------MMSSD
Q9M0W2_ARATH_180259/1-80    ------LKVTIKKGTNLA-------------------IRD-------------------------MMSSD
O49557_ARATH_215294/1-80    ------LKVTIKKGTNMA-------------------IRD-------------------------MMSSD
Q8L9H2_ARATH_183262/1-80    ------LKVTIKKGTNMA-------------------IRD-------------------------MMSSD
Q9FVJ3_ARATH_183262/1-80    ------LKVTIKKGTNMA-------------------IRD-------------------------MMSSD
Q1RV25_MEDTR_191270/1-80    ------LKVKVVKGTNLA-------------------IRD-------------------------MRTSD
Q49U73_ORYSA_166245/1-80    ------LNVKVKGGTNLA-------------------IRD-------------------------MSSSD
Q6H738_ORYSA_166245/1-80    ------LNVKVKGGTNLA-------------------IRD-------------------------MSSSD
Q69V47_ORYSA_167246/1-80    ------IKVKVIRGTKLA-------------------VRD-------------------------ILSSD
Q6Z653_ORYSA_179258/1-80    ------LNITVVRGIQLA-------------------VRD-------------------------MLTSD
Q6L4C8_ORYSA_240319/1-80    ------IKVDIRRGTNLA-------------------VRD-------------------------VMSSD
Q8RZA2_ORYSA_227306/1-80    ------IKVNVIRGTNLA-------------------VRD-------------------------MMSSD
Q8L7A4_ARATH_231310/1-80    ------IKVNVVKGTNLA-------------------VRD-------------------------VMTSD
Q9SFC0_ARATH_219298/1-80    ------IKVNVVKGTNLA-------------------VRD-------------------------VMTSD
Q1RU67_MEDTR_887/1-80       ------IKVNVRKGTHLA-------------------IRD-------------------------VVTSD
Q9FIK8_ARATH_887/1-80       ------LQVTVIQGKKLV-------------------IRD-------------------------FKSSD
Q2A9R2_BRAOL_887/1-80       ------LQVTVIRGKKLA-------------------IRD-------------------------FKSSD
Q2HV28_MEDTR_887/1-80       ------LKVIVVQGKRLV-------------------IRD-------------------------FKTSD
Q6K295_ORYSA_1594/1-80      ------LKVVVASGTNLA-------------------VRD-------------------------FTSSD
Q8LI73_ORYSA_1594/1-80      ------VKVKVVRGTNLA-------------------VRD-------------------------VFSSD
Q7XPV3_ORYSA_600693/1-94    ------LELGILGAQGIVP---------------MK-TRDGK------------------------GSSD
Q259Q9_ORYSA_600693/1-94    ------LELGILGAQGIVP---------------MK-TRDGK------------------------GSSD
Q84TJ7_ARATH_606693/1-88    ------LELGILNAVGLHP---------------MK-TREGR------------------------GTSD
Q9T0C8_ARATH_452539/1-88    ------LELGILNAVGLHP---------------MK-TREGR------------------------GTSD
Q43085_PEA_150/1-50         ----------------------------------------------------------------------
Q2HRE0_MEDTR_630702/1-73    --------------------------------------RDGR------------------------GAAD
O64492_ARATH_604694/1-91    ------LEIGILSATGLMP---------------MK-VRDGK----------------------CGGIAD
O48584_ARATH_329399/1-71    ------LVLGVISASGSIP---------------MK-SRDG------------------------RGTTD
O49435_ARATH_363455/1-93    ------LELGVLNATGLMP---------------MK-SRGG------------------------RGTTD
Q94JQ8_ARATH_364455/1-92    ------LELGILNATGLMP---------------MK-TKDG------------------------RGTTD
Q9M2R0_ARATH_364455/1-92    ------LELGILNATGLMP---------------MK-TKDG------------------------RGTTD
Q9C8H3_ARATH_365458/1-94    ------LELGVLNATGLMP---------------MK-AKEGG-----------------------RGTTD
Q60EW9_ORYSA_365456/1-92    ------LELGILTAQGLLP---------------MK-TKDG------------------------RGTTD
Q93ZA2_ARATH_258351/1-94    ------LEVGILSAQGLSP---------------MK-TKDG------------------------KATTD
Q9FL59_ARATH_383476/1-94    ------LEVGILSAQGLSP---------------MK-TKDG------------------------KATTD
Q9LXU2_ARATH_364451/1-88    ------LEVGIISAHGLMP---------------MK-SKDG------------------------KGTTD
Q1RSQ4_MEDTR_784876/1-93    ------LEMGILGAKGLLP---------------MK-MKDG------------------------HGSTD
Q1S9Y9_MEDTR_407504/1-98    ------LEVGILGAQKLLP---------------MK-MNNS------------------------RGSTD
Q9FI32_ARATH_626718/1-93    ------LEIGILGANGLVP---------------MK-LKDG------------------------RGSTN
Q69T22_ORYSA_212314/1-103   ------LEVGILGAAGLQP---------------MK-NRDG------------------------RGTTD
Q765H8_FLATR_33118/1-86     ------LEMGILGAHGLPP---------------MK-SKDG------------------------WTTTD
Q7XR21_ORYSA_405496/1-92    ------LEVGVLGAQGLPP---------------MKTAADGG-----------------------RGTTD
```

FIG. 3J

C2 C3

```
        80        90        100       110       120       130       140       150
PFVVITM------------GSQKLKTRVVE---NNCN------PEWNE----ELTLALRHP----------DEPVNLIV
PFVVITM------------GSQKLKTRVVE---NNCN------PEWNE----ELTLALRHP----------DEPVNLIV
PFVVITM------------GSQVF-------------------------------------------------------
PFVVITM------------GPQKLKSFTVK---NNCN------PEWNE----ELTLAIEDP----------NEPVKLMV
PFVVVTM------------GSQKLKTRGVE---NSCN------PEWDD----ELTLGINDP----------NQHVTLEV
PYVVITL------------ANQKLKTRVIN---NNCN------PVWNE----QLTLSIKDV----------NDPIRLTV
PYIVLNV------------ADQTLKTRVVK---KNCN------PVWNE----EMTVAIKDP----------NVPIRLTV
PYVVVNIG-----------HEQKLKTRVVK---NNCN------PEWNE----ELTLSIRDV----------RVPICLTV
PYVVVKM------------GKQKLKTRVIN---KDVN------PEWNE----DLTLSVTDS----------NLTVLLTV
PYVVVKM------------AKQKLKTRVIY---KNVN------PEWNE----DLTLSVSDP----------NLTVLLTV
PYAVVKM------------GKQRLKTHVIK---KDVN------PEWNE----DLTLSITDP----------VVPFKLTV
PYIVVHC------------GKQKLKTRVVK---HSVN------PEWND----DLTLSVTDP----------NLPIKLTV
PYVIVRM------------GKQKLRTRVMK---KNLN------TEWNE----DLTLSVTDP----------TLPVKIMV
PYVVLKL------------GRQKLKTKVVK---QNVN------PQWQE----DLSFTVTDP----------NLPLTLIV
PYVVLNL------------GKQKLQTTVMN---SNLN------PVWNQ----ELMLSVPES----------YGPVKLQV
PYVVLNL------------GKQKLQTTVMN---SNLN------PVWNQ----ELMLSVPES----------YGPVKLQV
PYVVLTL------------GQQKAQSTVVK---SNLN------PVWNE----ELMLSVPHN----------YGSVKLQV
PYVVLTL------------GQQKAQSTVVK---SNLN------PVWNE----ELMLSVPHN----------YGSVKLQV
PYVVLTL------------GQQKAQSTVVK---SNLN------PVWNE----ELMLSVPHN----------YGSVKLQV
PYVVLKL------------GQQTVQTTVIR---SNLN------PVWNE----ELMLSVPQQ----------FGPISLEV
PYVVLTL------------GQQKAQTSVIK---ANLN------PVWNE----ELKLSVPQQ----------YGPLKLQA
PYVVLTL------------GQQKAQTSVIK---ANLN------PVWNE----ELKLSVPQQ----------YGPLKLQV
PYVVLTL------------GQQKAKTKVIK---SNLN------PVWNE----VLTLSVPQK----------YGPLKLQV
PYVVLTL------------GEQKAQTTVKP---SDLN------PVWNE----VLKISIPRN----------YGPLKLEV
PYVMLNL------------GHQTMKTKVIK---NTLN------PVWNE----RLMLSIPHP----------VPPLKLQV
PYVILNL------------GHQSMKTKVIK---SSLN------PVWNE----RILLSIPDP----------IPMLKLQV
PYVILAL------------GQQSVKTRVIK---NNLN------PVWNE----TLMLSIPEP----------MPPLKVLV
PYVILAL------------GQQSVKTRVIK---NNLN------PVWNE----TLMLSIPEP----------MPPLKVLV
PYVILSL------------GHQSVKTRVIR---NNLN------PVWNE----SLMLSIPEN----------IPPLKVLV
PYVIVKL------------GNESAKTKVIN---NCLN------PVWNE----ELNFTLKDP----------AAVLALEV
PYVIVKL------------GNESAKTKVIN---NCLN------PVWDE----ELSFTLKDP----------AAVLSLEV
PYVVLKL------------GNQTAKTKVIN---SCLN------PVWNE----ELNFTLTEP----------LGVLNLEV
PYVVVRL------------AAMNKKTKVIN---SCLN------PVWNE----EMSFSIEEP----------AGVIKFEV
PYVVLKL------------GNQEVRTRTVR---KNTN------PVWNE----DLTLIVQDLN---------HLLVTLEV
TYCVAKY------------GSKWVRTRTIV---NNPG------PKFNE----QYTWEVYDP----------ATVLTVGV
TYCVAKY------------GSKWVRTRTIV---NNPG------PKFNE----QYTWEVYDP----------ATVLTVGV
TFCVGKY------------GQKWVRTRTMV---DNLC------PKYNE----QYTWEVFDP----------ATVLTVGV
TFCVGKY------------GQKWVRTRTMV---DNLC------PKYNE----QYTWEVFDP----------ATVLTVGV
--------------------------RTIS---NSLD------PKYHE----QYTWEVFDP----------ATVLTVGV
VYCVAKY------------GHKWVRTRTIV---GSLS------PKFHE----QYYWEVYDP----------STVLTLGV
SYCVAKY------------GPKWVRTRTVV---DSLC------PKWNE----QYTWEVYDP----------CTVVTVGV
AYCVAKY------------GQKWVRTRTIV---DSLS------PKWSE----QYTWEVYDP----------YTVITVAV
AYCVAKY------------GTKWVRTRTIV---DTFD------PKWNE----QYTWEVYDP----------YTVITIGV
AYCVAKY------------GQKWIRTRTII---DSFT------PRWNE----QYTWEVFDP----------CTVVTVGV
AYCVAKY------------GQKWIRTRTII---DSFT------PRWNE----QYTWEVFDP----------CTVVTVGV
AYCVAKY------------GQKWIRTRTII---DSFT------PRWNE----QYTWEVFDP----------CTVVTVGV
AYCVAKY------------GQKWVRTRTII---DSFT------PKWNE----QYTWEVYDP----------CTVITIGV
PYCVAKY------------GQKWVRTRTII---DSSS------PKWNE----QYTWEVYDP----------CTVITLGV
PYCVAKY------------GQKWVRTRTII---DSSS------PKWNE----QYTWEVYDP----------CTVITLGV
AYCVAKY------------GQKWIRTRTIV---DSFT------PKWNE----QYTWEVFDT----------CTVITFGA
AYCVAKY------------GQKWIRTRTLL---DTFS------PKWNE----QYTWEVYDP----------CTVITLGV
AYCVAKY------------GQKWIRTRTIL---DTFS------PKWNE----QYTWEVYDP----------CTVITLGV
AYCVAKY------------GQKWVRTRTIL---DTLS------PRWNE----QYTWEVYDP----------CTVITLGV
AYCVAKY------------GQKWVRTRTML---GTFS------PTWNE----QYTWEVFDP----------CTVITIGV
AYCVAKF------------GTKWVRTRTIT---NNFH------PKWNE----QYTWEVFDP----------CSIITIGV
AYCVAKY------------GHKWVRTRTVV---DSST------PRWNE----QYTWEVYDP----------CTVLTLAV
```

FIG. 3K

```
                                          C4
                                  |<-------------------------------------->|
              160        170        180  |    190        200        210        220        230        240
               |          |          |   |     |          |          |          |          |          |
YDK----DTFT-----------------SHDKMGDAK----------------------------------------------------------
YDK----DTFT-----------------SHDKMGDAK----------------------------------------------------------
-----------------------------------------------------------------------------------------------
YDK----DTFT-----------------ADDKMGDAQ----------------------------------------------------------
YDK----DTFT-----------------SHDPMGDAE----------------------------------------------------------
FDK----DRFS-----------------GDDKMGDAE----------------------------------------------------------
FDW----DKFT-----------------GDDKMGDAN----------------------------------------------------------
FDK----DTFF-----------------VDDKMGDAE----------------------------------------------------------
YDH----DMFS-----------------KDDKMGDAE----------------------------------------------------------
YDY----DTFT-----------------KDDKMGDAE----------------------------------------------------------
YDY----DTFS-----------------KDDKMGDAE----------------------------------------------------------
YDY----DLLS-----------------ADDKMGEAE----------------------------------------------------------
YDR----DRFS-----------------RDDKMGDAI----------------------------------------------------------
YDH----DFFS-----------------KDDKMGDAE----------------------------------------------------------
YDY----DTFS-----------------ADDIMGEAD----------------------------------------------------------
YDY----DTFS-----------------ADDIMGEAD----------------------------------------------------------
FDY----DTFS-----------------ADDIMGEAE----------------------------------------------------------
FDY----DTFS-----------------ADDIMGEAE----------------------------------------------------------
FDY----DTFS-----------------ADDIMGEAE----------------------------------------------------------
FDH----DLFS-----------------ADDIMGEAQ----------------------------------------------------------
FDH----DMLS-----------------KDDLMGEAE----------------------------------------------------------
FDH----DMLS-----------------KDDLMGEAE----------------------------------------------------------
YDH----DVLS-----------------RDDIMGEAE----------------------------------------------------------
YDH----DTFS-----------------ADDIMGEAE-------------------------------------------------------
FDK----DTFS-----------------SDDRMGDVE----------------------------------------------------------
YDK----DTFT-----------------TDDRMGEAE----------------------------------------------------------
YDK----DTFS-----------------TDDFMGEAE----------------------------------------------------------
YDK----DTFS-----------------TDDFMGEAE----------------------------------------------------------
YDK----DTFS-----------------TDDFMGEAE----------------------------------------------------------
FDK----DRFK-----------------ADDKMGHAS----------------------------------------------------------
FDK----DRFK-----------------ADDKMGHAT----------------------------------------------------------
FDK----DLLK-----------------ADDKMGNAF----------------------------------------------------------
FDW----DRFK-----------------YDDKMGHAF----------------------------------------------------------
YDR----DPF------------------VDDPMGAAF----------------------------------------------------------
FDN----GQLG---------EKGGEKTSSSKDAKIGKVR--------------------------------------------------------
FDN----GQLG---------EKGGEKTSSSKDAKIGKVR--------------------------------------------------------
FDN----GQLG---------EKG------NRDVKIGKIR--------------------------------------------------------
FDN----GQLG---------EKG------NRDVKIGKIR--------------------------------------------------------
FDN----CQVN---------GPD------NKDLLIGKVR--------------------------------------------------------
FNN----GQLN---------DSN-----DSNDSKIGKVR--------------------------------------------------------
FDN----ARVN---------ENN-----NSRDVRIGKVR--------------------------------------------------------
FDN--------------------------------------------------------------------------------------------
FDN----LKLF---------GAGNENRLIN-DSRIGKIR--------------------------------------------------------
FDN----CHLH---------GGEK-IGGAK-DSRIGKVR--------------------------------------------------------
FDN----CHLH---------GGEK-IGGAK-DSRIGKVR--------------------------------------------------------
FDN----CHLH---------GGDKNNGGGK-DSRIGKVR--------------------------------------------------------
FDN----CHLN---------GGEK-ANGAR-DTRIGKVR--------------------------------------------------------
FDN----CHLG---------GSEKSNSGAKVDSRIGKVR--------------------------------------------------------
FDN----CHLG---------GSEKSNSGAKVDSRIGKVR--------------------------------------------------------
FDN----GHIP---------GGSG-----K-DLRIGKVR--------------------------------------------------------
FDN----CHLG--------EKAPSGSS--IKDSRIGKVR--------------------------------------------------------
FDN----CHLGGGG-----EKAPSGGSNAARDSRIGKVR--------------------------------------------------------
FDN----SHLG---------SAQSGTAD-SRDARIGKVR--------------------------------------------------------
FDN----NHLGNGNGNGNNAGGGGGGSPPARDARVGKIR--------------------------------------------------------
FDNN---FHLQ---------GGDK---------RIGKVR--------------------------------------------------------
FDN----CNLG--------NGGGGG----KDQRIGKVR---------------------------------------------------------
```

FIG. 3L

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```
                                C1
                                |<------------->|
                                         10        20        30        40        50        60        70
                                          |         |         |         |         |         |         |
Q6K6B6_ORYSA_587682/1-96    ------LELGVLGATGLIP-------------MK-ARDGR-------------------------GATSD
Q9SKA3_ARATH_624711/1-88    ------LELGILSARNLMP-------------MK-GKDG---------------------------RMTD
O80558_ARATH_378465/1-88    ------LELGILSARNLMP-------------MK-GKDG---------------------------RMTD
Q5TKJ0_ORYSA_399486/1-88    ------LELGILGARNLIP-------------MK-GKDG---------------------------RTTD
Q7XKA3_ORYSA_621701/1-81    ------LELGILGARNLA--------------G-GK---------------------------------S
O65279_ARATH_285357/1-73    ------------------------------------R----------------------------KGTSD
Q8RXU9_ARATH_598688/1-91    ------LELGILNANVFHS-------------MK-TREG--------------------------KGTSD
Q9M2D4_ARATH_565653/1-89    ------LELGILRIEGLN--------------LS-QEGK--------------------------KETVD
Q8H2Q5_ORYSA_599693/1-95    ------LEVGILSANGLNP-------------TK-TKHE--------------------------RGSCD
Q6EUH5_ORYSA_383461/1-79    ------------------------------------RDG--------------------------RGSCD
Q9FJG3_ARATH_636729/1-94    ------VELGIIGCKNLLP-------------MKT-VNG--------------------------KGSTD
Q7XID7_ORYSA_400497/1-98    ------VELGIVGCKGLLP-------------MRT-ADG--------------------------KGCTD
Q9SSF7_ARATH_671762/1-92    ------LELGILGARGLLP-------------MKA-KNGG-------------------------KGSTD
Q9CA47_ARATH_671762/1-92    ------LELGILGARGLLP-------------MKA-KNGG-------------------------KGSTD
Q8S1FB_ORYSA_670764/1-95    ------LELGIIGACGLLP-------------MKT-KGGA-------------------------KGSTD
Q7XZZ4_ORYSA_639736/1-98    ------LEVGIRGAANLVP-------------MKIAKDGA-------------------------SGSTD
Q9SS68_ARATH_606698/1-93    ------LEVGIRGATNLLP-------------VKT-RDGT-------------------------RGTTD
Q9LZE5_ARATH_351437/1-87    ------LEIGILGATGLKG-------------SDERKQG-----------------------------ID
Q9M366_ARATH_360447/1-88    ------LEIGILGATGLKG-------------SDEKKQT-----------------------------ID
Q2QWP5_ORYSA_478560/1-83    ------VHLGILRATGLP-----------------LRMG--------------------------KSTVN
Q7XTM4_ORYSA_443525/1-83    ------LSVTVISGEDLPA-------------MDMNGK------------------------------SD
Q25A82_ORYSA_443525/1-83    ------LSVTVISGEDLPA-------------MDMNGK------------------------------SD
O23994_HORVU_146/1-46       ----------------------------------------------------------------------
Q8L706_ARATH_437519/1-83    ------LSVTVISAEEIPI-------------QDLMGK------------------------------AD
Q9ZVY8_ARATH_405487/1-83    ------LSVTVISAEEIPI-------------QDLMGK------------------------------AD
Q1S2I1_MEDTR_434516/1-83    ------LSVTVISAEDLPI-------------VDFMGK------------------------------AD
Q1SF66_MEDTR_443525/1-83    ------LSVTVISAEDLPA-------------VDFMGK------------------------------SD
Q6UU05_ORYSA_295377/1-83    ------LSVTVISAEDLPP-------------MDVMGK------------------------------AD
Q69UK6_ORYSA_435517/1-83    ------LSVTVISAEDLPP-------------MDVMGK------------------------------AD
Q9FY55_ARATH_450532/1-83    ------LSVTVVAAEDLPA-------------VDFMGK------------------------------AD
P92940_ARATH_248329/1-82    ------LIVTVVKATNLKN-------------KELIGK------------------------------SD
Q9LEX1_ARATH_265346/1-82    ------LIVTVVKATNLKN-------------KELIGK------------------------------SD
Q9LDM1_ARATH_216259/1-44    ----------------------------------------------------------------------
Q5MD17_BRANA_179/1-79       ---------TVVKATNLKN-------------KEFIGK------------------------------SD
O48645_LYCES_264346/1-83    ------LTVTIVKANGLKN-------------HEMIGK------------------------------SD
Q7XAL6_ORYSA_264346/1-83    ------LTVTVVKATSLKN-------------KELIGK------------------------------SD
Q6UU05_ORYSA_124208/1-85    ------LEVKLVEARDLTN-------------KDLVGK------------------------------SD
Q69UK6_ORYSA_264348/1-85    ------LEVKLVEARDLTN-------------KDLVGK------------------------------SD
Q9ZVY8_ARATH_232316/1-85    ------LEVKLVQAKNLTN-------------KDLVGK------------------------------SD
Q8L706_ARATH_264348/1-85    ------LEVKLVQAKNLTN-------------KDLVGK------------------------------SD
Q7XTM4_ORYSA_264348/1-85    ------LEVKLVQARDLTN-------------KDLIGK------------------------------SD
Q25A82_ORYSA_264348/1-85    ------LEVKLVQARDLTN-------------KDLIGK------------------------------SD
Q1SF66_MEDTR_264348/1-85    ------LEVKLVQAKELTN-------------KDIIGK------------------------------SD
Q1S2I1_MEDTR_251335/1-85    ------LDVKLVQAKNLSN-------------KDIIGK------------------------------SD
Q9FY55_ARATH_273357/1-85    ------LDVKVVQAKDLAN-------------KDMIGK------------------------------SD
Q5MD16_BRANA_182/1-82       ---------KVVRAVGLRK-------------KDMMGG------------------------------AD
Q9SKR2_ARATH_262346/1-85    ------VHVKVVRAVGLRK-------------KDLMGG------------------------------AD
Q9SKR0_ARATH_269/1-68       -------------------------------------GM-----------------------------IN
Q1T680_MEDTR_262346/1-85    ------LHVKVLHAMKLKK-------------KDLLGA------------------------------SD
Q9LNT5_ARATH_260344/1-85    ------LSVKVIKAIKLKK-------------KDLLGG------------------------------SD
Q6ETC4_ORYSA_262346/1-85    ------LHVNIVRAVKLTK-------------KDFLGK------------------------------SD
Q3E9M4_ARATH_41125/1-85     ------LHVSILRARNLLK-------------KDLLGT------------------------------SD
Q7XA06_ARATH_263347/1-85    ------LHVSILRARNLLK-------------KDLLGT------------------------------SD
Q9FYD9_ARATH_306390/1-85    ------LHVSILRARNLLK-------------KDLLGT------------------------------SD
Q655F0_ORYSA_262346/1-85    ------LHVKVIRAMNLLK-------------MDLLGK------------------------------SD
Q5QLZ9_ORYSA_262340/1-79    ------LLVKVLRAQNLRE-------------KGPLGK------------------------------RD
```

FIG. 3M

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```
            C2                                        C3
             80        90        100       110       120       130       140       150
             |         |         |         |         |         |         |         |
AYCVAKY------------GQKWIRTRTVV---DSVC------PRWNE----QYTWEVFDP----------CTVITVGV
PYCVAKY------------GNKWVRTRTLL---DALA------PKWNE----QYTWEVHDP----------CTVITIGV
PYCVAKY------------GNKWVRTRTLL---DALA------PKWNE----QYTWEVHDP----------CTVITIGV
AYCVAKY------------GPKWVRTRTIL---NTLN------PQWNE----QYTWEVFDP----------CTVITVVV
PYCVAKY------------GAKWVRTRTLV---GTAA------PRWNE----QYTWEVFDL----------CTVVTVAV
TYVVAKY------------GHKWVRSRTVI---NSMN------PKYNE----QYTWEVFDP----------ATVLTICV
TYVVAKY------------GHKWVRSRTVI---NSMN------PKYNE----QYTWEVFDP----------ATVLTICV
AYCVAKY------------GTKWVRTRTVT---NCLN------PRFNE----QYTWEVYEP----------ATVITIGV
AYCVAKY------------GQKWVRTRTIV---DNLN------PRFNE----QYTWDVFDH----------GTVLTIGL
AYCVAKY------------GVKWYRTRTVT---DSIS------PRFHQ----QYHWEVHDH----------CTVLTVAV
AYTVAKY------------GSKWVRTRTVS---DSLD------PKWNE----QYTWKVYDP----------CTVLTIGV
AYAVAKY------------GPKWARTRTIS---DSFD------PAWNE----QYTWPVYDP----------CTVLTVGV
AYCVAKY------------GKKWVRTRTIT---DSFD------PRWHE----QYTWQVYDP----------CTVLTVGV
AYCVAKY------------GKKWVRTRTIT---DSFD------PRWHE----QYTWQVYDP----------CTVLTVGV
AYCVAKY------------GKKWVRTRTVT---DSLN------PRWNE----QYTWQVYDP----------CTVLTVAV
AYVVLKY------------GPKWARTRTIL---DQFN------PRWNE----QYAWDVFDP----------CTVLTIAV
AYVVAKY------------GPKWIRTRTIL---DRFN------PRWNE----QYTWDVYDP----------CTVLTIGV
SYVVAKY------------GNKWARTRTVV---NSVT------PKWNE----QYSWDDYEK----------CTVLTLGI
SYVVAKY------------GNKWARTRTVV---NSVS------PKWNE----QYSWDVYEK----------CTVLTLGI
PYCVAKY------------GDKWVRTRTIL---DGPE------HVFNE----QHTWSVYDI----------ATVLTAGV
PYVVLSLKK---------SKTK-YKTRVVS---ESLN------PVWNQ----TFDFVVEDGLHD---------MLMLEV
PYVVLSLKK---------SKTK-YKTRVVS---ESLN------PVWNQ----TFDFVVEDGLHD---------MLMLEV
--------------------------RVVN---ESLN------PVWNQ----TFDFVVEDGLHD---------MLVLEV
PYVVLSMKK---------SGAK-SKTRVVN---DSLN------PVWNQ----TFDFVVEDGLHD---------MLVLEV
PYVVLSMKK---------SGAK-SKTRVVN---DSLN------PVWNQ----TFDFVVEDGLHD---------MLVLEV
PFVVLALKK---------SEKK-QKTRVVN---ETLN------PVWNQ----TFDFVVEDGLHD---------MLIVEL
PFVVLTLKK---------AETK-NKTRVVN---NSLN------PVWNQ----TFDFVVEDGLHD---------MLLVEV
PFVVLYLKK---------GETK-KKTRVVT---ETLN------PIWNQ----TFDFVVEDALHD---------LLMVEV
PFVVLYLKK---------GETK-KKTRVVT---ETLN------PIWNQ----TFDFVVEDALHD---------LLMVEV
AFVVITLKK---------SETK-SKTRVVP---DSLN------PVWNQ----TFDFVVEDALHD---------LLTLEV
PYATIYIRP---------VFK--YKTNAID---NNLN------PVWDQ----TFELIAEDKETQ---------SLTVEV
PYATIYIRP---------VFK--YKTKAIE---NNLN------PVWDQ----TFELIAEDKETQ---------SLTVEV
----------------------------IE---NNLN------PVWDQ----TFELIVEDKETQ---------SLTVEV
PYATIHIRP---------VFK--YNTKAIE---NNLN------PVWDQ----TFDLIAEDKETQ---------SLTIEV
PYAVVHIRP---------LFK--VKTKTID---NNLN------PVWDQ----TFELIAEDKETQ---------SLFIEV
PYVILYVRP---------MFK--VKTKVID---DNLN------PEWNE----TFPLIVEDKETQ---------SVIFEV
PFAVLYIRP---------LQDKMKKSKTIN---NDLN------PIWNE----HYEFVVEDTSTQ---------RLTVKI
PFAVLYIRP---------LQDKMKKSKTIN---NDLN------PIWNE----HYEFVVEDTSTQ---------RLTVKI
PFAKMFIRP---------LREKTKRSKTIN---NDLN------PIWNE----HFEFVVEDASTQ---------HLVVRI
PFAKMFIRP---------LREKTKRSKTIN---NDLN------PIWNE----HFEFVVEDASTQ---------HLVVRI
PFAIVYVRP---------LPDKMKRSKTIN---NDLN------PIWNE----HFEFIVEDADTQ---------TVTVKI
PFAIVYVRP---------LPDKMKRSKTIN---NDLN------PIWNE----HFEFIVEDADTQ---------TVTVKI
PYAVLYIRP---------LRNRTKKSKTIN---NDLN------PIWNE----HFEFIVEDASTQ---------HLFVKV
PFAVVFVRP---------LRDKTKTSKIIN---NQLN------PIWNE----HFEFIIEDESTQ---------HLTIRI
PYAIVFIRP---------LPDRTKKTKTIS---NSLN------PIWNE----HFEFIVEDVSTQ---------HLTVRV
PYVKIKLSE---------DKIPSKKTTVKH---KNLN------PEWNE----EHKFSVRDPQTQ---------VLEFSV
PFVKIKLSE---------DKIPSKKTTVKH---KNLN------PEWNE----EFKFSVRDPQTQ---------VLEFSV
PYVQIELSE---------DKISSKKTTVKH---KNLN------PEWNE----EFKFSVRDPKTQ---------VLEFNV
PYVKLKLTD---------DKMPSKKTTVKH---KNLN------PEWNE----EFNLVVKDPETQ---------VLQLNV
PYVKLTLSG---------DKVPGKKTVVKH---SNLN------PEWNE----EFDLVVKEPESQ---------ELQLIV
PYVKLKLTE---------EKLPSKKTSVKR---SNLN------PEWNE----DFKLVVKDPESQ---------ALELTV
PYVKLSLTG---------EKLPAKKTTIKK---RNLN------PEWNE----HFKLIVKDPNSQ---------VLQLEV
PYVKLSLTG---------EKLPAKKTTIKK---RNLN------PEWNE----HFKLIVKDPNSQ---------VLQLEV
PYVKLSLTG---------EKLPAKKTTIKK---RNLN------PEWNE----HFKLIVKDPNSQ---------VLQLEV
PYVKLRLSG---------EKLPSKKTSIKM---SNLN------PEWNE----HFRFIVKDPETQ---------ILELRM
PYVKLKMSG---------SKLPSKKTAVKH---SNLN------PEWNQ----EFKFVIRDPETQ---------ELDIN-
```

FIG. 3N

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```
                                       C4
                                   |<--------------------------------------------------------------------->|
        160        170        180        190        200        210        220        230        240
         |          |          |          |          |          |          |          |          |
FDN----CHVD--------KPASGNTTLAVRDNCIGKVR------------------------------------------------------------
FDN----SHVN--------DGGD------FKDQRIGKVR------------------------------------------------------------
FDN----SHVN--------DGGD------FKDQRIGKVR------------------------------------------------------------
FDN----NQIG--------KNGD------ARDESIGKVR------------------------------------------------------------
FDN----CHLT--------GGGD------AKDQRIGKVR------------------------------------------------------------
FDN----AHFA---------AGDGG---NKRDQPIGKVR------------------------------------------------------------
FDN----AHFA---------AGDGG---NKRDQPIGKVR------------------------------------------------------------
FDN----NQIN---------SGNG----NKGDGKIGKIR------------------------------------------------------------
FDN----CHIS--------ADSNHSSSPGHMDKPIGKVR------------------------------------------------------------
FHN----SQIG--------DKGGLVAGDPVKDVLLGKVR------------------------------------------------------------
FDS----WGVY---------EVDGGKEATRQDLRIGKVR------------------------------------------------------------
FDDPPPPSPSQ---------LPDGAKDAAAFSRPMGKVR------------------------------------------------------------
FDN----WRMF---------S--DASDD-RPDTRIGKIR------------------------------------------------------------
FDN----WRMF---------S--DASDD-RPDTRIGKIR------------------------------------------------------------
FDN----WRMF---------AFAGAGDEQRQDYRIGKVR------------------------------------------------------------
FDNVR--YRSA---------EASGDAGKLPKDARIGKLR------------------------------------------------------------
FDNGR--YKRD---------ES----GKQGRDVRVGKIR------------------------------------------------------------
YDN----RQIFKE--------------DQANDVPIGKVR------------------------------------------------------------
YDN----RQILEDK-------------NKANDVPIGKVR------------------------------------------------------------
FDH---FPHTR------------------KAHREIGKVQ------------------------------------------------------------
YDH----DTFS-------------------RD-YMGRCI------------------------------------------------------------
YDH----DTFS-------------------RD-YMGRCI------------------------------------------------------------
YDH----DTFS-------------------RD-YMGRCI------------------------------------------------------------
WDH----DTFG-------------------KD-YIGRCI------------------------------------------------------------
WDH----DTFG-------------------KD-YIGRCI------------------------------------------------------------
WDH----DTFG-------------------KE-KMGKVI------------------------------------------------------------
YDH----DTFG-------------------KD-YMGRVI------------------------------------------------------------
WDH----DTFG-------------------KD-YIGRCI------------------------------------------------------------
WDH----DTFG-------------------KD-YIGRCI------------------------------------------------------------
WDH----DKFG-------------------KD-KIGRVI------------------------------------------------------------
FDK----D-VG-------------------QDERLGLVK------------------------------------------------------------
FDK----D-VG-------------------QDERLGLVK------------------------------------------------------------
FDK----D-VG-------------------QDERLGLVK------------------------------------------------------------
FDK----D-VG-------------------QDERLGLVK------------------------------------------------------------
FDK----DNIG-------------------QDQRMGVAK------------------------------------------------------------
YDE----DRLQ-------------------QDKKLGVAK------------------------------------------------------------
YDD----EGLQ-------------------ASELIGCAR------------------------------------------------------------
YDD----EGLQ-------------------ASELIGCAR------------------------------------------------------------
YDD----EGVQ-------------------ASELIGCAQ------------------------------------------------------------
YDD----EGVQ-------------------ASELIGCAQ------------------------------------------------------------
YDD----DGIQ-------------------ESELIGCAQ------------------------------------------------------------
YDD----DGIQ-------------------ESELIGCAQ------------------------------------------------------------
YDD----EGLQ-------------------SSELIGCTD------------------------------------------------------------
FDD----EGIQ-------------------AAELIGCAQ------------------------------------------------------------
FDD----EGVG-------------------SSQLIGAAQ------------------------------------------------------------
YDW----GQLG-------------------KHDKMGMNV------------------------------------------------------------
YDW----EQVG-------------------NPEKMGMNV------------------------------------------------------------
YDW----EKIG-------------------KHDKMGMNV------------------------------------------------------------
YDW----EQVG-------------------KHDKMGMNV------------------------------------------------------------
YDW----EQVG-------------------KHDKIGMNV------------------------------------------------------------
YDW----EQVG-------------------KHDKIGMSV------------------------------------------------------------
FDW----DKVG-------------------GHDRLGMQM------------------------------------------------------------
FDW----DKVG-------------------GHDRLGMQM------------------------------------------------------------
FDW----DKVG-------------------GHDRLGMQM------------------------------------------------------------
FDW----EKVK-------------------MHDKLGMQV------------------------------------------------------------
--------FG-------------------KDEKLGMCK-------------------------------------------------------------
```

FIG. 3O

```
                                       C1
                                 10        20        30        40        50        60        70
                                  |         |         |         |         |         |         |
Q69JE2_ORYSA_262346/1-85  ------LLVKVLRAQNLRK-------------KDLLGK------------------------------SD
Q8L626_ARATH_403488/1-86  ------LSVTLVDAQKLRY-------------M-FFGK------------------------------TD
Q9SX44_ARATH_391476/1-86  ------LSVTLVDAQKLRY-------------M-FFGK------------------------------TD
Q9LT26_ARATH_388473/1-86  ------LSVTLVNAQKLPY-------------M-FSGR------------------------------TD
Q1T4J1_MEDTR_78119/1-42   ------LSVTLVDARKLPY---------------FFGK------------------------------TD
Q6K9U1_ORYSA_403488/1-86  ------LSVTLVDARKLSF-------------V-LFGK------------------------------TD
O04042_ARATH_262345/1-84  -----------FRCVNLDN-------------KDLFSK------------------------------SD
Q5XQC7_ARATH_202285/1-84  -----------FRCVNLDN-------------KDLFSK------------------------------SD
Q1KS96_ARATH_202285/1-84  -----------FRCVNLDN-------------KDLFSK------------------------------SD
Q5S1W2_ARATH_199283/1-85  ----------VFRGLNLES-------------KDTFSK------------------------------SD
Q94EW4_ARATH_199283/1-85  ----------VFRGLNLES-------------KDTFSK------------------------------SD
Q9LY30_ARATH_217301/1-85  ----------VFRGLNLES-------------KDTFSK------------------------------SD
Q9FH53_ARATH_199283/1-85  ----------VFRCSNLES-------------KDLFSK------------------------------SD
Q941L3_ARATH_199283/1-85  ----------VFRCSNLES-------------KDLFSK------------------------------SD
Q6H563_ORYSA_198286/1-89  ------IMEMVFRCSDLEI-------------KDLLSK------------------------------SD
Q5S1W2_ARATH_53146/1-94   -----------FSASNLRD-------------RDVISK------------------------------SD
Q94EW4_ARATH_53146/1-94   -----------FSASNLRD-------------RDVISK------------------------------SD
Q9LY30_ARATH_71164/1-94   -----------FSASNLRD-------------RDVISK------------------------------SD
Q9FH53_ARATH_54147/1-94   -----------FSASNLRD-------------RDVLSK------------------------------SD
Q941L3_ARATH_54147/1-94   -----------FSASNLRD-------------RDVLSK------------------------------SD
Q6H563_ORYSA_58151/1-94   -----------LSASNLGD-------------QEFFTK------------------------------SN
Q1KS96_ARATH_58151/1-94   -----------LSASNLLD-------------CDITSK------------------------------SD
Q5XQC7_ARATH_58151/1-94   -----------LSASNLLD-------------CDITSK------------------------------SD
O04042_ARATH_58145/1-88   ------VNQLTLSASNLLD-------------CDITSK------------------------------SD
Q6I5P8_ORYSA_65157/1-93   -----------FSASKLRN-------------MDAFSK------------------------------SD
Q66VB0_ORYSA_606687/1-82  ------MTVALIEGT-----------------GITNSNSK------------------------ELFDM-
Q6Z7A3_ORYSA_632713/1-82  ------LTVALIEGS-----------------GVVGSGTP------------------------GLPDP-
Q6Z8U1_ORYSA_590672/1-83  ------LTVALIEGT-----------------KLAPVDAT------------------------GFSDP-
Q5Z6I4_ORYSA_558640/1-83  ------LTVALIDGT-----------------NLAATKSS------------------------GYSDP-
Q9ZVT9_ARATH_537619/1-83  ------LTVALIEGV-----------------DLAAVDPS------------------------GHCDP-
Q9FGS8_ARATH_541623/1-83  ------LTIALIKGT-----------------NLASVEAT------------------------ELFDP-
Q7XKT6_ORYSA_549630/1-82  ------LTVALLEAT-----------------SLPPVS-S------------------------GSVDP-
Q7XQ16_ORYSA_166209/1-44  ----------------------------------------------------------------------
Q9T0H5_ARATH_90154/1-65   ----------------------------------------------------------------GTSDP-
Q56W08_ARATH_430523/1-94  ------LKVKIYTGEGWDL-------------DFHHTHFD------------------------QYSPPD
Q56W08_ARATH_430523/1-94  ------LKVKIYTGEGWDL-------------DFHHTHFD------------------------QYSPPD
Q9SZN3_ARATH_392485/1-94  ------LKVKIYTGEGWDL-------------DFHHTHFD------------------------QYSPPD
Q38811_ARATH_392485/1-94  ------LKVKIYTGEGWDL-------------DFHHTHFD------------------------QYSPPD
Q39032_ARATH_432524/1-93  ------LKVKIYTGEGWNM-------------DFPLDHFD------------------------RYSPPD
O49970_ARATH_432524/1-93  ------LKVKIYTGEGWNM-------------DFPLDHFD------------------------RYSPPD
Q2V2X4_ARATH_362454/1-93  ------LKVKVCMGDGWLL-------------DFKKTHFD------------------------SYSPPD
Q940R9_ARATH_464556/1-93  ------LKVKVCMGDGWLL-------------DFKKTHFD------------------------SYSPPD
Q944C1_ARATH_470562/1-93  ------LKVKVCMGDGWLL-------------DFKKTHFD------------------------SYSPPD
Q75IL8_ORYSA_471563/1-93  ------LKVTVYMGDGWRF-------------DFRKTHFD------------------------KCSPPD
Q39033_ARATH_454546/1-93  ------LRVTVYMGEGWYF-------------DFRHTHFD------------------------QYSPPD
Q8LG47_ARATH_57149/1-93   ------LRVTVYMGEGWYF-------------DFRHTHFD------------------------QYSPPD
Q56XL3_ARATH_136228/1-93  ------LRVTVYMGEGWYF-------------DFRHTHFD------------------------QYSPPD
Q9XEK4_BRANA_454546/1-93  ------LRVTIYMGEGWYF-------------DFRHTHFD------------------------QYSPPD
Q9LY51_ARATH_457549/1-93  ------LRVTIYMGEGWYY-------------DFPHTHFD------------------------RYSPPD
Q43443_SOYBN_471563/1-93  ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QYSPPD
Q43439_SOYBN_471563/1-93  ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QYSPPD
Q6SA76_9FABA_36128/1-93   ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QYSPPD
Q2PEW5_TRIPR_476568/1-93  ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QFSPPD
Q93YX8_MEDTR_466558/1-93  ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QFSPPD
O24297_PEA_467559/1-93    ------LKVTVYMGEGWYY-------------DFKHTHFD------------------------QFSPPD
Q8LLW1_PEA_467559/1-93    ------LKVTVYMGEGWYY-------------DFDHTHFD------------------------QFSPPD
Q43444_SOYBN_424516/1-93  ------LKVTIYMGEGWFL-------------DFKHTHFD------------------------KFSPPD
```

FIG. 3P

```
C2                                C3
80        90        100       110        120       130       140       150
PYVKLKMSD--------DKLPSKKTTVKR---SNLN------PEWNE----DFKFVVTDPETQ---------ALEINV
PYAILRLGDQ------VIRSKRNSQTTVIG---APGQ------PIWNQ----DFQFLVSNPREQ---------VLQIEV
PYAILRLGDQ------VIRSKRNSQTTVIG---APGQ------PIWNQ----DFQFLVSNPREQ---------VLQIEV
PYVILRIGDQ------VIRSKKNSQTTVIG---APGQ------PIWNQ----DFQFLVSNPREQ---------VLQIEV
PYVILSLGDQ------TIRSKKNSQTTVI-------------------------------------------------
PYVVMILGDQ------EIKSKKNSQTTVIG---QPGE------PIWNQ----DFHMLVANPRKQ---------KLCIQV
PFLRISRVVE------TSAAVPICRTEVVD---NNLN------PMWRP----VCLTMQQFGSKDT--------PLVIEC
PFLRISRVVE------TSAAVPICRTEVVD---NNLN------PMWRP----VCLTMQQFGSKDT--------PLVIEC
PFLRISRVVE------TSAAVPICRTEVVD---NNLN------PMWRP----VCLTMQQFGSKDT--------PLVIEC
PFLVISKIVE------HGTPIPVSKTEVLK---NDPN------PLWKP----VSLSVQQVGSKDS--------PLVIEC
PFLVISKIVE------HGTPIPVSKTEVLK---NDPN------PLWKP----VSLSVQQVGSKDS--------PLVIEC
PFLVISKIVE------HGTPIPVSKTEVLK---NDPN------PLWKP----VSLSVQQVGSKDS--------PLVIEC
PFLVVSKIVE------HGTPIPVSKTEVRK---NDLN------PIWKP----VFLSVQQVGSKDS--------PVIIEC
PFLVVSKIVE------HGTPIPVSKTEVRK---NDLN------PIWKP----VFLSVQQVGSKDS--------PVIIEC
PFLLISRISE------SGVPVPICKTEVRK---NDLN------PKWKP----VILNLQQIGSKEN--------PLIIEC
AMVVVYTKGR------DGTLAELFRSEVVL---NSLN------PKWIK----NFTIGYQFEIVQ---------TLLFRV
AMVVVYTKGR------DGTLAELFRSEVVL---NSLN------PKWIK----NFTIGYQFEIVQ---------TLLFRV
AMVVVYTKGR------DGTLAELFRSEVVL---NSLN------PKWIK----NFTIGYQFEIVQ---------TLLFRV
PMVVVYQKEK------DATLSEVFRSEVVL---NSLA------PKWIK----KFIVAYHFETVQ---------TLVFRV
PMVVVYQKEK------DATLSEVFRSEVVL---NSLA------PKWIK----KFIVAYHFETVQ---------TLVFRV
PMVIVYSKSK------EGALEELGRTEVIL---NSLN------PSWNA----RINVHYQFEVLQ---------PIVFQV
PMAVMYLRKK------DGRLEEIGRTEVIL---NNLN------PKWIE----KITVSFQFEAVQ---------TLVFHV
PMAVMYLRKK------DGRLEEIGRTEVIL---NNLN------PKWIE----KITVSFQFEAVQ---------TLVFHV
PMAVMYLRKK------DGRLEEIGRTEVIL---NNLN------PKWIE----KITVSFQFEAVQ---------TLVFHV
PMLVIYIR-K------DARLEEIGRTEVIL---NSLE------PSWIT----KATISYQFEIIQ---------PLVFKI
-YAVFTCNA-------KRKTSSVKFQTSE--------------PKWNE----IYEFDAMDDPPSR---------MDVAI
-YVVFTCNG-------KRKTSSVKFQTSE--------------PKWNE----IFEFNAMDDPPSR---------LEVVV
-YVVFTCNG-------KSKTSSIKFQTLE--------------PQWND----IFEFDAMDDPPSV---------MNVHV
-YVVFTCNG-------KTKTSSIKFHTLE--------------PRWNE----IFEFDAMEDPPSV---------MKINV
-YIVFTSNG-------KTRTSSIKFQKSN--------------PQWNE----IFEFDAMADPPSV---------LNVEV
-YVVFTCNG-------KTRTSSVKLQAQD--------------PQWNE----VIEFDAMEEPPSV---------LDVEV
-YVVFSCNG-------ITRTSSVQLQTHD--------------PQWNE----IMEFDAMEEPPAT---------LDVEV
------------------------RRTKE--------------PTWNE----EFTFNISLSRENL---------LQVAA
-YVVMDLDG-------QVAKSKTKWGTKE--------------PKWNE----DFVFNIKLPPAKK---------IEIAA
FFVKIGIAG-------VPRDTVSYRTETAV---DQWF------PIWGND---EFLFQLSVPELAL---------LWFKV
FFVKIGIAG-------VPRDTVSYRTETAV---DQWF------PIWGND---EFLFQLSVPELAL---------LWFKV
FFVKIGIAG-------VPRDTVSYRTETAV---DQWF------PIWGND---EFLFQLSVPELAL---------LWFKV
FFVKIGIAG-------VPRDTVSYRTETAV---DQWF------PIWGND---EFLFQLSVPELAL---------LWFKV
FYAKVGIAG-------VPLDTASYRTEIDK---DEWF------PIWDK----EFEFPLRVPELSL---------LCITV
FYAKVGIAG-------VPLDTASYRTEIDK---DEWF------PIWDK----EFEFPLRVPELSL---------LCITV
FFVRVGIAG-------APVDEVMEKTKIEY---DTWT------PIWNK----EFTFPLAVPELAL---------LRVEV
FFVRVGIAG-------APVDEVMEKTKIEY---DTWT------PIWNK----EFTFPLAVPELAL---------LRVEV
FFVRVGIAG-------APVDEVMEKTKIEY---DTWT------PIWNK----EFTFPLAVPELAL---------LRVEV
FYARVGIAG-------VEADTRMEQTKVKM---DTWI------PAWDH----EFEFPLSVPELAL---------LRVEV
FYTRVGIAG-------VPGDTVMKKTKTLE---DNWI------PAWDE----VFEFPLTVPELAL---------LRLEV
FYTRVGIAG-------VPGDTVMKKTKTLE---DNWI------PAWDE----VFEFPLTVPELAL---------LRLEV
FYTRVGIAG-------VPGDTVMKKTKTLE---DNWI------PAWDE----VFEFPLTVPELAL---------LRLEV
FYTRVGIAG-------VPADTVMKKTKTLE---DNWV------PSWDE----VFEFPLTVPELAL---------LRLEV
FYTRVGIAG-------VPADTVMKKTKTLE---DNWI------PAWDE----VFEFPLTVPELAL---------LRIEV
FYTRVGIAG-------VPNDTIMKRTKAIE---DNWL------PTWNE----AFEFPLTVPELAL---------LRIEV
FYTRVGIAG-------VPNDTIMKRTKAIE---DNWL------PTWNE----VFEFPLTVPELAL---------LRIEV
FYTRVGIAG-------VPSDTVMKKTKANK---DNWL------PTWNE----TFEFPLSVPELAL---------LRIEV
FYARIGIAG-------VPFDTVMKKTKSIE---DSWL------PSWNE----VFEFPLSVPELAL---------LRIEV
FYARVGIAG-------VPFDTVMKKTKSIE---DSWL------PSWNE----VFEFPLSVPELAL---------LRIEV
FYARVGIAG-------VPFDTIMKKTKTVE---DSWL------PSWNE----VFEFPLSVPELAL---------LRIEV
FYARVGIAG-------VPFDTIMKKTKTVE---DSWL------PSWNE----VFEFPLSVPELAL---------LRIEV
FYARVGIAG-------VPNDTVMKKTEKVE---DNWS------PSWNQ----VFKFPLAVPELAL---------LRVEV
```

FIG. 3Q

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```
                                   |<----------------------------- C4 ----------------------------->|
          160       170       180       190       200       210       220       230       240
           |         |         |         |         |         |         |         |         |
FDW----EQVG-------------------KHEKMGMNN----------------------------------------------------------------
NDR----LGFA-------------------DM-AIGTGE----------------------------------------------------------------
NDR----LGFA-------------------DM-AIGTGE----------------------------------------------------------------
NDC----LGFA-------------------DM-AIGIGE----------------------------------------------------------------
-------------------------------------------------------------------------------------------------------
KDS----VGLT-------------------DV-TIGTGE----------------------------------------------------------------
LDF----NTS-------------------GNHELIGKTE----------------------------------------------------------------
LDF----NTS-------------------GNHELIGKTE----------------------------------------------------------------
LDF----NTS-------------------GNHELMKDRE----------------------------------------------------------------
LDF----NGN-------------------GNHDLIGKVQ----------------------------------------------------------------
LDF----NGN-------------------GNHDLIGKVQ----------------------------------------------------------------
LDF----NGN-------------------GNHDLIGKVQ----------------------------------------------------------------
SDF----NSN-------------------GKHSLIGKVQ----------------------------------------------------------------
SDF----NSN-------------------GKHSLIGKVQ----------------------------------------------------------------
FNF----SSN-------------------GKHDLIGKIV----------------------------------------------------------------
YDI----DTQFQNSK--------EELLKLDEQQFLGEAT----------------------------------------------------------------
YDI----DTQFQNSK--------EELLKLDEQQFLGEAT----------------------------------------------------------------
YDI----DTQFQNSK--------EELLKLDEQQFLGEAT----------------------------------------------------------------
YDV----DTKFQNSR--------EEMLKLDEQQFLGEAT----------------------------------------------------------------
YDV----DTKFQNSR--------EEMLKLDEQQFLGEAT----------------------------------------------------------------
YDI----DPQFHDVN--------EKMLKLEEQQFLGEAV----------------------------------------------------------------
YDV----DTRYHNVP--------VKTLKLKDQDFLGEGT----------------------------------------------------------------
YDV----DTRYHNVP--------VKTLKLKDQDFLGEGT----------------------------------------------------------------
YDV----DTRYHNVP--------VKVIF-------
YDI----DTRYHNTP--------VKTLNLAQQDFLGEAC----------------------------------------------------------------
HDANG----------------------PFDQSP-IGHAE----------------------------------------------------------------
HDSEG----------------------PHNKIP-IGQTE----------------------------------------------------------------
YDFDG----------------------PFDEVTSLGHAE----------------------------------------------------------------
YDFDG----------------------PFDEVESLGHAE----------------------------------------------------------------
FDFDG----------------------PFDEAVSLGHAE----------------------------------------------------------------
FDFDG----------------------PFDQGASLGHAE----------------------------------------------------------------
FNFDG----------------------PFDLAVSLGHAE----------------------------------------------------------------
WDAN-----------------------LVTPHKRMGNAG----------------------------------------------------------------
WDAN-----------------------LVTPHKRMGNSE----------------------------------------------------------------
QDYD------------------------NDTQNDFAGQTC---------------------------------------------------------------
QDYD------------------------NDTQNDFAGQTC---------------------------------------------------------------
QDYD------------------------NDTQNDFAGQTC---------------------------------------------------------------
QDYD------------------------NDTQNDFAGQTC---------------------------------------------------------------
KDYD------------------------SNTQNDFAGQTC---------------------------------------------------------------
KDYD------------------------SNTQNDFAGQTC---------------------------------------------------------------
HEHD------------------------VNEKDDFGGQTC---------------------------------------------------------------
HEHD------------------------VNEKDDFGGQTC---------------------------------------------------------------
HEHD------------------------VNEKDDFGGQTC---------------------------------------------------------------
HESD------------------------NHQKODFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQIC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQAC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
```

FIG. 3R

```
                                      C1
                                   |<------->|
                                            10        20        30        40        50        60        70
                                             |         |         |         |         |         |         |
Q6TM10_9FABA_464556/1-93        ------LKVTIYMGEGWFH-------------DFKHTHFD------------------------QYSPPD
Q9M5Q5_TOBAC_459551/1-93        ------LKVTVFMGEGWYI-------------DFKHTHFD------------------------AYTPPD
Q9M5Q2_TOBAC_461553/1-93        ------LKVTVFMGEGWYY-------------DFNHTHFD------------------------AYAPPD
O49952_SOLTU_458550/1-93        ------LKVTVFMGEGWYY-------------DFEHTHFD------------------------AYSPPD
O49950_SOLTU_468560/1-93        ------LKVKVYMGKGWHL-------------DFKRTHFD------------------------AYSPPD
Q2QNK2_ORYSA_463555/1-93        ------LKVKVYMGDGWRM-------------DFSKTHFD------------------------TFSPPD
Q8RW31_ORYSA_153245/1-93        ------LKVKVYMGDGWRM-------------DFSKTHFD------------------------TFSPPD
Q6QJ78_MAIZE_459551/1-93        ------LKVKVYMGDRWRM-------------DFSKTHFD------------------------AFSPPD
Q6Z3Y9_ORYSA_471563/1-93        ------LKVKVYMGDGWRM-------------DFTQTHFD------------------------QYSPPD
Q9AXF1_ORYSA_472564/1-93        ------LKVKVYMGDGWRM-------------DFTQTHFD------------------------QYSPPD
Q2YGU1_9LILI_406498/1-93        ------LKVKVYMGDGWRM-------------DFKSTHFD------------------------TYSPPD
Q2YGU0_9LILI_420512/1-93        ------LKVKVYMGDGWRM-------------DFKQTYFD------------------------AYSPPD
O49902_NICRU_461553/1-93        ------LKVKVYMGDGWHL-------------DFKQTHFD------------------------LYSPPD
P93341_NICRU_461553/1-93        ------LKVKVYMGDGWHL-------------DFKQTHFD------------------------LYSPPD
Q5GA62_LYCES_449539/1-91        ------LQVRVYMGDGWRL-------------DFSHTHFD------------------------AYSPPD
Q8GV43_ARATH_417509/1-93        ------LKVKVYMGDGWRM-------------DFSHTHFD------------------------AYSPPD
Q9FSW1_9POAL_504595/1-92        ------LKVKVYMGEGWHK-------------DFKQTHFD------------------------TYSPPD
O49951_SOLTU_438530/1-93        ------LKVTVYMGDGWDK-------------DFDQTHFD------------------------TYSPPD
Q5GA63_LYCES_456548/1-93        ------LKVTVYMGDGWOK-------------DFDQTDFD------------------------TYSPPD
P93620_VIGUN_422514/1-93        ------LKVKVYLGKGWSL-------------DFSPSDFD------------------------SYSPPD
Q6TM09_9FABA_321413/1-93        ------LKVKVYLGKGWSL-------------DFSPSDFD------------------------SYSPPD
Q43442_SOYBN_426518/1-93        ------LKVKVYMGNGWSS-------------DFSKTHFD------------------------SFSPPD
Q1SDI4_MEDTR_462553/1-92        ------LKVKVYKGVGWRS-------------DFSPTHFD------------------------RFSPPD
Q1SDG3_MEDTR_461552/1-92        ------LKVKVYKGVGWSS-------------DFSPTHFD------------------------RFSPPD
Q944C2_ARATH_451543/1-93        ------LKVKVYMGKGWDS-------------GFQRTCFN------------------------TWSSPN
Q9LUZ0_ARATH_451543/1-93        ------LKVKVYMGKGWDS-------------GFQRTCFN------------------------TWSSPN
Q766D4_PHYPA_521593/1-73        ---------------------------------------D------------------------LFSPPD
Q6NMA7_ARATH_405496/1-92        ------LKVKIYMGDGWIV-------------DFKKR-IG------------------------RLSKPD
Q9SD51_ARATH_387478/1-92        ------LKVKIYMGDGWIV-------------DFKKR-IG------------------------RLSKPD
Q42582_ARATH_405496/1-92        ------LKVKIYMGDGWIV-------------DFKKR-IG------------------------RLSKPD
Q9STZ3_ARATH_405496/1-92        ------LKVKIYMGDGWIV-------------DFKKR-IG------------------------RLSKPD
Q762E2_PHYPA_515603/1-89        ------LKVTVLLGTDWHK-------------N-----YD------------------------VFKKPG
Q8RUY6_ARATH_271/1-70           --------------------------------------KQ------------------------SVGNPS
Q6NPD6_ARATH_191271/1-81        ------LVVTIKRGN---------------------NMKQ------------------------SVGNPS
Q700A9_CICAR_120200/1-81        ------LVVIIKRGN---------------------NMKQ------------------------SVGNPS
Q1SJ53_MEDTR_20862166/1-81      ------LVVIVKRGN---------------------NMRQ------------------------SVGIPS
Q67UI5_ORYSA_864944/1-81        ------LTVTIKRGN---------------------NLRQ------------------------SVGNPS
Q9CAQ9_ARATH_19842064/1-81      ------LTVNVMRAN---------------------NLKQ------------------------SMATTN
Q8GXS1_ARATH_308388/1-81        ------LTVNVMRAN---------------------NLKQ------------------------SMATTN
Q2R9P0_ORYSA_20022082/1-81      ------LTVTILRGN---------------------NLKQ------------------------TMGSTN
Q9C6Y4_ARATH_19952071/1-77      ------LTVAIKRGD---------------------NLKR------------------------S----N
Q5HZ03_ARATH_53140/1-88         ------LEVYVHQARDIHNIC----------IYHKQDV--------------------------------
Q9FJ58_ARATH_87174/1-88         ------LEVYVHQARDIHNIC----------IYHKQDV--------------------------------
Q84W25_ARATH_53140/1-88         ------LEVYVHQARDIHNIC----------IYHKQDV--------------------------------
Q9LPS7_ARATH_41128/1-88         ------LEVFVHQARDIHNIC----------IYHKQDV--------------------------------
Q9C6Q0_ARATH_328415/1-88        ------LEVFVHQARDIHNIC----------IYHKQDV--------------------------------
Q8LAD1_ARATH_41128/1-88         ------LEVFVHQARDIHNIC----------IYHKQDV--------------------------------
Q8H7W2_ORYSA_41128/1-88         ------LDVFVHQARDIHNIC----------IYHKQDV--------------------------------
Q1SS74_MEDTR_58145/1-88         ------VDVYIHQARDIHKIC----------IYHKQDV--------------------------------
Q8H5M0_ORYSA_29118/1-90         ------VDVHVQSARDIQNIC----------IYHKQDV--------------------------------
Q94CL2_ARATH_23113/1-91         ------LQVYVHNARNINNIC----------IYDNQOV--------------------------------
Q941Z2_ORYSA_27120/1-94         ------LDIYVHGARGIHNIC----------IYAAQDV--------------------------------
O80843_ARATH_1094/1-85          ------LEIEVISAEGLKVDR------------KPLKKK-------------------------------
Q58FX0_ARATH_1094/1-85          ------LEIEVISAEGLKVDR------------KPLKKK-------------------------------
Q84N41_ARATH_1094/1-85          ------LEIEVISAEGLKVDR------------KPLKKK-------------------------------
Q941L2_ARATH_20101/1-82         ------LEIDLRSAEGLKLNR------------RPIKKK-------------------------------
```

FIG. 3S

```
|<------ C2 ------->|                          |<------------ C3 ------------->|
         80        90        100       110        120       130       140       150
          |         |          |         |          |         |         |         |
FYARVGIAG-------VPYDTVMKKTKSVE---DNWS------PSWNE----EFKFPLSVPELAL---------LRVEV
FYAKIGIAG-------VPADNVMKKTKTLE---DMDT------PTWDE----KFEFPLTVPELAL---------LRVEV
FYAKIGIAG-------VPADNVMKKTRTLE---NNWI------PTWDE----KFEFPLTVPELAL---------LRVEV
FYARIGIAG-------VDADIVMKKTKTLE---DNWI------PTWDE----QFEFPLTVPELAL---------LRVEV
FYVKIGIAG-------VAADSRVKKTKAIE---DNWI------PIWND----EFEFPLTVPELAL---------LRVEV
FYTRVGIAG-------VRADCVMKKTRTIE---DQWV------PMWDE----EFTFPLTVPELAV---------LRIEV
FYTRVGIAG-------VRADCVMKKTRTIE---DQWV------PMWDE----EFTFPLTVPELAV---------LRIEV
FYTKVGIAG-------VKADSVMKKTRVIE---DQWV------PMWDE----EFTFLLTVPELAL---------LRVEV
FYARVGIAG-------VPADSVMKRTRAIE---DNWV------PVWEE----DFTFKLTVPEIAL---------LRVEV
FYARVGIAG-------VPADSVMKRTRAIE---DNWV------PVWEE----DFTFKLTVPEIAL---------LRVEV
FYTRVGIAG-------VPADCTMKKTRTIE---DDWT------PVWDE----ELVFPLTVPELAL---------LRIEV
FYTRIGIAG-------VPADXVMKRTKAIE---DDWT------PVWNE----EFVFPLTVPEIAL---------LRIEV
FYTRVGIAG-------VPADEIMKKTKTKE---DKWT------PVWDE----AFTFPLTVPELAL---------LRIEV
FYTRVGIAG-------VPADEIMKKTKTKE---DKWT------PVWDE----EFTFPLTVPELAL---------LRIEV
FYTK--VIG-------VPADSRKKKTRILE---DDWC------PVWDE----EFNFPLTVPELAL---------LRIEV
FYTKMFIVG-------VPADNAKKKTKIIE---DNWY------PIWDE----EFSFPLTVPELAL---------LRIEV
FYVEVGIAG-------VPLDSVMRKTKAVE---DNWV------PVWEE----EFAFPLTVPEIAV---------LRVEV
FYAKLGIAG-------VPADEVKKRTKTMD---DNWI------PSWDE----QFEFPLTVPELAL---------LRIKV
FYAKLGIAG-------VPADEVKKRTETID---DNWI------PSWNE----QFEFPLTVPELAL---------LRIKV
FYVKVCIVG-------VPADMIKKKTSVIS---NNWF------PVWNE----EFDFPLTVPELAL---------LGIEV
FYVKVCIVG-------VPADMIKKKTSVIS---NNWF------PVWNE----EFDFPLTVPELAL---------LRIEV
FYTKVCIVG-------VPADKANKKTKVIQ---DNWF------PVWDE----EFEFPLTVPELAL---------LRIEV
FYTKVCIAG-------VGADSVKMKTSVKM---DNWY------PVWDE----EFEFQLTVPELAL---------LRIEV
FYTKVSIAG-------VRADCAKKKTSVKM---DNWN------PIWDE----EFEFRLTVPELAL---------LRIEV
FYTRVGITG-------VRGDKVMKKTKKEQ---KTWE------PFWNE----EFEFQLTVPELAL---------LRIEV
FYTRVGITG-------VRGDKVMKKTKKEQ---KTWE------PFWNE----EFEFQLTVPELAL---------LRIEV
FFTRLLVTG-------VPADVAKWKTSVID---DVWE------PHWNE----DHEFYLKCPELAL---------LRIEV
LYVRISIAG-------VPHDEKIMNTTVKN---NEWK------PTWGE----EFTFPLTYPDLAL---------ISFEV
LYVRISIAG-------VPHDEKIMNTTVKN---NEWK------PTWGE----EFTFPLTYPDLAL---------ISFEV
LYVRISIAG-------VPHDENIMKTTVKN---NEWT------PTWGE----EFTFPLTYPDLAL---------ISFEV
LYVRISIAG-------VPHDENIMKTTVKN---NEWT------PTWGE----EFTFPLTYPDLAL---------ISFEV
YFVKVAIHG-------MHDDEQKFKTHVCK---RSRE------PHWEVE---EFVFQIRVPKLAI---------LRLEV
VFCKITLGN-------NPP----RQTKVIS---TGPN------PEWDE----SFSWSFESPPKGQK--------LHISC
VFCKITLGN-------NPP----RQTKVIS---TGPN------PEWDE----SFSWSFESPPKGQK--------LHISC
VYCKITLGN-------NPP----RLTKVVS---TGPN------PEWDE----SFSWSFESPPKGQK--------LHISC
VYCKITLGN-------SPP----KLTKVVS---TGPN------PEWEE----SFTWSFESPPKGQK--------LHISC
AFCKLTLGN-------NPP----RLTKIVS---TGAT------PEWDE----AFAWAFDSPPKGQK--------LHISC
AFCQLTIGN-------CPP----RQTKVVS---NSTT------PEWKE----GFTWAFDVPPKGQK--------LHIIC
AFCQLTIGN-------CPP----RQTKVVS---NSTT------PEWKE----GFTWAFDVPPKGQK--------LHIIC
AFCCLQIGN-------GPP----RQTKVVN---NSIC------PVWNE----GFTWLFDIPPKGQK--------LYILC
AFCRLIIDN-------CPT----KKTKVVK---RSSS------PVWKE----SFTWDFAAPPRGQF--------LEIVC
-YAKLCLTSD------P-DKS--VSTKIING--GGRN------PVFDDNV-K-LDVRV---LDTSLKC----EIYMMSR
-YAKLCLTSD------P-DKS--VSTKIING--GGRN------PVFDDNV-K-LDVRV---LDTSLKC----EIYMMSR
-YAKLCLTSD------P-DKS--VSTKIING--GGRN------PVFDDNV-K-LDVRV---LDTSLKC----EIYMMSR
-YAKLCLTND------P-ENS--LSTKIING--GGQN------PVFDDTL-Q-FDVKN---LDCSLKC----EIFMMSR
-YAKLCLTND------P-ENS--LSTKIING--GGQN------PVFDDTL-Q-FDVKN---LDCSLKC----EIFMMSR
-YAKLCLTND------P-ENS--LSTKIING--GGQN------PVFDDTL-Q-FDVKN---LDCSLKC----EIFMMSR
-YAKLCLTSD------P-DVS--CSTKVING--GGRN------PVFDDGL-R-LDVRT---VDASLKC----EIWMLSR
-YAKISLTSD------P-ENS--VNTKIING--GGRN------PVFNDNL-R-LSVRT---VDSSLKC----EIWMLSR
-YARLSLPGE------G-APA--ASTQVING--GGRN------PVFDQSL-R-LGVRAG-DVDGALRC----EVWMLSR
-YAKFSLTYN------P-DDT--ISTRIIHR--AGKN------PEFNQKL-M-IDVTQIDAHAAVLKC----EIWMMSR
-YARLALTSS------P-DDAPALDTRVAAG--GGAN------PRFDERL-PPLRVRRARLGTDVLKC----EIWMRSC
TYSVVRIDEK------------SWASKVDEL--GGSY------PIWKD----RFDMEMPI----NASV----RFISIEV
TYSVVRIDEK------------SWASKVDEL--GGSY------PIWKD----RFDMEMPI----NASV----RFISIEV
TYSVXRIDEK------------SWASKVDEL--GGSY------PIWKD----RFDMEMPI----NASV----RFISIEV
TFAVVKIDEK------------CRKSNLDES--RRSN------PTWN------YKSEMPI----NGNE----QFIFIEV
```

FIG. 3T

C4

```
            160        170        180        190        200        210        220        230        240
             |          |          |          |          |          |          |          |          |
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFAGQTC---------------------------------------------------------------
HVYD------------------------MSEKDDFAGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFAGQTC---------------------------------------------------------------
HEYD------------------------MSEIDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKHDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKHDFGGQTC---------------------------------------------------------------
QEYD------------------------MSEKHDFGGQTV---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTV---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTV---------------------------------------------------------------
HEYD------------------------MSDKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFAGQTC---------------------------------------------------------------
HEYD------------------------MSEKDDFAGQTC---------------------------------------------------------------
REYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
REYD------------------------MSEKDDFGGQTC---------------------------------------------------------------
HEQD------------------------VSE-DDFGGQTA---------------------------------------------------------------
LDYN------------------------LSDKDEFAGQTC---------------------------------------------------------------
LDYN------------------------LSDKDEFAGQTC---------------------------------------------------------------
REDD------------------------KHQKDDFGGQTC---------------------------------------------------------------
REED------------------------KHQKDDFGGQTC---------------------------------------------------------------
REYD------------------------KHEKDDFGGQTC---------------------------------------------------------------
KDKD------------------------KG-SDDFAGQTC---------------------------------------------------------------
KDKD------------------------QT-KDDFAGQTC---------------------------------------------------------------
HDYN------------------------MPEKDDFSGQTC---------------------------------------------------------------
HDYN------------------------MPEKDDFSGQTC---------------------------------------------------------------
RDHD------------------------EGSQDEFEGQAC---------------------------------------------------------------
YDYE------------------------VSTPDYFCGQTC---------------------------------------------------------------
YDYE------------------------VSTPDYFCGQTC---------------------------------------------------------------
YDYE------------------------VSTADAFCGQTC---------------------------------------------------------------
YDYE------------------------VSTADAFCGQTC---------------------------------------------------------------
REYD------------------------RIVRDDMVGQSC---------------------------------------------------------------
KNKS------------------------KMGKSSFGKVT----------------------------------------------------------------
KNKS------------------------KMGKSSFGKVT----------------------------------------------------------------
KNKS------------------------KVGKSKFGKVT----------------------------------------------------------------
KNKS------------------------KVGKSKFGKVT----------------------------------------------------------------
KNNS------------------------KFGKKSFGKVT----------------------------------------------------------------
KSKS------------------------TFGKTTLGRVT----------------------------------------------------------------
KSKS------------------------TFGKTTLGRVT----------------------------------------------------------------
KSKN------------------------TFGKSTLGRVT----------------------------------------------------------------
KSNN------------------------IFRNKNLGKVR----------------------------------------------------------------
VKN------------------------YLEDQL-LGFTL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFTL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFTL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFSL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFSL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFSL----------------------------------------------------------------
VRN------------------------YLEDQL-LGFAL----------------------------------------------------------------
VKN------------------------YLEDQL-LGFAL----------------------------------------------------------------
VKN------------------------YLQDQL-LGFAL----------------------------------------------------------------
ARH------------------------YMEDQL-LGFAL----------------------------------------------------------------
ARR------------------------LLDDQL-LGFAL----------------------------------------------------------------
YYRTS---------------------GSGRDKN-VGYAK----------------------------------------------------------------
YYRTS---------------------GSGRDKN-VGYAK----------------------------------------------------------------
YYRTS---------------------GSGRDKN-VGYAK----------------------------------------------------------------
FYRT----------------------GSGHDKK-IGEAK----------------------------------------------------------------
```

FIG. 3U

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```
                                C1
                           |<-------->|
                                10         20         30         40         50         60         70
                                 |          |          |          |          |          |          |
Q8LBT3_ARATH_586/1-82      ------LEIDLRSAEGLKLNR-----------RPIKKK-----------------------------
Q9M2E5_ARATH_687/1-82      ------LEIDLRSAEGLKLNR-----------RPIKKK-----------------------------
Q8SA25_ORYSA_21115/1-95    ------LEVTLISAQGLKPPSG---------LRRRLLQA----------------------------
Q6K8N6_ORYSA_30117/1-88    ------LEVTVISAQDLHR--R---------LGRRVRAA----------------------------
O22783_ARATH_1094/1-85     ------LELNIISAQDLAPVS-----------RKMKT------------------------------
O23030_ARATH_892/1-85      ------LELNIISAQDLAPVA-----------RKTKT------------------------------
Q9SI42_ARATH_1094/1-85     ------LELNIISAQELAPVA-----------RCMKT------------------------------
Q1SSZ2_MEDTR_1195/1-85     ------LELNVISAQDLAEVG-----------RSMRT------------------------------
Q9M8Z2_ARATH_1197/1-87     ------LEINLISAQDLAPVS-----------RNMKT------------------------------
Q8L8S6_ARATH_1197/1-87     ------LEINLISAQDLAPVS-----------RNMKT------------------------------
Q9M148_ARATH_794/1-88      ------LEINLISAQGLKEPTG---------KLRRLQT-----------------------------
Q8W0F9_ORYSA_50140/1-91    ------LEVTVVSGKHLKNVNW---------RRGDLRA-----------------------------
Q9LNV0_ARATH_995/1-87      ------LVVTVVSAKHLKNVNW---------RNGDLKP-----------------------------
Q6ZBX9_ORYSA_795/1-89      ------VEVTVSSARDLKNVNW---------RNGDLKP-----------------------------
Q651B1_ORYSA_896/1-89      ------VEVTVASARDLKNVNW---------RNGDLKP-----------------------------
Q5DVL6_HORVD_795/1-89      ------VEVTVGAARDLKNVNW---------RNGDLKP-----------------------------
Q5PNU6_ARATH_895/1-88      ------VEVTISSAKDIKNVNW---------RNGPNKP-----------------------------
Q9FF85_ARATH_24111/1-88    ------VEVTISSAKDIKNVNW---------RNGPNKP-----------------------------
Q60EX0_ORYSA_899/1-92      ------LELTLLSASDLRGVN----------LVSKMEV-----------------------------
Q942Z3_ORYSA_691/1-86      ------LELTLISAKDLKDVN----------LLSKMEV-----------------------------
Q8GRM0_ORYSA_691/1-86      ------LEVTLISARNLKKVN----------LITPMEV-----------------------------
Q8GS52_ORYSA_693/1-88      ------LEVTLHSARDLKNVN----------FISRMEV-----------------------------
Q94172_ORYSA_48138/1-91    ------LELTLVSASDLKKVT----------LFSRMHV-----------------------------
Q93W71_ORYSA_696/1-91      ------LELTLVSASDLKKVT----------LFSRMHV-----------------------------
Q65XE8_ORYSA_696/1-91      ------LEVTLVSAKNLKKVT----------MFSKMRV-----------------------------
Q9LK74_ARATH_697/1-92      ------LELNVYSAKDLENVN----------LITKMDV-----------------------------
O23425_ARATH_41134/1-94    ------LELKIVSASDVNHID----------ATDKMDV-----------------------------
O23427_ARATH_388479/1-92   ------LELNINSARNLLNVN----------LITKMNV-----------------------------
O04133_SOYBN_898/1-91      ------LELNIISAKDIKNVN----------LFSKMDV-----------------------------
O23425_ARATH_232323/1-92   ------LELVIKFAKNIEDVN----------AFSSMDV-----------------------------
O04023_ARATH_695/1-90      ------LDLTIISAEDLKDVQ----------LIGKQDL-----------------------------
O81814_ARATH_695/1-90      ------LDLTIISAEDLKDVQ----------LIGKQDL-----------------------------
Q69P64_ORYSA_15113/1-99    ------LELTVYEADDLHN------AIHGRIIKAAES----LKESLG---------------VHRLAHR
Q8SAG6_ORYSA_15113/1-99    ------LELTVYEADDLHN------AIHGRIIKAAES----LKESLG---------------VHRLAHR
Q1RZP8_MEDTR_84121/1-38    -------------------------------------------------------------------
Q1RZP4_MEDTR_59118/1-60    -------------------------------------------------------------------
PLDA1_PIMBR_10109/1-100    ------LHVTIFEVDHLK-----AGSVVVFSESLRRT----LRKPLV---------------LAKGTPK
Q1T525_MEDTR_10109/1-100   ------LHATIFEVDKLK-----NIGGGNILSKIRQN----FEETVG---------------FGKGTTK
Q2HUA3_MEDTR_10109/1-100   ------LHATIFEVDKLK-----NIGGGNILSKIRQN----FEETVG---------------FGKGTTK
PLDA1_VIGUN_10109/1-100    ------LHATIYEVDELH-----GGGGGNFFSKLKQN----IEETVG---------------IGKGVTK
Q2Q0A8_CUCME_10109/1-100   ------LHATIYEIDRLH-----TGGSSNVFSMLRQN----FEEAVG---------------IGKGQTK
Q9XFX8_CRAPL_10109/1-100   ------LHVTIYEVDQLH-----SGGGGNFFTKLKAN----IEETVG---------------FGKGTPK
Q9XFX7_CRAPL_10109/1-100   ------LHVTVYEVDRLH-----AGGGGNIFSKLRAN----IEEKVG---------------FGKGTPK
Q70EW5_CYNCA_10109/1-100   ------LHVTVYEVDKLR-----EGGGPNVFGKLMAN----IQETVG---------------FGEGTPK
PLDA1_RICCO_10109/1-100    ------LHVTIYEVDKLH-----SGGGPHFFRKLVEN----IEETVG---------------FGKGVSK
Q2HWT8_ARAHY_10108/1-99    ------LHVTIYEVDKLK-----TSGG-NVFTKLVQN----IEETVG---------------FGKGVTK
PLDA1_BRAOC_10110/1-101    ------LHATIYEVDDLHT----GGLRSGFFGKILAN----VEETIG---------------VGKGETQ
PLDA1_ARATH_51110/1-60     -------------------------------------------------------------------
PLDA2_BRAOC_52111/1-60     -------------------------------------------------------------------
PLDA2_ARATH_10110/1-101    ------LHATIYEVDHLHA----EGGRSGFLGSILAN----VEETIG---------------VGKGETQ
Q9AWC0_LYCES_10110/1-101   ------LHVTIFEVDNLQG----EEEGGHFFSKIKQH----FEETVG---------------IGKGTPK
Q9SDZ6_LYCES_10110/1-101   ------LHVTIFEVDNLQG----EEEGGHFFSKIKQH----FEETVG---------------IGKGTPK
PLDA1_TOBAC_10109/1-100    ------LHVTIYEVDNLQ-----KEGGGHFFSKIKEH----VEETIG---------------FGKGTPA
Q533V0_FRAAN_13111/1-99    ------LHATIYEVDKLH------GSSGNFLRKITGK----LEETVG---------------LGKGVSK
PLDA1_ORYSA_10114/1-105    ------LHATIFEAASLSNPHRASGSAPKFIRKFVEG----IEDTVG---------------VGKGATK
PLDA1_MAIZE_10114/1-105    ------LHATIFEAESLSNPHRATGGAPKFIRKLVEG----IEDTVG---------------VGKGATK
```

FIG. 3V

```
            C2                                    C3
80        90         100        110        120        130        140        150
TFAVVKIDEK-----------CRKSNLDES--RRSN-----PTWN------YKSEMPI----NGNE----QFIFIEV
TFAVVKIDEK-----------CRKSNLDES--RRSN-----PTWN------YKSEMPI----NGNE----QFIFIEV
-YAVAWVDAA----------RRLQTRPDRA--GGVD-----PEWHE---RLLFRVHEAALADDSR----AAVTVEI
-YAVAWADAA----------HKLRTGVDLA--GGAD-----PTWND---RFLFRVEEAFLRSDT-----AAVTVEV
-YAVAWVHSE----------RKLTTRVDYT--GGGN-----PTWND---KFVFRVSEDFLYADT-----SAVVVEI
-YAVAWVHSE----------RKLTTRVDYN--GGTN-----PTWND---KFVFRVNEEFLYADT-----SAVVIEI
-YAIAWIDPE----------RKLTTRVDNT--GGTS-----PTWND---KFVFRLDEEALYDAT-----SIVVIEI
-YAVAWVDPD----------RKLSTRVDSQ--SGTN-----PAWND---KFVFRVDEDFLYDEN-----STITIDI
-YSVAWINTD------P---MRKLTTRVDQS--NRAN-----PIWNE---KFVFRVNDKILYVDA-----SAIVIEI
-YSVAWINTD------P---MRKLTTRVDQS--NRAN-----PIWNE---KFVFRVNDKILDVDA-----SAIVIEI
-YASVWVDSS----------SKLRTRIDRI--GSEN-----PIWND---KFVFQVSPEFLSSET-----SGVSIEI
-YVVAYLDPS----------RRAATRPDDV--GGCK-----PAWNE---RVVLPLPPHLSPHDPS----LLLSLDV
-YVVLYLDQD----------HPLSTRSDDS--SSIK-----PVWNE---RITLPLTR--SVHES------VLNIEV
-YAVLWVDDG----------AKCSTRVDLD--NADN-----PNWDD---KLTLPLPP--SSRLDD----ALLYLDV
-YAVVWIDDG----------AKCSTRVDLD--NADN-----PTWDD---KLTVPLPP--STRLDD----AVLYLDV
-YAVLWIDAG----------ARCSTRVDLD--NGEN-----PTWDD---KVVVPLPP--ASRLQD----AVLYLDI
-YAVVWIDPK----------FKSSTRVDED--GNTC-----TTWNE---TFVIALPP--AND-DD----DKVYINI
-YAVVWIDPK----------FKSSTRVDED--GNTC-----TTWNE---TFVIALPP--AND-DD----DKVYINI
-YAVVYLAGD--------PRARQ-RVATDRA--GGRN-----PSWKGKD-ATVRLAVP---ASGAGS----GAVRVLL
-YAVVSLSGD--------RRSRQ-RIATDRA--GGRN-----PAWN--A-APLRFTVP---ASGAGS------LHVLL
-YAVVSVSGN--------PLARQ-QTLPDRH--GGRN-----PTWN---ATLHLAVP---AAAPGA-----FLHVLL
-YAVATISGD--------PLTRQ-QTPPDPY--GGRH-----PAWN---ATLRFTVPP-TAASAAG-----CLHVLL
-YAVASISGS------NVPMPMH-GTHADRN--GGSN-----PAWN---TVLHFPVP--ARFDTRG----LALHVQL
-YAVASISGS------NVPMPMH-GTHADRN--GGSN-----PAWN---TVLHFPVP--ARFDTRG----LALHVQL
-YAVASISGG------DPRVPTH-RTHADRE--GGRS-----PMWH---APLRFPIPD-AGADMRA----IALHVLL
-YAVVWITGD------DSRKNHKEKTPIDRT--GESE-----PTWN---HTVKFSVDQ-RLAHEGR----LTLVVKL
-YAVVSINGD------TTQQKQAAKTPIDYD--GGSN-----PTWN---HTVKFSVNE-REANEGL----LTITVKL
-FTAITINGE------NTRKKQKAKTTVDRY--GGSN-----PTWN---QTIKFSVDE-RSARGGH----SSLVMRV
-YAAVSLSGD-------PLHPQGATTHVHKD--AGSN-----PTWN---YPVKFSVNE-SLAKENR----LSLEIKL
-YASVAILKD------RKVKN-RINTPVAFA--AYTN-----PKWN---QMMKFSIDE-KSAQEGR----LMLLVEL
-YAVVSINGD------ARTKQ---KTKVDKD--CGTK-----PKWK---HQMKLTVDD-AAARDNR----LTLVFEI
-YAVVSINGD------ARTKQ---KTKVDKD--CGTK-----PKWK---HQMKLTVDD-AAARDNR----LTLVFEI
IYVDVDVG-----------AARVARTREVEF--HPTN-----PVWNQ----SFRLHCAYPAAP----------VAFTV
IYVDVDVG-----------AARVARTREVEF--HPTN-----PVWNQ----SFRLHCAYPAAP----------VAFTV
-------------------------------------S-----PKWNE---TFHIYSAHSISN----------IIFTV
-YATVDLD-----------KARVGRTRMIGN--QPSN-----PKWNE---TFEIYCAHYISN----------IVFTV
IYASIDLD-----------KARVGRTRMIEN--EPNN-----PKWNE---SFHIYCGHPSTN----------VIFTV
LYATIDLE-----------KARVGRTRIIEK--EHVN-----PQWNE---SFHIYCAHLASD----------IIFTV
LYATIDLE-----------KARVGRTRIIEK--EHVN-----PQWNE---SFHIYCAHLASD----------IIFTV
LYATIDLE-----------KARVGRTRIIEN--ETTN-----PKWNE---SFHIYCGHLASN----------IIFTV
LYATIDLE-----------KARVGRTRILES--EPSN-----PRWYE---SFHIYCAHKASN----------VIFTV
IYASIDLE-----------KARVGRTRMIEH--EPNN-----PRWYE---SFHIYCAHMASN----------VIFTV
IYASIDLE-----------KARVGRTRMIEH--EPTN-----PRWYE---SFHIYCAHLASN----------IIFTV
IYATIDLE-----------KSRVGRTRMIEN--EPQN-----PRWYE---SFHIYCAHHASN----------IIFTV
LYATIDLE-----------KARVGRTRILEN--EQSN-----PRWYE---SFHVYCAHQASN----------VIFTV
LYATIDLE-----------KARVGRTRIIEK--DHSN-----PRWYE---SFHIYCAHMASN----------IIFTV
LYATIDLQ-----------RARVGRTRKIKD--EAKN-----PKWYE---SFHIYCAHLASD----------IIFTV
-YATIDLQ-----------KARVGRTRKIKN--EPKN-----PKWYE---SFHIYCAHLASD----------IIFTV
-YATIDLQ-----------KARVGRTRKITD--EPKN-----PKWYE---SFHIYCAHMASD----------IIFTV
LYATIDLE-----------KARVGRTRKITK--EPKN-----PKWFE---SFHIYCGHMAKH----------VIFTV
LYATIDLE-----------KARVGRTRIIEN--EPKN-----HRWYE---SFHIYCAHMASN----------VIFTI
LYATIDLE-----------KARVGRTRIIEN--EPKN-----HRWYE---SFHIYCAHMASN----------VIFTI
IYATVDLE-----------KARVGRTRKIKN--EPNN-----PRWYE---SFHIYCAHMASN----------VIFTV
LYATVDLE-----------RARVGRTRVIEK--EPSN-----PNWSE---SFHIYCAHVAAN----------VIFTV
VYSTIDLE-----------KARVGRTRMITN--EPIN-----PRWYE---SFHIYCAHMASN----------VIFTV
IYATVDLE-----------KARVGRTRMISN--EPVN-----PRWYE---SFHIYCAHMAAD----------VIFTV
```

FIG. 3W

```
                                   C4
                                   |<--------------------------------------------------------------->|
          160       170       180       190       200       210       220       230       240
           |         |         |         |         |         |         |         |         |
FYRT----------------------GSGHDKK-IGEAK----------------------------------------------------------------
FYRT----------------------GSGHDKK-IGEAK----------------------------------------------------------------
YAAPAG------------------GWHIGGDSL-VGSAR----------------------------------------------------------------
RAP----------------------RRFGGDAV-LGVTR----------------------------------------------------------------
YAL-----------------------HWFRDVH-VGTVR----------------------------------------------------------------
YAL-----------------------HWFRDVH-VGTVR----------------------------------------------------------------
YAL-----------------------HWFKDIH-VGTVQ----------------------------------------------------------------
YAI-----------------------HWFKDIH-VGTAH----------------------------------------------------------------
YAA-----------------------AWAKDAL-VGTVN----------------------------------------------------------------
YAA-----------------------AWAKDAL-VGTVN----------------------------------------------------------------
YAV-----------------------GYLRDHL-IGTVR----------------------------------------------------------------
FHS---------------------KPSDSPKPL-VGSAR----------------------------------------------------------------
FHS---------------------NSSDLAKTL-VGSVR----------------------------------------------------------------
VHA---------------------NAAEGVKPL-VGSAR----------------------------------------------------------------
VHA---------------------NAAEGVKPL-VGSAR----------------------------------------------------------------
VHA---------------------NAPEGVKPL-VGSAR----------------------------------------------------------------
VHA---------------------GREENTKPL-IGSAH----------------------------------------------------------------
VHA---------------------GREENTKPL-IGSAH----------------------------------------------------------------
RAERA---------------------GLGGDRD-VGEVF----------------------------------------------------------------
RAERA----------------------LG-DRD-VGEVH----------------------------------------------------------------
RTERA----------------------LG-DRD-VGEVF----------------------------------------------------------------
RAERS----------------------LG-DRD-IGEVI----------------------------------------------------------------
RARRS----------------------FGGHRD-VGDVF----------------------------------------------------------------
RARRS----------------------FGGHRD-VGDVF----------------------------------------------------------------
RAERV----------------------FG-DSD-VGEVF----------------------------------------------------------------
VCDR----------------------IFGDKD--LGEVQ----------------------------------------------------------------
FSYW----------------------LEGDNDLYLGEVN----------------------------------------------------------------
ISRR----------------------VLGNKE--IGRVN----------------------------------------------------------------
ISDR----------------------TLGDTV--IGTVH----------------------------------------------------------------
MSHRP---------------------FLGDKE--IGFVR----------------------------------------------------------------
VADRP---------------------IAGDKP--VGEVS----------------------------------------------------------------
VADRP---------------------IAGDKP--VGEVS----------------------------------------------------------------
KSQH------------------------LVGAGVLGAAR----------------------------------------------------------------
KSQH------------------------LVGAGVLGAAR----------------------------------------------------------------
KQDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRTY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLLGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDAN------------------------PIGATLIGRGY----------------------------------------------------------------
KDDN------------------------PFGASLIGRAY----------------------------------------------------------------
KDDN------------------------PFGASLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KESN------------------------PIGASLIGRAY----------------------------------------------------------------
KIDN------------------------PIGATNIGRAY----------------------------------------------------------------
KIDN------------------------SIGASLIGRAY----------------------------------------------------------------
```

FIG. 3X

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```
                                  C1
                                  |<-------->|
                                           10         20        30        40        50        60        70
                                            |         |         |         |         |         |         |
Q8VWE9_PAPSO_10114/1-105      ------LHVTIFEANSISHPDRKTGGAPKFFRKLVEN----IEETVG----------------FGKGASM
Q8W1B2_PAPSO_10114/1-105      ------LHVTIFEANSISHPDRKTGGAPKFFRKLVEN----IEETVG----------------FGKGASM
Q9AWB8_LYCES_1775/1-59        ----------------------------------------------------------------------
Q9FR61_LYCES_10108/1-99       ------LHVTIFEVDKLR-----TNFGREIFNKVVQG----IEGAIG----------------FNKTAST
Q9AWB9_LYCES_10108/1-99       ------LHVTIFEVDRLH-----TNFGRDFFNKVVQG----IEGAIG----------------FNKAASR
Q75KP6_ORYSA_72130/1-59       ----------------------------------------------------------------------
Q65XR9_ORYSA_10114/1-105      ------MHVTIFEAESLSNPSRPSSQAPQFLRKLVEG----IEDTVG----------------VGKGTSK
PLDA2_ORYSA_10100/1-91        ------LEATILEADHLSNPTRATGAAPGIFRKFVEG----FEDSLG----------------LGKGATR
Q69X20_ORYSA_10114/1-105      ------LEATILEADHLSNPTRATGAAPGIFRKFVEG----FEDSLG----------------LGKGATR
Q69X21_ORYSA_10118/1-109      ------LDATIFEATNLTNPTRLTGNAPEGFRKWWEGLENGLEKTTG----------------LGPGGTR
Q9LKM2_ORYSA_10118/1-109      ------LDATIFEATNLTNPTRLTGNAPEGFRKWWEGLENGLEKTTG----------------LGPGGTR
Q69X22_ORYSA_11115/1-105      ------LDATIFEATNLTNPTRLTGSAPEGIRKWWEG----VEKTTG----------------VGQGGTR
Q9LKM3_ORYSA_11115/1-105      ------LDATIFEATNLTNPTRLTGSAPEGIRKWWEG----VEKTTG----------------VGQGGTR
Q8H1U0_GOSHI_15129/1-115      ------LDLTIVEARRLPNMDFMVNHLRSCLT-CEPCKSPAQTAAKE-------GDS-KIRGHRKIITSD
Q8H6B9_GOSHI_15129/1-115      ------LDLTIVEARRLPNMDFMVNHLRSCLT-CEPCKSPAQTAAKE-------GDS-KIRGHRKIITSD
Q8H1T9_GOSHI_16133/1-118      ------LDLTIIEARKLPNMDIVSNHLRKCLT-CETCKAPSQAAAAQEP-----GEVGKVHHHHKIMTSD
Q3E9Q5_ARATH_16138/1-123      ------LDLKIVKARRLPNMDMFSEHLRRLFTACNACARPTDTDDVDPRDKGEFGDK-NIRSHRKVITSD
Q8L891_ARATH_7129/1-123       ------LDLKIVKARRLPNMDMFSEHLRRLFTACNACARPTDTDDVDPRDKGEFGDK-NIRSHRKVITSD
PLDD1_ARATH_16138/1-123       ------LDLKIVKARRLPNMDMFSEHLRRLFTACNACARPTDTDDVDPRDKGEFGDK-NIRSHRKVITSD
Q7XJ06_ORYSA_25139/1-115      ------LDLWVVEARLLPNMDMFSEHVRRCFA---ACKPPTSCATARQP------RHARGHHRRKIITSD
Q9LKM1_ORYSA_22137/1-116      ------LDIWITEAKCLPNMDIMSERMRRFFTGYGACGSSCAG--DNA------RRGGVGVRPKKIITSD
Q6AVR2_ORYSA_22139/1-118      ------LDIWITEAKCLPNMDIMSERMRRFFTGYGACGSSCGGTGDNA------RRAGGGVRPKKIITSD
Q8LGW5_ORYSA_18128/1-111      ------LDIQIVEAKCLPNMDLMTERMRKCFTGYGACSTECGK-----------SDPHTDVR--KIITSD
Q1RUP7_MEDTR_19130/1-112      ------LDLFIIEAKSLPNLDLSTEAIRKCLTMGNSCTPPFVKG----------LKTHSGKD--KIITSD
PLDG2_ARATH_29113/1-85        ---------LMVELLH--------------------GRRIRKVD----------------GEKSSKFTSD
Q3EA52_ARATH_38145/1-108      ------LDIWVKEAKHLPNMICYRNKLVGGISFSELGRRIRKVD----------------GEKSSKFTSD
PLDG1_ARATH_44147/1-104       ------LDIWVKEAKHLPNMDGFHN-RLGGMLSG-LGRK--KVE----------------GEKSSKITSD
PLDG3_ARATH_48154/1-107       ------LDIWVKEAKHLPNMDGFHNTLVGGMFFG-LGRRNHKVD----------------GENSSKITSD
Q9AWB7_LYCES_39142/1-104      ------LDIWVREAKNLPNMDLFHKKLDN--LLGGLAKLGSKKE----------------G--SPKITSD
PLDB2_ARATH_119221/1-103      ------LDIWVSCANNLPNLDLFHK-TLGVVFGGMTN----MIE----------------GQLSKKITSD
PLDB1_ARATH_158260/1-103      ------LDIWIYHAKNLPNMDMFHK-TLGDMFGRLPG----KIE----------------GQLTSKITSD
Q9AWB6_LYCES_99193/1-95       ------LEIWVYEAKNLPNMDMFHK-TIGDMFG----------------------------QMSNKITSD
Q9XGT0_GOSHI_20126/1-107      ------LDIWVLEANNLPNMDMFHR-TLGDMFANFSSNISKKVG----------------GRSDEKITSD
Q8H1U1_GOSHI_353459/1-107     ------LDIWVLEANNLPNMDMFHR-TLGDMFANFSSNISKKVG----------------GRSDEKITSD
Q8H1U2_GOSHI_275381/1-107     ------LDIWVLEAKNLPNMDMFHK-TLGDMFGNFSSNISKKIG----------------GRSEGKNTSD
Q710M6_ORYSA_31135/1-105      ------LDVWVYDARNLPNKDLFSK-RVGDLLG--PRLIGAVGS----------------KMSSANMTSD
Q8H093_ORYSA_243347/1-105     ------LDVWVYDARNLPNKDLFSK-RVGDLLG--PRLIGAVGS----------------KMSSANMTSD
Q8H048_ORYSA_102202/1-101     ------LDIWIHEARNLPNMDIVSK-TVVDILG--TKKK----K----------------KAANGAMTSD
Q8SAG7_ORYSA_102202/1-101     ------LDIWIHEARNLPNMDIVSK-TVVDILG--TKKK----K----------------KAANGAMTSD
Q6YUS5_ORYSA_38161/1-124      ------LDLTIHEARGLPNMDFLSTLLRRLCLCLRPPARRPSPGQSRGSVPADEDGRRQPHGHHLLPTSD
Q6ESI0_ORYSA_58121/1-64       ----------------------------------------------------------------------
Q39485_CHLEU_1073/1-64        ------LDVTLKSASDLRE-------------DMSVK-------------------------------LD
Q9LZI7_ARATH_697/1-92         ------LEINVTSAKGLKK----------------------------------------------VSKMD
Q9MA57_ARATH_796/1-90         ------VEINVLSAQDLNS------------INLLFR-------------------------------PT
Q9FGS8_ARATH_384/1-82         ------LYVYILQAKDLPA-------------------------------------------------KE
Q9SS68_ARATH_283366/1-84      ------LYIRVAKAKRAKN----------------DGS------------------------------NP
Q9C7Z6_ARATH_26602763/1-104------MTVQILEAKGLHI--------------IDDGN-----------------------------SHS
Q2HRV4_MEDTR_7107/1-101       ------IDLKIISCKDINA-------------FNFFQK------------------------------LT
Q2R360_ORYSA_1396/1-84        ------VTIRSISCRGVKA-------------FVPFQK------------------------------PP
Q1T1V3_MEDTR_14104/1-91       ------FELRIIQARNIES----------------VKS-----------------------------TKN
```

FIG. 3Y

```
C2                                                C3
        80        90        100       110         120       130       140       150
LYASVDLD-----------KARVGRTRIIKD--EPVN------PKWYE----SFHIYCAHMAAN----------VIFTV
LYASVDLD-----------KARVGRTRIIKD--EPVN------PKWYE----SFHIYCAHMAAN----------VIFTV
-YATIDLG-----------KARVGRTRLLD---EHKN------PRWYE----SFHIYCAHMASD----------VVFTV
LYATIDLG-----------KARVGRTRLLD---EHKN------PRWYE----SFHIYCAHMASD----------VVFTV
LYATIDLG-----------KARVGRTRLLD---DHKN------PRWYE----SFHIYCAHMAAN----------VIITV
-YATVDID-----------KARVARTRTVE---PTGT------PRWKE----SFHIYCAHYAGD----------VIFTV
VYATIGLD-----------KARVGRTRTLAD--DTAA------PRWYE----SFHVYCAHLATH----------VAFTL
LYATIDLG-----------RARVGRTRVVDD--EPVN------PRWYE----VFHIYCAHFAAD----------VVFSV
LYATIDLG-----------RARVGRTRVVDD--EPVN------PRWYE----VFHIYCAHFAAD----------VVFSV
LYATVDLG-----------RARLGRTRVIDD--EPVS------PRWDE----RFHFYCAHFAEN----------VVFSV
LYATVDLG-----------RARLGRTRVIDD--EPVS------PRWDE----RFHFYCAHFAEN----------VVFSV
LYATVDLG-----------KARLGRTRVIDD--EPVN------PRWDE----RFHLYCAHFADN----------VVFSV
LYATVDLG-----------KARLGRTRVIDD--EPVN------PRWDE----RFHLYCAHFADN----------VVFSV
PYVTVCLP-----------QATVARTRVLK---NSQN------PKWNE----HFIIPLAHPVTE----------LDINV
PYVTVCLP-----------QATVARTRVLK---NSQN------PKWNE----HFIIPLAHPVTE----------LDINV
PYVTITVP-----------QSTLARTPVLK---SADN------PEWNE----RFIIPMAHPLTE----------LEINV
PYVTVVVP-----------QATLARTRVLK---NSQE------PLWDE----KFNISIAHPFAY----------LEFQV
PYVTVVVP-----------QATLARTRVLK---NSQE------PLWDE----KFNISIAHPFAY----------LEFQV
PYVTVVVP-----------QATLARTRVLK---NSQE------PLWDE----KFNISIAHPFAY----------LEFQV
PYVTLSVA-----------GAVVARTRVIP---NDQD------PVWDE----RFAVPLAHYAAA----------LEFHV
PYVSVCLA-----------GATVACTRVIP---NSEN------PRWEE----RFRVEVAHAVSR----------LEFHV
PYVSVCLA-----------GATVACTRVIP---NSEN------PRWEE----RFRVEVAHAVSR----------LEFHV
PYVSVCLS-----------GATVACTRVIA---NSEN------PKWDE----HFYVQVAHSVSR----------VEFHV
PYVSICLA-----------GATIACTRVIP---NCEN------PLWDE----HFLVPVAHPAHK----------IEFLV
PYVTVSIS-----------GAVIGRTFVIS---NSEN------PVWMQ----HFDVPVAHSAAE----------VHFVV
PYVTVSIS-----------GAVIGRTFVIS---NSEN------PVWMQ----HFDVPVAHSAAE----------VHFVV
PYVTVSIS-----------GAVIGRTFVIS---NSEN------PVWMQ----HFDVPVAHSAAE----------VHFVV
PYVTVSIS-----------GAVIGRTFVIS---NSEN------PVWMQ----HFDVPVAHSAAK----------VHFVV
PYVTVSVS-----------NAVVARTYVIN---NSEN------PIWMQ----HFYVPVAHYASE----------VHFVV
PYVSISVA-----------GAVIGRTYVIS---NSEN------PVWQQ----HFYVPVAHHAAE----------VHFVV
PYVSVSVA-----------GAVIGRTYVMS---NSEN------PVWMQ----HFYVPVAHHAAE----------VHFVV
PYVSINIA-----------DATIGRTYVIN---NNEN------PVWMQ----HFNVPVAHYAAE----------VQFLV
PYVTIAVA-----------GAVIGRTFVIS---NNEN------PVWMQ----HFNVPVAHHAXE----------VQFVV
PYVTIAVA-----------GAVIGRTFVIS---NNEN------PVWMQ----HFNVPVAHHAAE----------VQFVV
PYVTIAVS-----------GAVIGRTFVIN---NDEN------PVWRQ----HFYVPVAHHAAE----------VQFVV
PYVTIQVS-----------YATVARTYVVP---NNEN------PVWTQ----NFLVPVGHDAAE----------VEFVV
PYVTIQVS-----------YATVARTYVVP---NNEN------PVWTQ----NFLVPVGHDAAE----------VEFVV
PYVTVQLA-----------SATVARTYVVN---DDEN------PVWAQ----HFLIPVAHEAPA----------VHFLV
PYVTVQLA-----------SATVARTYVVN---DDEN------PVWAQ----HFLIPVAHEAPA----------VHFLV
PYAAVVVA-----------GNTLARTHVVR---DSED------PEWST----HVLLHLAHHATG----------VAFHV
-YVNIQF------------GDQIFTSKITQG--KGKK------VWWNE----KFRFPLSSDECKEL------AKVTLKI
AYCVVSC------------ASTAHRSNTVTD--AGKT------MNWEQ----TFHFDKVASTS----------VLKLE-
VFVAVKLSGDP-----KCSDHREQRTQAARD--GGTS------PKWSN---DVMKFILDQNLAEAN-----RLVITFKI
VYVSVSVTR----------GSRDKQVTPAAAWDKKFL-------RWNY----RMKFYIEDDKVRRN-----ESVFVFQI
TFAKLHV------------GRHKSKTRVAR---DTSS------PIWNE----EFVFRISDVDEGD--------DVVVSI
VYAKLVI------------GTNGVKTRSQT----GKD--------WDQ----VFAFEKESLNSTS---------LEVSV
FFCTLRLVVDSQGAEPQKLFPQSARTKCVKPSTTIVNDLMECTSKWNE----LFIFEIPRKGVAR---------LEVEV
LYAQVSISTTN---PKTKLTKQQQRTPTHRDTDDDGTN-----PEWNHQTRFNLSFLSSHPDPSE-------FFLSFER
LYAAVSLA-----------GRREKTSGDPD---GGEN------PDWDAA---VFAFDLPAAADG---------MLQFEV
LFARLYLP-----------TGNNKRIQLNSKSVSTKS-----VPFWDE---SFNLDCSCPQEFLEN--LNQQSLEVEL
```

FIG. 3Z

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C4

```
          160        170        180        190        200        210        220        230        240
           |          |          |          |          |          |          |          |          |
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KDDN------------------------PIGATLIGRAY----------------------------------------------------------------
KADN------------------------PIGAELIGRAY----------------------------------------------------------------
KADN------------------------PIGAELIGRAY----------------------------------------------------------------
KFDN------------------------PIGAEVIGRAY----------------------------------------------------------------
KAEN------------------------PVGATLIGRAY----------------------------------------------------------------
KAKN------------------------PIGASLLGVGY----------------------------------------------------------------
K------------------------------------------------------------------------------------------------------
KAAQ------------------------PIGATLIGRAY----------------------------------------------------------------
KVAL------------------------SVDAKLIGRAY----------------------------------------------------------------
KVAL------------------------SVDAKLIGRAY----------------------------------------------------------------
KVSL------------------------PIDAALIGRAY----------------------------------------------------------------
KVSL------------------------PIDAALIGRAY----------------------------------------------------------------
KDND------------------------LFGADAIGTAK----------------------------------------------------------------
KDND------------------------LFGADAIGTAK----------------------------------------------------------------
KDDD------------------------LLGAEVIGTTK----------------------------------------------------------------
KDDD------------------------VFGAQIIGTAK----------------------------------------------------------------
KDDD------------------------VFGAQIIGTAK----------------------------------------------------------------
KDDD------------------------VFGAQIIGTAK----------------------------------------------------------------
KDND------------------------TFGAQLIGTVT----------------------------------------------------------------
KDND------------------------VFGAQLIGVAS----------------------------------------------------------------
KDND------------------------VFGAQLIGVAS----------------------------------------------------------------
KDND------------------------VFGAELIGVAS----------------------------------------------------------------
KDND------------------------ILGAELIGVVE----------------------------------------------------------------
KDND------------------------PIGSKIIGVVG----------------------------------------------------------------
KDND------------------------PIGSKIIGVVG----------------------------------------------------------------
KDSD------------------------IIGSQIMGAVG----------------------------------------------------------------
KDSD------------------------IIGSQIIGAVE----------------------------------------------------------------
KDND------------------------VVGSQIIGAVG----------------------------------------------------------------
KDSD------------------------AVGSQLIGIVT----------------------------------------------------------------
KDSD------------------------VVGSQLIGLVT----------------------------------------------------------------
KDDD------------------------IVGSQLMGTVA----------------------------------------------------------------
KDSD------------------------ILGSDIIGVVA----------------------------------------------------------------
KDSD------------------------ILGSDIIGVVA----------------------------------------------------------------
KDID------------------------ILGSEIIGVVT----------------------------------------------------------------
KDND------------------------VFGAQLIGTVS----------------------------------------------------------------
KDND------------------------VFGAQLIGTVS----------------------------------------------------------------
KDSD------------------------VFGAELIGEVV----------------------------------------------------------------
KDSD------------------------VFGAELIGEVV----------------------------------------------------------------
KDAD------------------------PFGSDLIGVAI----------------------------------------------------------------
MERDK-----------------------FSEDSLVGETK----------------------------------------------------------------
-------------------------------------------------------------------------------------------------------
KCEQR-----------------------GGVDKDIGEVH----------------------------------------------------------------
KCKR-----------------------FFGSDQVVGKLF----------------------------------------------------------------
LHHEQ--QDHQS----------------IVSTGLIGKVR----------------------------------------------------------------
WSEEKIEKEDK---------------TTTTTESCLGTVS----------------------------------------------------------------
TNLAAK----------------------AGKGEVVGSLS----------------------------------------------------------------
RHDG-----------------------LILGNKFLGECR----------------------------------------------------------------
KAQVP-----------------------LLGSKLVGKVS----------------------------------------------------------------
RQRK------------------------IWGSQLIGKFE----------------------------------------------------------------
```

FIG. 3ZZ

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C1

```
1   ------------------------------MSS V------  oryza full
1   ------------------------------MSS D------  P09229  GI118170 oryzacysta
1   ----------MRKHRIVSLVAALLILLALA-VSS TRNAQE  CAA60610.1  GI809608 zea ma
1   ---------------LLAIVVPFTQTRTQSARDK AAM---  BAB18768.1  GI11559283 trit
1   MWKYRVLGSVAALLLLLAVVVPFTQTWTQSARDK AAM---  CAG38123.2  GI109238749 Hor
1   ----------MRKQRIVPLVAALLVLLALA-VSS TRNARE  BAB21558.1  GI12657579 Coi>
1   ----------MRKHRIVSLVAALLVLLALAAVSS TRSTQK  P31726  GI399334 zea mays 1
1   -------------ARVVPLVAALLVLLALA-VSS TRNRNA  CAA60634.1  GI809576 sorght
1   ------------------------------.AA ------  AAU21498.1  GI52001235 Arac
1   ------------------------------.AA L-----  CAA11899.1  GI4150974 Casta
1   ------------------------------.AE AHN---  AAM78598.1  GI31505485 sacc
1   ------------------------------.AA ------  Q06445  GI1169196 Vigna ung
```

C2

10 20 30

```
5   -------GGP VLGGVEPVG--NENDLHLVDLARFAVTEHN  oryza full
5   -------GGP VLGGVEPVG--NENDLHLVDLARFAVTEHN  P09229  GI118170 oryzacysta
30  DS-MADNTGT LAGGIKDVPG-NENPLHLQELARFAVDEHN  CAA60610.1  GI809608 zea ma
23  ----AEDAGP LVGGIKDSPMGQENDLDVIALARFAVSEHN  BAB18768.1  GI11559283 trit
38  ----AEDAGP LMGGIEDSPMGQENDLDVIALARFAVSEHN  CAG38123.2  GI109238749 Hor
30  EESMADDAGM LAGGIKDVPA-NENDLHLQELARFAVDEHN  BAB21558.1  GI12657579 Coi>
31  ES-VADNAGM LAGGIKDVPA-NENDLQLQELARFAVNEHN  P31726  GI399334 zea mays 1
27  QE--GEESMA LDGGIKDVPA-NENDLHLQELARFAVDEHN  CAA60634.1  GI809576 sorght
3   ---------- -VGAPREVAG-NENSLEIDSLARFAVDEHN  AAU21498.1  GI52001235 Arac
4   ---------- -VGGVSDVKG-HENSLQID.LARFAVDDHN  CAA11899.1  GI4150974 Casta
6   ----GRRVG- MVGDVRDAPAGHEN.LEAIELARFAVAEHN  AAM78598.1  GI31505485 sacc
3   ---------- -.GGNRDVAG-NQNSLEIDSLARFAVEEHN  Q06445  GI1169196 Vigna ung
```

C3

40 50 60 70

```
36  KKANSLLEFEKLVSV KQQVVAGT LYYFTLEVKEGD-AKKL  oryza full
36  KKANSLLEFEKLVSV KQQVVAGT LYYFTIEVKEGD-AKKL  P09229  GI118170 oryzacysta
68  KKANALLGFEKLVKA KTQVVAGT MYYLTIEVKDGE-VKKL  CAA60610.1  GI809608 zea ma
59  NKANALLEFENVVKL KKQTVAGT MHYITIRVTEGG-AKKL  BAB18768.1  GI11559283 trit
74  KKANALLEFENVVKL KKQTVAGT MYYITIRVTEGG-TKKL  CAG38123.2  GI109238749 Hor
69  KKANALLGYEKLVKA KTQVVAGT MYYLTIEVKDGE-VKKL  BAB21558.1  GI12657579 Coi>
69  QKANALLGFEKLVKA KTQVVAGT MYYLTIEVKDGE-VKKL  P31726  GI399334 zea mays 1
4   KKANALLGYEKLVKA KTQVVAGT MYYLTVEVKDGE-VKKL  CAA60634.1  GI809576 sorght
31  KKQNGLLEFKRVISA KQQVVAGT LHHITLEAASGD-SKNV  AAU21498.1  GI52001235 Arac
31  KKANTLLQFKKVVNA KQQVVSGT IYILTLEVEDGG-KKKV  CAA11899.1  GI4150974 Casta
40  SKTNAMLEFERLVKV RHQVVAGT MHHFTVQVKEAGGGKKL  AAM78598.1  GI31505485 sacc
30  KKQNALLEFGRVVSA QQQVVSGT LYTITLEAKDGG-QKKV  Q06445  GI1169196 Vigna ung
```

C4

80 90 100

```
75   YEAKVWE KPWM DFKELQEFKPVDASANA      oryza full
75   YEAKVWE KPWM DFKELQEFKPVDASANA      P09229  GI118170 oryzacysta
107  YEAKVWE KPWE NFKELQEFKPVDEGASA      CAA60610.1  GI809608 zea ma
98   YEAKVWE KPWE NFKQLQEFKPVEDAAIA      BAB18768.1  GI11559283 trit
113  YEAKVWE KLWE NFKQLEEFKPVQDAAIA      CAG38123.2  GI109238749 Hor
108  YEAKVWE KPWE NFKELLEFKPVEEDASA      BAB21558.1  GI12657579 Coi>
108  YEAKVWE KPWE NFKQLQEFKPVEEGASA      P31726  GI399334 zea mays 1
103  YEAKVWE KPWE NFKELQEFKPVEEGASA      CAA60634.1  GI809576 sorght
70   YEAKVWE KPWM NFKEVQEFKLAGDGSNA      AAU21498.1  GI52001235 Arac
70   YEAKIWE KPWL NFKEVQEFKLIGDAPTH HSA  CAA11899.1  GI4150974 Casta
80   YEAKVWE KVWE NFKQLQSFQPVGDA         AAM78598.1  GI31505485 sacc
69   YEAKVWE KPWL NFKELQEFKHVGDAPA       Q06445  GI1169196 Vigna ung
```

FIG. 4

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```
C1
C1                                      C2
         10          20            30
1  MAGSGVLEVHLVDAKG|LTGNDFLGK-ID|PYVVVQYRSQER  Os-FIERG2
1  MAGSGVLEVHFVDAKG|LTGNDFLGK-ID|PYVVVQYRSQER  fiergl
1  MV-QGTLEVLLVGAKG|LENTDYLCN-MD|PYAVLKCRSQEQ  Q7F9X0  GI73919340 er
1  MG-MGMMEVHLISGKG|LQAHDPLNKPID|PYAEINFKGQER  Q9ZT46  GI25090875 cu
1  MG-MGMMEVHLISGKG|LQAHDPLNKPID|PYAEINFKGQER  Q9ZT47  GI25090878 cu
1  MP-HGTLEVVLVSAKG|LEDADFLNN-MD|PYVQLTCRTQDQ  Q9C8S6  GI73920511 ar

                             C3
   40        50        60                70
40 K|SSVARDQGKNP|SWNEVFKFQINSTAATGQHKLFLRL|MDH  Os-FIERG2
40 K|SSVARDQGKNP|SWNEVFKFQINSTAATGQHKLFLRL|MDH  fiergl
39 K|SSVASGKGSDP|EWNETFMFSVT----HNATELIIKL|MDS  Q7F9X0  GI73919340 er
40 M|SKVAKNAGPDP|IWNEKFKFLVEYPGSGGDFHILFKV|MDH  Q9ZT46  GI25090875 cu
40 M|SKVAKNAGPNP|LWDEKFKFLAEYPGSGGDFHILFKV|MDH  Q9ZT47  GI25090878 cu
39 K|SNVAEGMGTTP|EWNETFIFTVS----EGTTELKAKI|FDK  Q9C8S6  GI73920511 ar

                            C4
   80         90        100               110
80 DTFSRDDFL|GEATINVTDLISLGMEHGTWEMSESKHRVVL  Os-FIERG2
80 DTFSRDDFL|GEATINVTDLISLGMEHGTWEMSESKHRVVL  fiergl
75 DSGTDDDFV|GEATISLEAIYTEG------SIPPTVYNVVK  Q7F9X0  GI73919340 er
80 DAIDGDDYI|GDVKIDVQNLLAEGVRKGWSELPPRMYQVLA  Q9ZT46  GI25090875 cu
80 DAIDGDDYI|GDVKIDVKNLLAEGVRKGKSEMPPRMYHVLA  Q9ZT47  GI25090878 cu
75 DVGTEDDAV|GEATIPLEPVFVEG------SIPPTAYNVVK  Q9C8S6  GI73920511 ar

    120       130        140       150
120 ADKTYHGEIRVSLTFTASAKAQD--HAEQVGGWAHSFRQ|  Os-FIERG2
120 ADKTYHGEIRVSLTFTASAKAQD--HAQQVGGWAHSFRQ|  fiergl
109 EEE-YRGEIKVGLTFTPEDDRDRGLSEEDIGGWKQSS  |  Q7F9X0  GI73919340 er
120 HKIYFKGEIEVGVFFQRQG                    |  Q9ZT46  GI25090875 cu
120 HKIHFKGEIEVGVSFKLQGGGGCG----GCYPWEN    |  Q9ZT47  GI25090878 cu
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FIG. 5

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SEQUENCE LISTING

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Tyr Tyr Arg

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<400> 108

Arg Arg Thr Phe Trp Phe Val

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1 5

<210> 109
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 109

Glu Arg Lys Phe Trp Phe Phe
1 5

<210> 110
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 110

Ser Arg Arg Phe Trp Phe Phe
1 5

<210> 111
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 111

Ser Arg Arg Phe Trp Phe Phe
1 5

<210> 112
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 112

Ser Arg Glu Phe Trp Phe Glu
1 5

<210> 113
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 113

Ala Arg Leu Phe Trp Phe Lys
1 5

<210> 114
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 114

Val Arg Thr Phe Ser Phe Thr
1 5

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<210> 115
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 115

Ala Arg Glu Phe Trp Phe His
1 5

<210> 116
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 116

Ser Arg Glu Phe Trp Phe Lys
1 5

<210> 117
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 117

Ala Arg Lys Phe Trp Phe Glu
1 5

<210> 118
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 118

Ser Arg Glu Phe Trp Phe Val
1 5

<210> 119
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 119

Ser Arg Glu Phe Trp Phe Val
1 5

<210> 120
<211> 7
<212> PRT
<213> Phaseolus vulgaris

<400> 120

Ala Arg Glu Phe Trp Phe Glu
1 5

<210> 121

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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
<222> 1
<223> Xaa = Met, Val, Glu, Pro, Gln, Thr, Ala or Phe

<220>
<220>
<221> VARIANT
<222> 2
<223> Xaa = Asp, Glu, Asn, Val, Ser, Ile or Ala

<220>
<220>
<221> VARIANT
<222> 3
<223> Xaa = Glu, Ala, lys or Asp

<220>
<220>
<221> VARIANT
<222> 4
<223> Xaa = Pro, Lys or Leu

<220>
<220>
<221> VARIANT
<222> 6
<223> Xaa = Ser, Pro, Lys, His or Thr

<220>
<220>
<221> VARIANT
<222> (7)...(0)
<223> Xaa = Ser, Asn, Lys or Thr

<400> 121

Xaa Xaa Xaa Xaa Gly Xaa Xaa
1   5

<210> 122
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
<220>
<221> VARIANT
<222> 2
<223> Xaa = Lys, Arg, Thr or Phe

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<220>
<220>
<221> VARIANT
<222> 3
<223> Xaa = Tyr or Phe

<220>
<220>
<221> VARIANT
<222> 4
<223> Xaa = Tyr, Phe or His

<220>
<220>
<221> VARIANT
<222> 5
<223> Xaa = Asn, Thr, Lys, Asp or Glu

<220>
<220>
<221> VARIANT
<222> 7
<223> Xaa = Thr, Ser, Asn, Lys or Glu

<220>
<220>
<221> VARIANT
<222> (9)...(0)
<223> Xaa = Gly or Pro

<400> 122

Tyr Xaa Xaa Xaa Xaa Tyr Xaa Ser Xaa
1 5

<210> 123
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
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<221> VARIANT
<222> 1
<223> Xaa = Val, Ile, Leu or Met

<220>
<220>
<221> VARIANT
<222> 2
<223> Xaa = Gly or Glu

<220>
<220>
<221> VARIANT
<222> 3
<223> Xaa = Leu, Ile, Val, Glu, Thr, Ser, Glu, Phe or
Lys

<220>
<220>
<221> VARIANT
<222> 4

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<223> Xaa = Arg, Gly, Glu or Asp

<220>
<220>
<221> VARIANT
<222> 5
<223> Xaa = Asn, His, Asp, Gln, Lys, Ser or Glu

<400> 123

Xaa Xaa Xaa Xaa Xaa Thr
1   5

<210> 124
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 124

Pro Gln Gln Val His Ile Thr Gln Gly Asp His Val Gly Lys Ala Val
1   5   10   15

Ile Val Ser Trp Val Thr Met Asp Glu Pro Gly Ser Ser Val Val Val
            20   25   30

Tyr Trp Ser Glu Asn Ser Lys Tyr Lys Lys Ser Ala Glu Gly Thr Val
        35   40   45

Thr Thr Tyr Arg Phe Tyr Asn Tyr Thr Ser Gly Tyr Ile His His Cys
    50   55   60

Tyr Ile Lys Gly Leu Glu Tyr Asp Thr Lys Tyr Tyr Tyr Val Val Gly
65   70   75   80

Ile Gly Asn Thr Ser Arg Glu Phe Trp Phe Arg
                85   90

<210> 125
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 125

Pro Gln Gln Val His Ile Thr Gln Gly Asp Leu Val Gly Lys Ala Val
1   5   10   15

Ile Val Ser Trp Val Thr Val Asp Glu Pro Gly Ser Ser Glu Val His
            20   25   30

Tyr Trp Ser Glu Asn Ser Asp Lys Lys Lys Ile Ala Glu Gly Lys Leu
        35   40   45

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Val Thr Tyr Arg Phe Phe Asn Tyr Ser Ser Gly Phe Ile His His Thr
50 55 60

Thr Ile Arg Asn Leu Glu Tyr Lys Thr Lys Tyr Tyr Tyr Glu Val Gly
65 70 75 80

Leu Gly Asn Thr Thr Arg Gln Phe Trp Phe Val
85 90

<210> 126
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 126

Pro Gln Gln Val His Ile Thr Gln Gly Asp Leu Val Gly Arg Ala Met
1 5 10 15

Ile Ile Ser Trp Val Thr Met Asp Glu Pro Gly Ser Ser Ala Val Arg
20 25 30

Tyr Trp Ser Glu Lys Asn Gly Arg Lys Arg Ile Ala Lys Gly Lys Met
35 40 45

Ser Thr Tyr Arg Phe Phe Asn Tyr Ser Ser Gly Phe Ile His His Thr
50 55 60

Thr Ile Arg Lys Leu Lys Tyr Asn Thr Lys Tyr Tyr Tyr Glu Val Gly
65 70 75 80

Leu Arg Asn Thr Thr Arg Arg Phe Ser Phe Ile
85 90

<210> 127
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 127

Gly Asp Asp Leu Gly Lys Lys Leu His Leu Ala Ala Ser Arg Gly His
1 5 10 15

Leu Glu Ile Val Arg Val Leu Val Glu Ala Gly Ala Asp Val Asn Ala
20 25 30

Leu Asp Lys Phe Gly Arg Thr Ala Leu His Ile Ala Ala Ser Arg Gly
35 40 45

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His Leu Glu Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn
50 55 60

Ala Leu Asp Lys Phe Gly Arg Thr Ala Leu His Leu Ala Ala Ser Arg
65 70 75 80

Gly His Leu Glu Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val
85 90 95

Asn Ala Leu Asp Lys Phe Gly Asp Thr Ala Leu His Val Ser Ile Asp
100 105 110

Asn Gly Asn Glu Asp Ile Ala Glu Ile Leu Gln
115 120

<210> 128
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 128

Gly Asp Asp Leu Gly Lys Lys Leu His Leu Ala Ala Ser Arg Gly His
1 5 10 15

Leu Glu Ile Val Arg Val Leu Val Glu Ala Gly Ala Asp Val Asn Ala
20 25 30

Leu Asp Lys Phe Gly Arg Thr Pro Leu His Ile Ala Ala Ser Lys Gly
35 40 45

Asn Glu Gln Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro Asn
50 55 60

Ala Leu Asp Lys Phe Gly Arg Thr Pro Leu His Ile Ala Ala Ser Lys
65 70 75 80

Gly Asn Glu Gln Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro
85 90 95

Asn Ala Gln Asp Lys Phe Gly Asp Thr Ala Leu His Val Ser Ile Asp
100 105 110

Asn Gly Asn Glu Asp Ile Ala Glu Ile Leu Gln
115 120

<210> 129
<211> 123
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 129

Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1   5   10   15

Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20   25   30

Leu Asp Lys Phe Gly Arg Thr Pro Leu His Ile Ala Ala Ser Lys Gly
        35   40   45

Asn Glu Gln Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro Asn
    50   55   60

Ala Leu Asp Lys Phe Gly Arg Thr Pro Leu His Ile Ala Ala Ser Lys
65   70   75   80

Gly Asn Glu Gln Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro
                85   90   95

Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp
            100   105   110

Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
        115   120

<210> 130
<211> 102
<212> PRT
<213> Oryza sativa

<400> 130

Met Ser Ser Val Gly Gly Pro Val Leu Gly Gly Val Glu Pro Val Gly
1   5   10   15

Asn Glu Asn Asp Leu His Leu Val Asp Leu Ala Arg Phe Ala Val Thr
            20   25   30

Glu His Asn Lys Lys Ala Asn Ser Leu Leu Glu Phe Glu Lys Leu Val
        35   40   45

Ser Val Lys Gln Gln Val Val Ala Gly Thr Leu Tyr Tyr Phe Thr Leu
    50   55   60

Glu Val Lys Glu Gly Asp Ala Lys Lys Leu Tyr Glu Ala Lys Val Trp
65   70   75   80

Glu Lys Pro Trp Met Asp Phe Lys Glu Leu Gln Glu Phe Lys Pro Val
                85   90   95

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Asp Ala Ser Ala Asn Ala
100

<210> 131
<211> 156
<212> PRT
<213> Oryza sativa

<400> 131

Met Ala Gly Ser Gly Val Leu Glu Val His Leu Val Asp Ala Lys Gly
1 5 10 15

Leu Thr Gly Asn Asp Phe Leu Gly Lys Ile Asp Pro Tyr Val Val Val
20 25 30

Gln Tyr Arg Ser Gln Glu Arg Lys Ser Ser Val Ala Arg Asp Gln Gly
35 40 45

Lys Asn Pro Ser Trp Asn Glu Val Phe Lys Phe Gln Ile Asn Ser Thr
50 55 60

Ala Ala Thr Gly Gln His Lys Leu Phe Leu Arg Leu Met Asp His Asp
65 70 75 80

Thr Phe Ser Arg Asp Asp Phe Leu Gly Glu Ala Thr Ile Asn Val Thr
85 90 95

Asp Leu Ile Ser Leu Gly Met Glu His Gly Thr Trp Glu Met Ser Glu
100 105 110

Ser Lys His Arg Val Val Leu Ala Asp Lys Thr Tyr His Gly Glu Ile
115 120 125

Arg Val Ser Leu Thr Phe Thr Ala Ser Ala Lys Ala Gln Asp His Ala
130 135 140

Glu Gln Val Gly Gly Trp Ala His Ser Phe Arg Gln
145 150 155

<210> 132
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 132

Gly Glu Val Ile Gly Ile Ser Val Asn Asp Pro Arg Val Lys Glu Ile
1 5 10 15

Ala Glu Phe Ala Leu Lys Gln His Ala Glu Gln Asn
20 25

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<210> 133
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 133

Gly Glu Val Ile Gly Ile Gln Val Asn Asp Pro Arg Val Lys Glu Ile
1   5   10   15

Ala Glu Phe Ala Leu Lys Gln His Ala Glu Gln Asn
            20   25

<210> 134
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 134

Gly Gly Val Ile Gly Ile Ser Val Asn Asp Pro Arg Val Lys Glu Ile
1   5   10   15

Ala Glu Phe Ala Leu Lys Gln His Ala Glu Gln Asn
            20   25

<210> 135
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 135

Gly Gly Tyr Val Pro Cys Lys Asp Pro Asn Asp Pro His Val Lys Asp
1   5   10   15

Ile Ala Glu Trp Ala Val Ala Glu Tyr Asn Lys Ser Gln Gly His His
            20   25   30

Leu Thr Leu Val Ser Ile Leu Lys Cys Glu Ser Gln Val Val Ala Gly
        35   40   45

Val Asn Trp Arg Leu Val Leu Lys Cys Lys Asp Glu Asn Asn Gly Glu
    50   55   60

Gly Asn Tyr Glu Thr Val Val Trp Glu Lys Ile Trp Glu Asn Phe Arg
65   70   75   80

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```
Gln Leu Ile Thr Phe Asp His Leu Leu
                85


<210>  136
<211>  54
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetically generated peptide

<400>  136

Gly Gly Tyr Ser Pro Ile Lys Asn Leu Asn Asp His His Leu Ile Glu
1               5                   10                  15


Ile Ala Asn Phe Ala Val Thr Glu Tyr Gly Lys Gln Gln Gly Ile Lys
            20                  25                  30


Gln Ile Lys Leu Glu Lys Ile Thr Lys Gly Glu Thr Gln Val Val Asp
        35                  40                  45


Gly Thr Asn Tyr Arg Leu
    50


<210>  137
<211>  55
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetically generated peptide

<400>  137

Gly Gly Tyr Ser Pro Ile Lys Asn Leu Asn Asp Pro His Val Ile Glu
1               5                   10                  15


Ile Ala Asn Phe Ala Val Thr Glu Tyr Gly Lys Gln Gln Arg Phe Tyr
            20                  25                  30


Ser Lys Leu Asp Lys Ile Ile Lys Gly Glu Ser Gln Ala Val Asp Gly
        35                  40                  45


Thr Asn Tyr Arg Phe Ile Leu
    50                  55


<210>  138
<211>  73
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetically generated peptide

<400>  138

Gly Gly Trp Ser Pro Ile Lys Asp Ile Asn Asp Pro His Val Ile Val
1               5                   10                  15
```

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```
Ile Ala Asn Phe Ala Val Thr Glu Tyr Asn Lys His Thr Gly Ala Asn
            20                  25                  30

Leu Lys Leu Asp Lys Leu Ile Lys Gly Glu Ser Gln Val Thr Ser Gly
        35                  40                  45

Ile Tyr Tyr Asp Leu Ile Leu Ser Ala Gly Asp Gly Ser His Ser Asn
    50                  55                  60

Ile Tyr Lys Ala Leu Val Trp Glu Lys
65                  70
```

<210> 139
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 139

```
Gly Gly Trp Glu Pro Ile Lys Asn Ile Asn Asp Pro His Val Ile Asp
1               5                   10                  15

Ile Ala Asn Tyr Ala Val Thr Glu His Asp Lys Gln Ala Gly Leu Asn
            20                  25                  30

Leu Lys Leu Glu Lys Val Ile Ser Gly Glu Thr Lys Val Val Asp Gly
        35                  40                  45

Ile Ile Tyr Cys Leu Asn Ile Thr Ala Ser Asp Gly Ser Ala Ser Asn
    50                  55                  60

Lys Tyr Asn Leu Ala Val Leu Glu Lys Leu Gln His
65                  70                  75
```

<210> 140
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 140

```
Gly Asn Leu Ser Pro Ile Asn Asn Ile Asn Asp Pro Lys Val Ile Asp
1               5                   10                  15

Val Ala Asn Phe Ala Val Lys Glu Tyr Asn Asn Arg Arg Arg Lys Pro
            20                  25                  30

Glu Glu Lys Leu Arg Leu Trp Lys Val Ile Lys Gly Glu Ser Gln Ile
        35                  40                  45
```

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Val Ala Asp Gly Val Asn Tyr Arg Leu Thr Leu Ser Ala Thr Lys
    50   55   60

<210> 141
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 141

Leu Gln Phe Ser Arg Val Val Ser Ala Gln Lys Gln Val Val Ala Gly
1   5   10   15

Leu Lys Tyr Tyr Leu Arg Ile Glu Val Thr Gln Pro Asn Gly Ser
            20   25   30

<210> 142
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 142

Leu Gln Phe Ser Arg Val Val Ser Ala Gln Lys Gln Val Val Ala Gly
1   5   10   15

Leu Lys Tyr Tyr Leu Arg Ile Glu Val Thr Gln Pro Asn Gly Ser
            20   25   30

<210> 143
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 143

Gly Ala Arg Thr Glu Val Pro Asp Val Glu Gly Asp Gly Glu Val Gln
1   5   10   15

Glu Leu Gly Arg Phe Ser Val Ala Glu Tyr Asn Arg Gln Leu Arg Glu
            20   25   30

Gly Gly Gly Gly Gly Gly Arg Leu Glu Phe Gly Arg Val Val Ala Ala
        35   40   45

Gln Arg Gln Val Val Ser Gly Leu Lys Tyr Tyr Leu Arg Val Val Ala
    50   55   60

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Val Glu
65

<210> 144
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 144

Gly Ala Arg Thr Glu Val Arg Asp Val Glu Gly Asp Gly Glu Val Gln
1 5 10 15

Glu Leu Gly Arg Phe Ser Val Ala Glu Tyr Asn Arg Gln Leu Arg Asp
20 25 30

Gly Gly Gly Gly Gly Arg Leu Glu Phe Gly Arg Val Val Ala Ala Gln
35 40 45

Arg Gln Val Val Ser Gly Leu Lys Tyr Tyr Leu Arg Val Val Ala Val
50 55 60

Glu
65

<210> 145
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 145

Gly Gly Arg Thr Glu Val Arg Asp Val Glu Gly Asp Arg Glu Val Gln
1 5 10 15

Glu Leu Gly Arg Phe Ser Val Glu Glu His Asn Arg Arg Arg Arg Ser
20 25 30

Arg Asp Cys Gly Asp Val Arg Leu Glu Phe Gly Arg Val Val Ala Ala
35 40 45

Gln Arg Gln Val Val Ser Gly Leu Lys Tyr Tyr Leu Arg Val Ala Ala
50 55 60

Ala Glu
65

<210> 146
<211> 70
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 146

Gly Gly Arg Thr Glu Ile Arg Asp Val Gly Ser Asn Lys Ala Val Gln
1 5 10 15

Ser Leu Gly Arg Phe Ala Val Ala Glu His Asn Arg Arg Leu Arg His
20 25 30

Gly Gly Ser Gly Gly Pro Ala Asp Pro Val Pro Val Lys Leu Ala Phe
35 40 45

Ala Arg Val Val Glu Ala Gln Lys Gln Val Val Ser Gly Val Ala Tyr
50 55 60

Tyr Leu Lys Val Ala Ala
65 70

<210> 147
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 147

Gly Gly Arg Lys Glu Ile Glu Asn Val Lys Thr Asn Lys Glu Val Gln
1 5 10 15

Glu Leu Gly Arg Phe Ser Val Glu Glu Tyr Asn Arg Gln Arg Gly Thr
20 25 30

Gln Lys Met Asp Gly Gly Gly Glu Leu Gln Phe Leu Glu Val Val Glu
35 40 45

Ala Gln Ser Gln Val Val Ser Gly Ile Lys Tyr Tyr Leu Lys Val Ser
50 55 60

Ala Val Arg
65

<210> 148
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 148

Gly Gly Arg Thr Lys Val Lys Asn Val Lys Thr Asp Thr Glu Ile Gln
1 5 10 15

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Gln Leu Gly Ser Tyr Ser Val Asp Glu Tyr Asn Arg Leu Gln Arg Thr
20 25 30

Lys Lys Thr Gly Ala Gly Asp Leu Lys Phe Ser Gln Val Ile Ala Ala
35 40 45

Glu Thr Gln Val Val Ala Gly Thr Lys Tyr Tyr Leu Lys Ile Glu Ala
50 55 60

<210> 149
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 149

Gly Gly Arg Thr Glu Ile Pro Asp Val Glu Ser Asn Glu Glu Ile Gln
1 5 10 15

Gln Leu Gly Glu Tyr Ser Val Glu Gln Tyr Asn Gln Gln His His Asn
20 25 30

Gly Asp Gly Gly Asp Ser Thr Asp Ser Ala Gly Asp Leu Lys Phe Val
35 40 45

Lys Val Val Ala Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr Tyr
50 55 60

Leu Lys Ile Val Ala Ala Lys Gly Gly His Lys Lys Lys Phe Asp Ala
65 70 75 80

Glu Ile Val Val Gln Ala Trp Lys Lys Thr Lys Gln Leu Met Ser Phe
85 90 95

Ala Pro Ser His
100

<210> 150
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 150

Phe Ser Val Asp Glu Tyr Asn Ser Lys Asn Lys Ser Asn Leu Lys Leu
1 5 10 15

Leu Lys Val Val Lys Ala Glu Glu Gln Val Val Ala Gly Lys Lys Tyr
20 25 30

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Tyr Leu Lys Ile Ser Ala
35

<210> 151
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 151

Gly Gly Val Glu Pro Val Gly Asn Glu Asn Asp Leu His Leu Val Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Thr Glu His Asn Lys Lys Ala Asn Ser Leu
20 25 30

Leu Glu Phe Glu Lys Leu Val Ser Val Lys Gln Gln Val Val Ala Gly
35 40 45

Thr Leu Tyr Tyr Phe Thr Ile Glu Val Lys Glu Gly Asp Ala Lys Lys
50 55 60

Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Met Asp Phe Lys Glu
65 70 75 80

Leu Gln Glu Phe Lys Pro Val Asp
85

<210> 152
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 152

Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Tyr Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

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Glu Leu Leu Glu Phe Lys Pro Val Glu
85

<210> 153
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 153

Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Tyr Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Val Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 154
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 154

Gly Gly Ile Lys Asp Val Pro Gly Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

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Glu Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 155
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 155

Gly Gly Ile Lys Asp Val Pro Gly Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 156
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 156

Gly Gly Ile Lys Asp Val Pro Gly Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

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Glu Leu Gln Glu Phe Lys Pro Val Asp
85

<210> 157
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 157

Gly Gly Ile Gln Asp Val Pro Gly Ser Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Val Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Leu Lys
65 70 75 80

Gly Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 158
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 158

Gly Gly Ile Gln Asp Val Pro Gly Ser Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Leu Lys
65 70 75 80

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Gly Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 159
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 159

Gly Gly Ile Lys Asp Val Pro Gly Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Leu Lys
65 70 75 80

Gly Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 160
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 160

Gly Gly Ile Gln Asp Val Pro Gly Ser Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

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Glu Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 161
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 161

Gly Gly Ile Gln Asp Val Pro Glu Asn Glu Asn Asp Leu His Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Lys Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 162
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 162

Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu Gln Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asn Glu His Asn Gln Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Asn
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

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Gln Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 163
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 163

Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu Gln Leu Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asn Glu His Asn Gln Lys Ala Asn Ala
20 25 30

Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly Glu Val Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

Gln Leu Gln Glu Phe Lys Pro Val Glu
85

<210> 164
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 164

Val Ser Glu His Lys Asn Lys Thr Asn Ala Leu Leu Glu Phe Glu Lys
1 5 10 15

Val Val Arg Leu Lys Gln Gln Val Val Ala Gly Met Met Tyr Tyr Ile
20 25 30

Thr Ile Gln Val Asn Glu Gly Gly Ala Lys Lys Met Tyr Glu Ala Lys
35 40 45

Val Trp Glu Arg Pro Trp Met Asp Phe Lys Lys Leu Met Glu Phe Arg
50 55 60

Pro Ala Glu
65

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<210> 165
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 165

Leu Ala Arg Phe Ala Val Ser Glu His Lys Asn Lys Thr Asn Ala Leu
1 5 10 15

Leu Glu Phe Glu Lys Val Val Arg Leu Lys Gln Gln Val Val Ala Gly
20 25 30

Met Thr Tyr Tyr Ile Thr Ile Gln Val Asn Glu Gly Gly Ala Lys Lys
35 40 45

Met Tyr Glu Ala Lys Val Trp Glu Arg Pro Trp Met Asp Phe Lys Lys
50 55 60

Leu Met Glu Phe Arg Pro Ala Glu
65 70

<210> 166
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 166

Gly Gly Ile Val Asp Ser Leu Arg Arg Glu Asn Asp Pro Tyr Ile Val
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Ser Glu His Asn Lys Glu Gly Asn Thr
20 25 30

Gln Leu Glu Leu Glu Lys Val Val Lys Val Lys Glu Gln Ala Val Ala
35 40 45

Gly Arg Leu Tyr Tyr Ile Thr Ile Gln Val Asp Glu Gly Gly Ala Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Leu Glu Gln Leu Trp Leu Asp Val Lys
65 70 75 80

Lys Leu Val Glu Phe Lys Pro Ala Glu
85

<210> 167
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 167

Gly Gly Ile Val Asp Ser Leu Gly Arg Glu Asn Asp Pro Tyr Ile Val
1   5   10   15

Asp Leu Ala Arg Phe Ala Val Ser Glu His Asn Lys Glu Gly Asn Thr
            20   25   30

Gln Leu Glu Leu Glu Lys Val Val Lys Val Lys Glu Gln Ala Val Ala
        35   40   45

Gly Arg Leu Tyr Tyr Ile Thr Ile Gln Val Asp Glu Gly Gly Ala Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Leu Glu Gln Leu Trp Leu Asp Val Lys
65   70   75   80

Lys Leu Val Glu Phe Lys Pro Ala Glu
                85

<210> 168
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 168

Gly Gly Ile Val Asp Ser Pro Gly Arg Glu Asn Asp Pro Tyr Ile Val
1   5   10   15

Asp Leu Ala Arg Phe Ala Val Ser Gln His Asn Lys Glu Ala Asn Thr
            20   25   30

Gln Leu Glu Leu Glu Lys Val Val Lys Val Lys Glu Gln Ala Ile Ala
        35   40   45

Gly Arg Leu Tyr Tyr Ile Thr Ile Gln Val Asp Glu Gly Gly Ala Lys
    50   55   60

Lys Leu Tyr Lys Ala Lys Val Leu Glu Gln Leu Trp Leu Asp Val Lys
65   70   75   80

Lys Leu Leu Glu Phe Lys Pro Ala Glu
                85

<210> 169
<211> 90

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 169

Gly Gly Ile Ser Asp Ser Pro Met Gly Gln Glu Asn Asp Leu Asp Val
1 5 10 15

Ile Ala Leu Ala Arg Phe Ala Val Ser Glu His Asn Asn Lys Ala Asn
20 25 30

Ala Leu Leu Glu Phe Glu Asn Val Val Lys Val Lys Lys Gln Thr Val
35 40 45

Ala Gly Thr Met His Tyr Ile Thr Ile Arg Val Thr Glu Gly Gly Ala
50 55 60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe
65 70 75 80

Lys Lys Leu Glu Glu Phe Lys Leu Val Glu
85 90

<210> 170
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 170

Gly Gly Ile Ser Asp Ser Pro Met Gly Gln Glu Asn Asp Leu Asp Val
1 5 10 15

Ile Ala Leu Ala Arg Phe Ala Val Ser Glu His Asn Asn Lys Ala Asn
20 25 30

Ala Leu Leu Glu Phe Glu Asn Val Val Lys Val Lys Lys Gln Thr Val
35 40 45

Ala Gly Thr Met His Tyr Ile Thr Ile Arg Val Thr Glu Gly Gly Ala
50 55 60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe
65 70 75 80

Lys Lys Leu Glu Glu Phe Lys Leu Val Glu
85 90

<210> 171
<211> 88

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 171

Gly Gly Ile Lys Asp Ser Pro Met Gly Gln Glu Asn Asp Leu Asp Val
1   5   10   15

Ile Ala Arg Phe Ala Val Ser Glu His Asn Asn Lys Ala Asn Ala Leu
            20   25   30

Leu Glu Phe Glu Asn Val Val Lys Leu Lys Lys Gln Thr Val Ala Gly
        35   40   45

Thr Met His Tyr Ile Thr Ile Arg Val Thr Glu Gly Gly Ala Lys Lys
    50   55   60

Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln
65   70   75   80

Leu Gln Glu Phe Lys Pro Val Glu
                85

<210> 172
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 172

Gly Asp Val Arg Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala
1   5   10   15

Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn
            20   25   30

Ala Met Leu Glu Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val
        35   40   45

Ala Gly Thr Leu His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly
    50   55   60

Gly Glu Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Ala Trp Glu
65   70   75   80

Asn Phe Lys

<210> 173
<211> 92

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 173

Gly Asp Val Arg Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala
1 5 10 15

Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn
20 25 30

Ala Met Leu Glu Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val
35 40 45

Ala Gly Thr Leu His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly
50 55 60

Gly Glu Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Ala Trp Glu
65 70 75 80

Asn Phe Lys Gln Leu Gln Ser Phe Glu Leu Val Gly
85 90

<210> 174
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 174

Glu Asn Asp Leu Glu Ala Ile Glu Leu Ala Arg Phe Ala Val Ala Glu
1 5 10 15

His Asn Ser Lys Thr Asn Ala Met Leu Glu Phe Glu Arg Leu Val Lys
20 25 30

Val Arg His Gln Val Val Ala Gly Thr Met His His Phe Thr Val Gln
35 40 45

Val Lys Glu Ala Gly Gly Gly Lys Lys Leu Tyr Glu Ala Lys Val Trp
50 55 60

Glu Lys Val Trp Glu Asn Phe Lys Gln Leu Gln Ser Phe Gln Pro Val
65 70 75 80

Gly

<210> 175
<211> 90

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 175

Gly Gly Val Gln Asp Ala Pro Ala Gly Arg Glu Asn Asp Leu Glu Thr
1 5 10 15

Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ala Lys Ala Asn
20 25 30

Ala Leu Leu Glu Phe Glu Lys Leu Val Lys Val Arg Gln Gln Val Val
35 40 45

Ala Gly Cys Met His Tyr Phe Thr Ile Glu Val Lys Glu Gly Gly Ala
50 55 60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Ala Trp Glu Asn Phe
65 70 75 80

Lys Gln Leu Gln Glu Phe Lys Pro Ala Ala
85 90

<210> 176
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 176

Gly Gly Val Gln Asp Ala Pro Ala Gly Arg Glu Asn Asp Leu Glu Thr
1 5 10 15

Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ala Lys Ala Asn
20 25 30

Ala Leu Leu Glu Phe Glu Arg Leu Val Lys Val Arg Gln Gln Val Val
35 40 45

Ala Gly Cys Met His Tyr Phe Thr Ile Glu Val Lys Glu Gly Gly Ala
50 55 60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Ala Trp Glu Asn Phe
65 70 75 80

Lys Gln Leu Gln Glu Phe Lys Pro Ala Ala
85 90

<210> 177
<211> 91

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 177

Gly Gly Ile His Asp Ala Pro Ala Gly Arg Glu Asn Asp Leu Thr Thr
1 5 10 15

Val Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ser Lys Ala Asn
20 25 30

Ala Met Leu Glu Leu Glu Arg Val Val Lys Val Arg Gln Gln Val Val
35 40 45

Gly Gly Phe Met His Tyr Leu Thr Val Glu Val Lys Glu Pro Gly Gly
50 55 60

Ala Asn Lys Leu Tyr Glu Ala Lys Val Trp Glu Arg Ala Trp Glu Asn
65 70 75 80

Phe Lys Gln Leu Gln Asp Phe Lys Pro Leu Asp
85 90

<210> 178
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 178

Gly Gly Ile Tyr Asp Ala Pro Leu Asn Asn Glu Asn Gly Phe Asp Lys
1 5 10 15

Glu Asp Leu Ala Arg Phe Ala Val Arg Glu Tyr Asn Asn Lys Asn Asn
20 25 30

Ala Leu Leu Glu Phe Val Arg Val Val Lys Ala Lys Glu Gln Val Val
35 40 45

Ser Gly Met Met His Tyr Leu Thr Val Glu Val Asn Asp Ala Gly Lys
50 55 60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Gln Val Trp Met Asn Phe
65 70 75 80

Arg Gln Leu Gln Glu Phe Thr Tyr Leu Gly
85 90

<210> 179
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 179

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Gly Thr Ser Arg Asp Val Asp Pro Asn Ala Asn Asp Leu Gln Val Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Val
            20                  25                  30

Ser Leu Glu Tyr Arg Arg Leu Ile Gly Ala Lys Thr Gln Val Val Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Val Glu Val Ala Asp Gly Glu Thr Lys
    50                  55                  60

Lys Val Tyr Glu Ala Lys Val Leu Glu Lys Ala Trp Glu Asn Leu Lys
65                  70                  75                  80

Lys Leu Glu Asp Phe Thr His Leu Arg
                85
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<210> 180
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 180

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Gly Gly Val Arg Asp Val Asp Pro Asn Ala Asn Asp Leu Gln Val Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Val
            20                  25                  30

Ser Leu Glu Tyr Arg Arg Leu Ile Gly Ala Lys Thr Gln Val Val Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Val Glu Val Ala Asp Gly Glu Thr Lys
    50                  55                  60

Lys Val Tyr Glu Ala Lys Val Leu Glu Lys Ala Trp Glu Asn Leu Lys
65                  70                  75                  80

Lys Leu Glu Asp Phe Thr His Leu Arg
                85
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<210> 181
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 181

Gly Gly Val Arg Asp Ile Asp Ala Asn Ala Asn Asp Leu Gln Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Asn Glu Asn Leu
20 25 30

Thr Leu Glu Tyr Lys Arg Leu Leu Gly Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Val Glu Val Ala Asp Gly Glu Thr Asn
50 55 60

Lys Val Tyr Glu Ala Lys Val Leu Glu Lys Ala Trp Glu Asn Leu Lys
65 70 75 80

Gln Leu Glu Ser Phe Asn His Leu His
85

<210> 182
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 182

Gly Gly Val Arg Asp Ile Asp Ala Asn Ala Asn Asp Leu Gln Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Asn Glu Asn Leu
20 25 30

Thr Leu Glu Tyr Lys Arg Leu Leu Gly Ala Lys Thr Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Val Glu Val Ala Asp Gly Glu Thr Asn
50 55 60

Lys Val Tyr Glu Ala Lys Val Leu Glu Lys Ala Trp Glu Asn Leu Lys
65 70 75 80

Gln Leu Glu Ser Phe Asn His His His
85

<210> 183
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 183

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 184
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 184

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 185
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 185

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Ala Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 186
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 186

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Val Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Ala Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 187
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 187

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Val Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu His Glu Phe Lys Asp Ala Ser
                85

<210> 188
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 188

Gly Gly Val Gln Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Arg Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu His Glu Phe Lys Asp Ala Ser
                85

<210> 189
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 189

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Pro Lys Asp Gln Val Phe Ala
35 40 45

Gly Pro Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Asn Glu Ala Lys Val Trp Val Asn Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 190
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 190

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Pro Lys Glu Gln Val Phe Ala
35 40 45

Gly Pro Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Asn Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 191
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 191

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Pro Lys Glu Gln Val Phe Ala
        35   40   45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85

<210> 192
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 192

Gly Gly Val Gln Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Phe Ala
        35   40   45

Gly Pro Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Ser His Glu Phe Lys Asp Ala Gly
                85

<210> 193
<211> 89

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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetically generated peptide

<400>  193

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1               5                   10                  15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Phe Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65                  70                  75                  80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85


<210>  194
<211>  89
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetically generated peptide

<400>  194

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1               5                   10                  15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Phe Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65                  70                  75                  80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85


<210>  195
<211>  89
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2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 195

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Phe Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 196
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 196

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Leu Val Lys Ala Lys Asp Gln Val Phe Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Asn Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 197
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 197

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Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1               5                   10                  15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Ile Leu Glu Phe Ala Arg Leu Val Lys Ala Lys Glu Gln Val Val Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65                  70                  75                  80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85
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<210> 198
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 198

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Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1               5                   10                  15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Ile Leu Glu Phe Ala Arg Leu Val Lys Ala Lys Glu Gln Val Val Ala
        35                  40                  45

Gly Thr Met His His Leu Thr Val Glu Ala Ile Glu Ala Gly Lys Lys
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65                  70                  75                  80

Glu Leu His Glu Phe Lys Asp Ala Ser
                85
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<210> 199
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 199

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Pro Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 200
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 200

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Pro Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 201
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 201

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 202
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 202

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 203
<211> 89

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 203

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 204
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 204

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Leu Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Arg Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Gly
85

<210> 205
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 205

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Ile Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85

<210> 206
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 206

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu His Glu Phe Lys Asp Ala Gly
                85

<210> 207
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 207

Gly Gly Val His Asp Ser Gln Thr Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ile Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 208
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 208

Gly Gly Val His Asp Ser Gln Ser Ser Gln Asn Ser Ala Glu Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Met Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu His Glu Phe Lys Asp Ala Ser
85

<210> 209
<211> 90

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 209

Gly Gly Val His Asp Ser Pro Gln Gly Thr Ala Asn Asn Ala Glu Ile
1 5 10 15

Asp Gly Ile Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn
20 25 30

Ala Met Val Glu Phe Gly Arg Val Leu Lys Ala Lys Glu Gln Val Val
35 40 45

Ala Gly Thr Leu His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys
50 55 60

Lys Lys Ile Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65 70 75 80

Lys Glu Leu Gln Glu Phe Lys His Ala Thr
85 90

<210> 210
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 210

Gly Gly Val His Glu Ser His Gly Ala Gln Asn Ser Ala Glu Val Glu
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Gln Glu His Asn Asn Lys Glu Asn Ala
20 25 30

Leu Leu Glu Phe Val Ser Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Ile Glu Ala Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Gln Ala Lys Val Trp Val Lys Pro Trp Met Gly Phe Lys
65 70 75 80

Glu Val Gln Glu Phe Lys His Ala Asp
85

<210> 211
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 211

Gly Gly Ile Val Asp Val Glu Gly Ala Gln Asn Ser Ala Glu Val Glu
1   5   10   15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Leu Leu Gln Phe Ser Arg Leu Val Lys Ala Lys Gln Gln Val Val Ser
        35   40   45

Gly Ile Met His His Leu Thr Val Glu Val Ile Glu Gly Gly Lys Lys
    50   55   60

Lys Val Tyr Glu Ala Lys Val Trp Val Gln Ala Trp Leu Asn Ser Lys
65   70   75   80

Lys Leu His Glu Phe Ser Pro Ile Gly
                85

<210> 212
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 212

Gly Gly Val Gly Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Leu His His Leu Thr Leu Glu Ile Ala Gly Gln Lys Lys Leu
    50   55   60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65   70   75   80

Gln Glu Phe Lys Pro Ala Ser
                85

<210> 213
<211> 87

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 213

Gly Gly Val Gly Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Leu Glu Ile Ala Gly Gln Lys Lys Leu
50 55 60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65 70 75 80

Gln Glu Phe Lys Pro Ala Ser
85

<210> 214
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 214

Gly Gly Val Gly Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Leu Glu Ile Ala Gly Gln Lys Lys Leu
50 55 60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65 70 75 80

Gln Glu Phe Lys Pro Ala Ser
85

<210> 215
<211> 87

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 215

Gly Gly Val Gly Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Leu His His Leu Thr Leu Glu Ile Ala Gly Gln Lys Lys Leu
    50   55   60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65   70   75   80

Gln Glu Phe Thr Pro Ala Ser
                85

<210> 216
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 216

Gly Gly Val Arg Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Leu His His Leu Thr Leu Glu Ile Ala Gly Glu Lys Lys Leu
    50   55   60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65   70   75   80

Gln Glu Phe Lys Pro Ala Ser
                85

<210> 217
<211> 88

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 217

Gly Gly Val Arg Asp Val Pro Ala Asn Gln Asn Ser Gly Glu Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Leu Glu Ile Ile Glu Ala Gly Lys Lys
50 55 60

Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu
65 70 75 80

Leu Gln Glu Phe Lys Pro Ala Ser
85

<210> 218
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 218

Gly Gly Val Arg Asp Val Pro Ser Asn Glu Asn Ser Val Glu Val Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Met His His Leu Thr Leu Glu Ile Ile Glu Ala Gly Lys Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Ser Thr
85

<210> 219
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 219

Gly Gly Val Arg Asp Leu Pro Ala Asn Glu Asn Ser Val Glu Val Glu
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
            20   25   30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met His His Leu Thr Leu Glu Ile Ile Glu Ala Gly Lys Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu Gln Glu Phe Lys Pro Ala Ser
                85

<210> 220
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 220

Gly Gly Val His Asp Leu Arg Gly Asn Gln Asn Ser Gly Glu Ile Glu
1   5   10   15

Ser Leu Ala Arg Phe Ala Ile Gln Glu His Asn Lys Gln Gln Asn Lys
            20   25   30

Ile Leu Glu Phe Lys Lys Ile Val Lys Ala Arg Glu Gln Val Val Ala
        35   40   45

Gly Thr Met Tyr His Leu Thr Leu Glu Ala Lys Glu Gly Asp Gln Thr
    50   55   60

Lys Asn Phe Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65   70   75   80

Gln Leu Gln Glu Phe Lys Glu Ser Ser
                85

<210> 221
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 221

Gly Gly Val His Asp Leu Arg Gly Asn Gln Asn Ser Gly Glu Ile Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Ile Gln Glu His Asn Lys Gln Gln Asn Lys
20 25 30

Ile Leu Glu Phe Lys Lys Ile Val Lys Ala Arg Glu Gln Val Val Ala
35 40 45

Gly Thr Met Tyr His Leu Thr Leu Glu Ala Lys Glu Gly Asp Gln Thr
50 55 60

Lys Asn Phe Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65 70 75 80

Gln Leu Gln Glu Phe Lys Glu Ser Ser
85

<210> 222
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 222

Gly Gly Val His Asp Leu Arg Gly Asn Gln Asn Ser Gly Glu Ile Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Ile Gln Glu His Asn Lys Gln Gln Asn Lys
20 25 30

Ile Leu Glu Phe Lys Lys Ile Val Lys Ala Arg Glu Gln Val Val Ala
35 40 45

Gly Thr Met Tyr His Leu Thr Leu Glu Ala Lys Glu Gly Asp Gln Thr
50 55 60

Lys Asn Phe Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65 70 75 80

Gln Leu Gln Glu Phe Lys Glu Ser Ser
85

<210> 223
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 223

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Gly Gly Val His Asp Leu Arg Gly Asn Gln Asn Ser Gly Glu Ile Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Ile Gln Glu His Asn Lys Gln Gln Asn Lys
            20                  25                  30

Ile Leu Glu Phe Lys Lys Ile Val Lys Ala Arg Glu Gln Val Val Ala
        35                  40                  45

Gly Thr Met Tyr His Leu Thr Leu Glu Ala Lys Glu Gly Asp Gln Thr
    50                  55                  60

Lys Asn Phe Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65                  70                  75                  80

Gln Leu Gln Glu Phe Lys Glu Ser Ser
                85
```

<210> 224
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 224

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Gly Gly Ile Gln Asp Ser Pro Ser Ser Glu Asn Ser Leu Glu Ile Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Val Asp Gln His Asn Ala Lys Gln Asn Ser
            20                  25                  30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Arg Glu Gln Val Val Ala
        35                  40                  45

Gly Thr Leu His His Leu Thr Leu Glu Ala Ile Asp Ala Gly Glu Lys
    50                  55                  60

Lys Ile Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65                  70                  75                  80

Glu Leu Thr Glu Phe Lys His Ala Gly
                85
```

<210> 225
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 225

Gly Gly Ile Gln Asp Ser Pro Ser Ser Glu Asn Ser Leu Glu Ile Glu
1 5 10 15

Ser Leu Ala Arg Phe Ala Val Asp Gln His Asn Ala Lys Gln Asn Ser
20 25 30

Leu Leu Glu Phe Ala Arg Val Val Lys Ala Arg Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Leu Glu Ala Ile Asp Ala Gly Glu Lys
50 55 60

Lys Ile Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65 70 75 80

Glu Leu Thr Glu Phe Lys His Ala Gly
85

<210> 226
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 226

Gly Gly Leu Arg Asp Ser Gln Gly Ser Gln Asn Ser Val Gln Thr Glu
1 5 10 15

Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Gln Asn Ser Leu Leu
20 25 30

Glu Phe Ser Arg Val Val Arg Thr Gln Glu Gln Val Val Ala Gly Thr
35 40 45

Leu His His Leu Thr Leu Glu Ala Ile Glu Ala Gly Glu Lys Lys Leu
50 55 60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe Lys Glu Leu
65 70 75 80

Gln Glu Phe Lys Pro Ala Gly
85

<210> 227
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 227

Gly Gly Val Lys Glu Asn Pro Ala Ala Ala Asn Ser Ala Asp Ser Asp
1 5 10 15

Gly Leu Gly Arg Phe Ala Val Asp Glu His Asn Arg Arg Glu Asn Ala
20 25 30

Leu Leu Glu Phe Val Arg Val Val Glu Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Leu Glu Ala Val Glu Ala Gly Arg Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asp Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Ser His Lys Gly
85

<210> 228
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 228

Gly Gly Val Lys Glu Asn Pro Ala Ala Ala Asn Ser Ala Glu Ser Asp
1 5 10 15

Gly Leu Gly Arg Phe Ala Val Asp Glu His Asn Arg Arg Glu Asn Ala
20 25 30

Leu Leu Glu Phe Val Arg Val Val Glu Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Leu His His Leu Thr Leu Glu Ala Val Glu Ala Gly Arg Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asp Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Ser His Lys Gly
85

<210> 229
<211> 89

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 229

Gly Gly Lys Ser Glu Asn Pro Ala Ala Ala Asn Ser Leu Glu Thr Asp
1   5   10   15

Gly Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Arg Glu Asn Ala
            20   25   30

Leu Leu Glu Phe Val Arg Val Val Glu Ala Lys Glu Gln Thr Val Ala
        35   40   45

Gly Thr Val His His Leu Thr Leu Glu Ala Leu Glu Ala Gly Arg Lys
    50   55   60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asp Phe Lys
65   70   75   80

Glu Leu Gln Glu Phe Arg His Thr Gly
                85

<210> 230
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 230

Gly Gly Ala His Asp Ala Pro Ser Ala Ala Asn Ser Val Glu Thr Asp
1   5   10   15

Ala Arg Phe Ala Val Asp Glu His Asn Lys Arg Glu Asn Ala Leu Leu
            20   25   30

Glu Phe Val Arg Val Val Glu Ala Lys Glu Gln Val Val Ala Gly Thr
        35   40   45

Leu His His Leu Thr Leu Glu Ala Leu Glu Ala Gly Arg Lys Lys Val
    50   55   60

Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asp Phe Lys Glu Leu
65   70   75   80

Gln Glu Phe Arg Asn Thr Gly
                85

<210> 231
<211> 90

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 231

Gly Gly Val His Asp Ser His Gly Ser Ser Gln Asn Ser Asp Glu Ile
1   5   10   15

His Ser Leu Ala Lys Leu Ala Val Asp Glu His Asn Lys Lys Glu Asn
            20   25   30

Ala Met Ile Glu Leu Ala Arg Val Val Lys Ala Gln Glu Gln Thr Val
        35   40   45

Ala Gly Lys Leu His His Leu Thr Leu Glu Val Met Asp Ala Gly Lys
    50   55   60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65   70   75   80

Lys Glu Leu Gln Glu Phe Lys His Val Glu
                85   90

<210> 232
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 232

Gly Gly Val His Asp Ser His Gly Ser Ser Gln Asn Ser Asp Glu Ile
1   5   10   15

His Ser Leu Ala Lys Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn
            20   25   30

Ala Met Ile Glu Leu Ala Arg Val Val Lys Ala Gln Glu Gln Thr Val
        35   40   45

Ala Gly Lys Leu His His Leu Thr Leu Glu Val Met Asp Ala Gly Lys
    50   55   60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65   70   75   80

Lys Glu Leu Gln Glu Phe Lys His Val Glu
                85   90

<210> 233
<211> 90

2013201171 18 Jun 2013

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 233

```
Gly Gly Ile Arg Asp Ser His Pro Glu Ser Gln Asn Ser Asp Glu Ile
1               5                   10                  15

His Ser Leu Ala Lys Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn
            20                  25                  30

Ala Met Phe Glu Leu Ala Arg Val Val Lys Ala Lys Glu Gln Val Val
        35                  40                  45

Ala Gly Thr Leu His His Leu Thr Leu Glu Val Val Asp Ala Gly Lys
    50                  55                  60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65                  70                  75                  80

Lys Glu Leu Gln Glu Phe Thr His Val Glu
                85                  90
```

<210> 234
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 234

```
Gly Gly Ile Ser Asp Ser Ala Ser Ala Glu Asn Ser Val Glu Ile Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Val Glu Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Met Ile Glu Leu Val Arg Val Val Lys Ala Glu Glu Gln Val Val Ala
        35                  40                  45

Gly Lys Leu His His Leu Thr Leu Glu Val Ile Asp Ala Gly Lys Arg
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Leu Lys Pro Trp Met Asn Phe Lys
65                  70                  75                  80

Glu Leu Gln Gly Phe Asn His Ile Glu
                85
```

<210> 235
<211> 89

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 235

```
Gly Gly Ile Ser Asp Ser Ala Ser Ala Glu Asn Ser Val Glu Ile Glu
1               5                   10                  15

Ser Leu Ala Arg Phe Ala Val Glu Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Met Ile Glu Leu Val Arg Val Val Lys Ala Glu Glu Gln Val Val Ala
        35                  40                  45

Gly Lys Leu His His Leu Thr Leu Glu Val Ile Asp Ala Gly Lys Arg
    50                  55                  60

Lys Leu Tyr Glu Ala Lys Val Trp Leu Lys Pro Trp Met Asn Phe Lys
65                  70                  75                  80

Glu Leu Gln Gly Phe Asn His Ile Glu
                85
```

<210> 236
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 236

```
Gly Gly Phe Ser Asp Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile
1               5                   10                  15

Asp Asp Ile Ala Leu Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn
            20                  25                  30

Ala Val Leu Glu Leu Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val
        35                  40                  45

Ala Gly Lys Leu Tyr Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu
    50                  55                  60

Lys Lys Ile Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe
65                  70                  75                  80

Lys Gln Leu Gln Glu Phe Lys Asn Ile Ile
                85                  90
```

<210> 237
<211> 90

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 237

Gly Gly Phe Ser Asp Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile
1 5 10 15

Asp Asp Ile Ala Leu Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn
20 25 30

Ala Val Leu Glu Leu Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val
35 40 45

Ala Gly Lys Leu Tyr Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu
50 55 60

Lys Lys Ile Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe
65 70 75 80

Lys Gln Leu Gln Glu Phe Lys Asn Ile Ile
85 90

<210> 238
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 238

Gly Gly Val His Asp Ser Asn Ser Asn Pro Asp Thr His Ser Leu Ala
1 5 10 15

Arg Phe Ala Val Asp Gln His Asn Thr Lys Glu Asn Gly Leu Leu Glu
20 25 30

Leu Val Arg Val Val Glu Ala Arg Glu Gln Val Val Ala Gly Thr Leu
35 40 45

His His Leu Val Leu Glu Val Leu Asp Ala Gly Lys Lys Lys Leu Tyr
50 55 60

Glu Ala Lys Ile Trp Val Lys Pro Trp Met Asp Phe Lys Gln Leu Gln
65 70 75 80

Glu Phe Lys His Val Arg
85

<210> 239
<211> 64

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 239

Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu Phe Thr Arg Val
1 5 10 15

Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu His Asp Leu Ile
20 25 30

Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala Lys Val Trp Val
35 40 45

Lys Pro Trp Glu Asp Phe Lys Ser Val Val Glu Phe Arg Leu Val Gly
50 55 60

<210> 240
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 240

Gly Val Leu Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu Asp Ala Ala
1 5 10 15

Arg Phe Ala Val Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu
20 25 30

Phe Thr Arg Val Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu
35 40 45

His Asp Leu Ile Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala
50 55 60

Lys Val Trp Val Lys Pro Trp Glu Asp Phe Lys Ser Val Val Glu Phe
65 70 75 80

Arg Leu Val Gly

<210> 241
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 241

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Gly Met Leu Ala Ala Ile Arg Arg Glu Gln Ala Glu Ala Glu Asp Ala
1   5   10   15

Ala Arg Phe Ala Val Ala Glu Tyr Asn Lys Asn Gln Gly Ala Glu Leu
            20   25   30

Glu Phe Ala Arg Ile Val Lys Ala Lys Arg Gln Val Val Thr Gly Thr
        35   40   45

Leu His Asp Leu Met Leu Glu Val Val Asp Ser Gly Lys Lys Ser Lys
    50   55   60

Ala Lys Val Trp Val Lys Pro Trp Leu Asp Phe Lys Ala Val Val Glu
65   70   75   80

Phe Arg His Val Gly
                85

<210> 242
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 242

Gly Ala Pro Arg Asp Val Pro Ala Gly Gly Glu Asn Ser Ala Asp Val
1   5   10   15

Glu Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Lys Lys Glu Asn
            20   25   30

Ala Leu Leu Glu Phe Gly Arg Val Val Lys Ala Lys Glu Gln Val Val
        35   40   45

Ala Gly Thr Leu His His Leu Thr Val Glu Ala Ile Asp Ala Gly Asn
    50   55   60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65   70   75   80

Lys Glu Leu Gln Glu Phe Arg His Ala Gly
                85   90

<210> 243
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 243

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Gly Gly Ile Arg Asp Ser Pro Ala Gly Ser Glu Asn Ser Leu Glu Thr
1   5   10   15

Glu Ala Leu Gly Arg Phe Ala Val Asp Asp His Asn Gln Lys Gln Asn
            20   25   30

Gly Met Leu Glu Phe Val Arg Val Val Lys Ala Lys Glu Gln Val Val
        35   40   45

Ala Gly Thr Leu His His Leu Val Val Glu Ala Ile Asp Gly Gly Lys
    50   55   60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Leu Asn Phe
65   70   75   80

Lys Gln Val Gln Glu Phe Lys His Ala Gly
                85   90

<210> 244
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 244

Gly Ala Val Arg Asp Asn Gln Gly Val Ala Asn Ser Val Glu Thr Glu
1   5   10   15

Ser Leu Ala Arg Tyr Ala Val Asp Glu His Asn Lys Lys Glu Asn Asp
            20   25   30

Leu Leu Glu Phe Val Arg Val Leu Asp Asp Lys Val Gln Val Val Ser
        35   40   45

Gly Thr Met His Tyr Leu Lys Ile Glu Ala Thr Glu Gly Gly Lys Lys
    50   55   60

Lys Val Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Glu Asn Phe Lys
65   70   75   80

Gln Val Gln Glu Phe Lys Pro Val Ser
                85

<210> 245
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 245

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Gly Gly Ile Thr Glu Val Lys Asp Phe Ala Asn Ser Leu Val Ile Asp
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Asp Glu Tyr Ser Lys Lys Gln Asn Thr
20 25 30

Leu Leu Glu Phe Glu Arg Val Leu Asp Ala Lys Gln Gln Ile Val Ala
35 40 45

Gly Thr Met Tyr Tyr Phe Ile Ala Thr Val Gly
50 55

<210> 246
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 246

Gly Gly Phe Thr Glu Val Lys Asp Phe Ala Asn Ser Ile Val Ile Asp
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Asp Glu Tyr Asn Lys Lys Gln Asn Thr
20 25 30

Leu Leu Glu Phe Arg Lys Val Leu Asn Ala Lys Glu Gln Ile Val Ser
35 40 45

Gly Thr Leu Tyr Tyr Ile Thr Leu Asp Ala Ala Asn Gly Gly Ile Ile
50 55 60

Lys Thr Tyr Glu Ala Lys Val Trp Val Lys Lys Trp Glu Asn Leu Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Val Asp
85

<210> 247
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 247

Gly Gly Ile Thr Glu Val Lys Asp Phe Ala Asn Ser Leu Glu Ile Glu
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Gln Asn Thr
20 25 30

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Leu Leu Glu Phe Gly Lys Val Leu Asn Ala Lys Glu Gln Ile Val Ala
35 40 45

Gly Lys Leu Cys Tyr Ile Thr Leu Glu Ala Thr Asp Gly Gly Val Lys
50 55 60

Lys Thr Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Glu Asn Phe Lys
65 70 75 80

Glu Leu Gln Glu Phe Lys Pro Val Asp
85

<210> 248
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 248

Gly Gly Ile Thr Glu Val Lys Asp Asn Asp Asn Ser Val Asp Phe Asp
1 5 10 15

Glu Leu Ala Lys Phe Ala Ile Ala Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Ala Leu Glu Phe Gly Lys Val Ile Glu Lys Lys Gln Gln Ala Val Gln
35 40 45

Gly Thr Met Tyr Tyr Ile Lys Val Glu Ala Asn Asp Gly Gly Glu Lys
50 55 60

Lys Thr Tyr Glu Ala Lys Val Trp Val Lys Leu Trp Glu Asn Phe Lys
65 70 75 80

Glu Leu Gln Glu Leu Lys Leu Val
85

<210> 249
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 249

Ser Leu Glu Ile Asp Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn
1 5 10 15

Lys Lys Gln Asn Ala Leu Leu Glu Phe Gly Lys Val Val Asn Thr Lys
20 25 30

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Glu Gln Val Val Ala Gly Lys Met Tyr Tyr Ile Thr Leu Glu Ala Thr
        35   40   45

Asn Gly Gly Val Lys Lys Thr Tyr Glu Ala Lys Val Trp Val Lys Pro
    50   55   60

Trp Glu Asn Phe Lys Glu Leu Gln Glu Phe Lys Pro Val Asp
65   70   75

<210> 250
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 250

Gly Gly Ile Lys Gln Val Glu Gly Ser Ala Asn Ser Leu Glu Val Glu
1   5   10   15

Ser Leu Ala Lys Phe Ala Val Glu Asp His Asn Lys Lys Gln Asn Ala
            20   25   30

Met Leu Glu Phe Ser Lys Val Val Asn Thr Lys Glu Gln Val Val Ala
        35   40   45

Gly Thr Met Tyr Tyr Ile Thr Leu Glu Ala Thr Asp Gly Gly Lys Lys
    50   55   60

Lys Val Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65   70   75   80

Gln Val Gln Glu Phe Lys Leu Leu Gly
                85

<210> 251
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 251

Gly Gly Ile Arg Glu Ala Gly Gly Ser Glu Asn Ser Leu Glu Ile Asn
1   5   10   15

Asp Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Gln Asn Ala
            20   25   30

Leu Leu Glu Phe Gly Lys Val Val Asn Val Lys Glu Gln Val Val Ala
        35   40   45

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Gly Thr Met Tyr Tyr Ile Thr Leu Glu Ala Thr Glu Gly Gly Lys Lys
50 55 60

Lys Ala Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Gln Asn Phe Lys
65 70 75 80

Gln Val Glu Asp Phe Lys Leu Ile Gly
85

<210> 252
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 252

Gly Gly Ile His Glu Lys Glu Gly Ser Ala Asn Ser Val Glu Met Asp
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Gln His Asn Lys Lys Gln Asn Ala
20 25 30

Leu Leu Glu Phe Val Lys Val Val Asn Val Lys Glu Gln Val Val Ser
35 40 45

Gly Thr Leu Tyr Tyr Ile Thr Leu Glu Ala Thr Gly Gly Gly Gln Lys
50 55 60

Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys
65 70 75 80

Glu Leu Gln Asp Phe Gln Leu Ala Ser
85

<210> 253
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 253

Gly Gly Ser Ser Ala Ile Ser Leu Glu Ile Asp Glu Leu Ala Lys Phe
1 5 10 15

Ala Val Asp His Tyr Asn Ser Ile Glu Asn Ala Leu Leu Glu Phe Pro
20 25 30

Arg Val Val Asn Thr Lys Glu Gln Val Val Ala Gly Thr Ile Tyr Tyr
35 40 45

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Ile Thr Leu Glu Ala Thr Asp Gly Gly Val Lys Lys Leu Tyr Glu Ala
    50   55   60

Asn Val Trp Val Lys Pro Gly Val Asn Phe Lys Glu Val Gln Val Phe
65   70   75   80

Lys Tyr Val Gly

<210> 254
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 254

Gly Gly Ile Lys Asp Ser Gly Gly Ser Ser Ala Asn Ser Leu Glu Ile
1   5   10   15

Asp Glu Leu Ala Lys Phe Ala Val Asp His Tyr Asn Ser Lys Glu Asn
            20   25   30

Ala Leu Leu Glu Phe Gln Arg Val Val Asn Thr Lys Glu Gln Val Val
        35   40   45

Ala Gly Thr Ile Tyr Tyr Ile Thr Leu Glu Ala Thr Asp Gly Gly Val
    50   55   60

Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Val Asn Phe
65   70   75   80

Lys Glu Val Gln Asp Phe Lys Tyr Val Gly
                85   90

<210> 255
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 255

Gly Gly Val Ser Asp Val Lys Gly His Glu Asn Ser Leu Gln Ile Asp
1   5   10   15

Asp Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Ala Asn Thr
            20   25   30

Leu Leu Gln Phe Lys Lys Val Val Asn Ala Lys Gln Gln Val Val Ser
        35   40   45

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Gly Thr Ile Tyr Ile Leu Thr Leu Glu Val Glu Asp Gly Gly Lys Lys
50 55 60

Lys Val Tyr Glu Ala Lys Ile
65 70

<210> 256
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 256

Gly Gly Val Ser Asp Val Lys Gly His Glu Asn Ser Leu Gln Ile Asp
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Ala Asn Thr
20 25 30

Leu Leu Gln Phe Lys Lys Val Val Asn Ala Lys Gln Gln Val Val Ser
35 40 45

Gly Thr Ile Tyr Ile Leu Thr Leu Glu Val Glu Asp Gly Gly Lys Lys
50 55 60

Lys Val Tyr Glu Ala Lys Ile
65 70

<210> 257
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 257

Gly Gly Val Ser Asp Val Lys Gly His Glu Asn Ser Leu Gln Ile Asp
1 5 10 15

Asp Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Ala Asn Thr
20 25 30

Leu Leu Gln Phe Lys Lys Val Val Asn Ala Lys Gln Gln Val Val Ser
35 40 45

Gly Thr Ile Tyr Ile Leu Thr Leu Glu Val Glu Asp Gly Gly Lys Lys
50 55 60

Lys Val Tyr Glu Ala Lys Ile Trp Glu Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

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Glu Val Gln Glu Phe Lys Leu Ile Gly
85

<210> 258
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 258

Gly Gly Leu Gln Asp Val Glu Gly Asp Ala Asn Asn Leu Glu Tyr Gln
1 5 10 15

Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Thr Asn Ala
20 25 30

Met Leu Gln Phe Lys Arg Val Val Asn Val Lys Gln Ala Val Val Glu
35 40 45

Gly Leu Lys Tyr Cys Ile Thr Leu Glu Ala Val Asp Gly His Lys Thr
50 55 60

Lys Val Tyr Glu Ala Glu Ile Trp Leu Lys Leu Trp Glu Asn Phe Arg
65 70 75 80

Ser Leu Glu Gly Phe Lys Leu Leu Gly
85

<210> 259
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 259

Glu Ser Val Glu Ile Asp Ser Leu Ala Arg Phe Ala Val Glu Glu His
1 5 10 15

Asn Lys Lys Gln Asn Ala Leu Leu Glu Phe Gly Arg Val Val Ser Ala
20 25 30

Gln Gln Gln Val Val Ser Gly Thr Leu Tyr Thr Ile Thr Leu Glu Ala
35 40 45

Lys Asp Gly Gly Gln Lys Lys Val Tyr Glu Ala Lys Val Trp Glu Lys
50 55 60

Pro Trp Leu Asn Phe Lys Glu Leu Gln Glu Phe Lys Leu Val Gly
65 70 75

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<210> 260
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 260

Gly Gly Asn Arg Asp Val Ala Gly Asn Gln Asn Ser Leu Glu Ile Asp
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Glu Glu His Asn Lys Lys Gln Asn Ala
            20   25   30

Leu Leu Glu Phe Gly Arg Val Val Ser Ala Gln Gln Gln Val Val Ser
        35   40   45

Gly Thr Leu Tyr Thr Ile Thr Leu Glu Ala Lys Asp Gly Gly Gln Lys
    50   55   60

Lys Val Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Leu Asn Phe Lys
65   70   75   80

Glu Leu Gln Glu Phe Lys His Val Gly
                85

<210> 261
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 261

Asn Ser Val Glu Ile Asp Ala Arg Phe Ala Val Glu Glu His Asn Lys
1   5   10   15

Lys Gln Asn Ala Leu Leu Glu Phe Glu Lys Val Val Thr Ala Lys Gln
            20   25   30

Gln Val Val Ser Gly Thr Leu Tyr Thr Ile Thr Leu Glu Ala Lys Asp
        35   40   45

Gly Gly Gln Lys Lys Val Tyr Glu Ala Lys Val Trp Glu Lys Ser Trp
    50   55   60

Leu Asn Phe Lys Glu Val Gln Glu Phe Lys Leu Val Gly
65   70   75

<210> 262
<211> 89
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 262

Gly Gly Ile Lys Glu Val Glu Glu Ser Ala Asn Ser Val Glu Ile Asp
1 5 10 15

Asn Leu Ala Arg Phe Ala Val Asp Asp Tyr Asn Lys Lys Gln Asn Ala
20 25 30

Leu Leu Glu Phe Lys Arg Val Val Ser Thr Lys Gln Gln Val Val Ala
35 40 45

Gly Thr Met Tyr Tyr Ile Thr Leu Glu Val Ala Asp Gly Gly Gln Thr
50 55 60

Lys Val Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Leu Asn Phe Lys
65 70 75 80

Glu Val Gln Glu Phe Lys Pro Ile Gly
85

<210> 263
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 263

Gly Gly Val Arg Asp Val Pro Gly Asn Gln Asn Ser Leu Ala Ile Asp
1 5 10 15

Gly Leu Ala Arg Phe Ala Val Glu Glu His Asn Lys Lys Gln Asn Ala
20 25 30

Leu Leu Glu Phe Ser Arg Val Ile Ser Ala Lys Glu Gln Val Val Ala
35 40 45

Gly Thr Ile His His Ile Thr Leu Glu Val Lys Asp Gly Val Asn Lys
50 55 60

Lys Val Tyr Glu Ala Lys Val Trp Glu Lys Ser Trp Met Asn Phe Lys
65 70 75 80

Glu Val Gln Glu Phe Lys Leu Val Glu
85

<210> 264
<211> 89
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 264

Gly Ala Pro Arg Glu Val Ala Gly Asn Glu Asn Ser Leu Glu Ile Asp
1   5   10   15

Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Gln Asn Gly
            20   25   30

Leu Leu Glu Phe Lys Arg Val Ile Ser Ala Lys Gln Gln Val Val Ala
        35   40   45

Gly Thr Leu His His Ile Thr Leu Glu Ala Ala Ser Gly Asp Ser Lys
    50   55   60

Asn Val Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Met Asn Phe Lys
65   70   75   80

Glu Val Gln Glu Phe Lys Leu Ala Gly
                85

<210> 265
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 265

Gly Gly Ile Thr Asp Val Pro Gly Ala Ala Asn Ser Val Glu Ile Ala
1   5   10   15

Asn Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Gln Asn Gly
            20   25   30

Val Leu Glu Phe Val Arg Val Ile Ser Ala Lys Gln Gln Val Val Ser
        35   40   45

Gly Ile Leu Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Glu Thr Lys
    50   55   60

Lys Val Tyr Lys Thr Lys Val Trp Val Arg Glu Trp Leu Asn Pro Lys
65   70   75   80

Glu Val Gln Glu Phe Asn Leu Val Thr
                85

<210> 266
<211> 89
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 266

Gly Gly Ile Thr Asp Val Pro Gly Ala Ala Asn Ser Val Glu Ile Ala
1 5 10 15

Asn Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Gln Asn Gly
20 25 30

Val Leu Glu Phe Val Arg Val Ile Ser Ala Lys Gln Gln Val Val Ser
35 40 45

Gly Ile Leu Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Glu Thr Lys
50 55 60

Lys Val Tyr Lys Thr Lys Val Trp Val Arg Glu Trp Leu Asn Pro Lys
65 70 75 80

Glu Val Gln Glu Phe Asn Leu Val Thr
85

<210> 267
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 267

Gly Gly Ile Ile Asp Val Ser Gly Ser Ala Asn Cys Leu Glu Ile Ala
1 5 10 15

Ile Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys Gln Asn Gly
20 25 30

Val Leu Glu Phe Val Arg Val Ile Ser Ala Lys Gln Gln Val Val Ser
35 40 45

Gly Ile Leu Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Glu Thr Lys
50 55 60

Lys Val Tyr Lys Thr Lys Val Trp Val Arg Glu Trp Leu Asn Pro Lys
65 70 75 80

Glu Val Gln Glu Phe Asn Leu Val Thr
85

<210> 268
<211> 89
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 268

Gly Gly Ile Thr Asp Val His Gly Ala Ala Asn Ser Val Glu Ile Asn
1 5 10 15

Asn Leu Ala Arg Phe Ala Val Glu Glu Gln Asn Lys Arg Glu Asn Ser
20 25 30

Val Leu Glu Phe Val Arg Val Ile Ser Ala Lys Gln Gln Val Val Ala
35 40 45

Gly Val Asn Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Leu Ile Lys
50 55 60

Asn Glu Tyr Glu Ala Lys Val Trp Val Arg Glu Trp Leu Asn Ser Lys
65 70 75 80

Glu Leu Leu Glu Phe Lys Pro Val Asn
85

<210> 269
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 269

Gly Gly Val Gly Asp Val Pro Ser Asp Thr Leu His Ile Glu Asn Leu
1 5 10 15

Ala Arg Phe Ala Val Asp Gln Tyr Asn Lys Asn Glu Asn Ala Asn Leu
20 25 30

Glu Phe Val Arg Val Ile Asp Ala Lys Glu Gln Val Val Glu Gly Phe
35 40 45

Ile Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Glu Ser Lys Asn Val
50 55 60

Tyr Glu Ala Lys Val Trp Glu Arg Ser Trp Leu Asn Ser Ile Glu Leu
65 70 75 80

Leu Glu Phe Lys Pro Val Asp
85

<210> 270
<211> 87
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 270

Gly Gly Val Gly Asp Val Pro Ser Asp Thr Leu His Ile Glu Asn Leu
1 5 10 15

Ala Arg Phe Ala Val Asp Gln Tyr Asn Lys Asn Glu Asn Ala Asn Leu
20 25 30

Glu Phe Val Arg Val Ile Asp Ala Lys Glu Gln Val Val Glu Gly Phe
35 40 45

Ile Tyr Tyr Ile Thr Leu Glu Ala Lys Asp Gly Glu Ser Lys Asn Val
50 55 60

Tyr Glu Ala Lys Val Trp Glu Arg Ser Trp Leu Asn Ser Ile Glu Leu
65 70 75 80

Leu Glu Phe Lys Pro Val Asp
85

<210> 271
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 271

Gly Gly Phe Thr Asp Ile Thr Gly Ala Gln Asn Ser Ile Asp Ile Glu
1 5 10 15

Asn Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala
20 25 30

Val Leu Glu Phe Val Arg Val Ile Ser Ala Lys Lys Gln Val Val Ser
35 40 45

Gly Thr Leu Tyr Tyr Ile Thr Leu Glu Ala Asn Asp Gly Val Thr Lys
50 55 60

Lys Val Tyr Glu Thr Lys Val Leu Glu Lys Pro Trp Leu Asn Ile Lys
65 70 75 80

Glu Val Gln Glu Phe Lys Pro Ile Thr
85

<210> 272
<211> 48
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 272

```
Gly Phe Thr Asp Ile Thr Gly Ala Gln Asn Ser Ile Asp Ile Glu Asn
1               5                   10                  15

Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu Asn Ala Val
            20                  25                  30

Leu Glu Phe Val Arg Val Lys Ser Ala Lys Lys Gln Val Val Ser Gly
        35                  40                  45
```

<210> 273
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 273

```
Gly Gly Val Thr Glu Cys Lys Asn Phe Glu Asn Asn Val Glu Ile Glu
1               5                   10                  15

Thr Ile Ala Lys Phe Ala Val Glu Glu His Asn Lys Lys Glu Asn Ala
            20                  25                  30

Thr Leu Glu Phe Val Lys Val Val Ser Ala Lys Glu Gln Val Val Ser
        35                  40                  45

Gly Lys Ile Tyr Tyr Ile Thr Ile Glu Thr Asn Asp Gly Lys Thr Tyr
    50                  55                  60

Glu Ala Lys Leu Trp Val Lys Pro Trp Glu Asn Phe Gln Glu Leu Gln
65                  70                  75                  80

Glu Phe Lys Pro Ala Ala
                85
```

<210> 274
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 274

```
Gly Gly Val Arg Asp Val Pro Asp His Asn Ser Ala Glu Thr Glu Glu
1               5                   10                  15

Leu Ala Arg Phe Ala Val Gln Glu His Asn Lys Lys Ala Asn Thr Arg
            20                  25                  30
```

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Leu Glu Phe Ser Arg Val Val Lys Ala Lys Glu Gln Val Val Ala Gly
35 40 45

Thr Met Tyr Tyr Ile Thr Leu Glu Val Val Glu Ala Gly Gln Lys Lys
50 55 60

Ile Tyr Glu Ala Lys Val Trp Val Lys Leu Trp Glu Asn Phe Lys Glu
65 70 75 80

Leu Gln Glu Phe Lys Pro Val Gly
85

<210> 275
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 275

His Leu Glu Tyr Val Glu Asn Leu Asn Val Lys Glu Gln Leu Val Ala
1 5 10 15

Gly Thr Leu Tyr Tyr Ile Thr Leu Val Ala Thr Asp Ala Gly Lys Lys
20 25 30

Lys Ile Tyr Glu Thr Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys
35 40 45

Lys Val Val Glu Phe Lys Leu Val Gly
50 55

<210> 276
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 276

Gly Asp Ile Val Asp Val Pro Asp Pro Asn Ile Pro Pro Leu Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Ala Gln Asn Ala His
20 25 30

Leu Glu Tyr Val Glu Asn Leu Asn Val Lys Glu Gln Leu Val Ala Gly
35 40 45

Thr Leu Tyr Tyr Ile Thr Leu Val Ala Thr Asp Ala Gly Lys Lys Lys
50 55 60

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Ile Tyr Glu Thr Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys Lys
65 70 75 80

Val Val Glu Phe Lys Leu Val Gly
85

<210> 277
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 277

Gly Gly Phe Thr Asp Val Pro Phe Pro Asn Asn Pro Glu Phe Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Lys Glu Asn Ala His
20 25 30

Leu Glu Tyr Val Glu Asn Leu Asn Val Lys Glu Gln Leu Val Ala Gly
35 40 45

Met Ile Tyr Tyr Ile Thr Leu Val Ala Thr Asp Ala Gly Lys Lys Lys
50 55 60

Ile Tyr Glu Ala Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys Lys
65 70 75 80

Val Val Glu Phe Lys Leu Val Gly
85

<210> 278
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 278

Gly Gly Ile Thr Asp Val Pro Phe Pro Asn Asn Pro Glu Phe Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Ile Gln Val Tyr Asn Lys Lys Glu Asn Val His
20 25 30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Gln Gln Val Val Ala Gly
35 40 45

Met Met Tyr Tyr Ile Thr Leu Ala Ala Ile Asp Ala Gly Lys Lys Lys
50 55 60

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Ile Tyr Glu Thr Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys Lys
65 70 75 80

Val Val Glu Phe Lys Leu Val Gly
85

<210> 279
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 279

Gly Gly Ile Val Asn Val Pro Asn Pro Asn Asn Thr Lys Phe Gln Glu
1 5 10 15

Leu Ala Arg Phe Ala Ile Gln Asp Tyr Asn Lys Lys Gln Asn Ala His
20 25 30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Val Val Ala Gly
35 40 45

Ile Met Tyr Tyr Ile Thr Leu Ala Ala Thr Asp Asp Ala Gly Lys Lys
50 55 60

Lys Ile Tyr Lys Ala Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys
65 70 75 80

Lys Val Val Glu Phe Lys Leu Val Gly
85

<210> 280
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 280

Gly Gly Ile Ile Ser Val Pro Phe Pro Asn Ser Pro Glu Phe Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Asn Thr Gln Asn Ala His
20 25 30

Leu Glu Phe Val Glu Asn Leu Ser Val Lys Glu Gln Leu Val Ser Gly
35 40 45

Met Met Tyr Tyr Ile Thr Leu Ala Ala Thr
50 55

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<210> 281
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 281

```
Gly Gly Ile Ile Asn Val Pro Asn Pro Asn Ser Pro Glu Phe Gln Asp
1               5                   10                  15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Asn Thr Gln Asn Ala His
            20                  25                  30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Leu Val Ser Gly
        35                  40                  45

Met Met Tyr Tyr Ile Thr Leu Ala Ala Thr Asp Ala Gly Asn Lys Lys
    50                  55                  60

Glu Tyr Glu Ala Lys Ile Trp Val Lys Glu Trp Glu Asp Phe Lys Lys
65                  70                  75                  80

Val Ile Asp Phe Lys Leu Val Gly
                85
```

<210> 282
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 282

```
Gly Gly Ile Ile Asn Val Pro Phe Pro Asn Asn Pro Glu Phe Gln Asp
1               5                   10                  15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Lys Glu Asn Ala His
            20                  25                  30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Leu Val Ala Gly
        35                  40                  45

Met Leu Tyr Tyr Ile Thr Leu Val Ala Ile Asp Ala Gly Lys Lys Lys
    50                  55                  60

Ile Tyr Glu Ala Lys Ile Trp Val Lys Glu Trp Glu Asn Phe Lys Lys
65                  70                  75                  80

Val Ile Glu Phe Lys Leu Ile Gly
                85
```

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<210> 283
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 283

Gly Gly Ile Thr Asn Val Pro Phe Pro Asn Leu Pro Glu Phe Lys Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Lys Glu Asn Ala His
20 25 30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Val Val Ala Gly
35 40 45

Ile Ile Tyr Tyr Ile Thr Leu Val Ala Thr Asp Ala Gly Lys Lys Lys
50 55 60

Ile Tyr Glu Thr Lys Ile Leu Val Lys Gly Trp Glu Asn Phe Lys Glu
65 70 75 80

Val Gln Asp Phe Lys Leu Val Gly
85

<210> 284
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 284

Gly Gly Ile Thr Asn Val Pro Phe Pro Asn Leu Pro Gln Phe Lys Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Lys Glu Asn Ala His
20 25 30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Val Val Ala Gly
35 40 45

Ile Ile Tyr Tyr Ile Thr Leu Val Ala Thr Asp Ala Gly Lys Lys Lys
50 55 60

Ile Tyr Glu Thr Lys Ile Leu Val Lys Gly Trp Glu Asn Phe Lys Glu
65 70 75 80

Val Gln Glu Phe Lys Leu Val Gly
85

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<210> 285
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 285

Gly Gly Ile Ile Ile Val Pro Phe Pro Asn Ser Pro Glu Phe Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Phe Asn Lys Lys Glu Asn Gly His
20 25 30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Glu Gln Val Val Ala Gly
35 40 45

Met Met Tyr Tyr Ile Thr Leu Ala Ala Thr Asp Ala Arg Lys Lys Glu
50 55 60

Ile Tyr Glu Thr Lys Ile Leu Val Lys Glu Trp Glu Asn Phe Lys Glu
65 70 75 80

Val Gln Glu Phe Lys Leu Val Gly
85

<210> 286
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 286

Gly Gly Leu Thr Asp Val Pro Phe Pro Asn Asn Pro Glu Phe Gln Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Lys Lys Glu Asn Gly His
20 25 30

Leu Glu Phe Val Glu Val Leu Asn Val Lys Glu Gln Val Val Ala Gly
35 40 45

Met Met Tyr Tyr Ile Thr Leu Ala Ala Thr
50 55

<210> 287
<211> 88
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 287

Gly Gly Phe Thr Glu Val Pro Phe Pro Asn Ser Pro Glu Phe Gln Asp
1   5   10   15

Leu Thr Arg Phe Ala Val His Gln Tyr Asn Lys Asp Gln Asn Ala His
            20   25   30

Leu Glu Phe Val Glu Asn Leu Asn Val Lys Lys Gln Val Val Ala Gly
        35   40   45

Met Leu Tyr Tyr Ile Thr Phe Ala Ala Thr Asp Gly Gly Lys Lys Lys
    50   55   60

Ile Tyr Glu Thr Lys Ile Trp Val Lys Val Trp Glu Asn Phe Lys Lys
65   70   75   80

Val Val Glu Phe Lys Leu Val Gly
                85

<210> 288
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 288

His Leu Glu Phe Val Glu Val Leu Asn Val Lys Glu Gln Val Val Ala
1   5   10   15

Gly Met Met Tyr Tyr Ile Thr Leu Ala Val Thr Asp Ala Gly Lys Lys
            20   25   30

Lys Ile Tyr Glu Ala Asn Ile Trp Val Lys Glu Trp Glu His Phe Ile
        35   40   45

Lys Val Val Glu Phe Lys Pro Val Ser
    50   55

<210> 289
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 289

Asn Ala His Leu Glu Phe Val Glu Val Leu Asn Val Lys Glu Gln Val
1   5   10   15

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Val Ala Gly Met Met Tyr Tyr Ile Thr Leu Val Ala Thr Asp Asp Gly
20 25 30

Tyr Lys Lys Ile Tyr Lys Thr Lys Ile Trp Val Lys Glu Trp Glu Asn
35 40 45

Phe Lys Glu Val Gln Glu Phe Lys Gln Ile Val
50 55

<210> 290
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 290

Gly Gly Leu Val Asp Val Pro Phe Glu Asn Lys Val Glu Phe Asp Asp
1 5 10 15

Leu Ala Arg Phe Ala Val Gln Asp Tyr Asn Gln Lys Asn Asp Ser Ser
20 25 30

Leu Glu Phe Lys Lys Val Leu Asn Val Lys Gln Gln Ile Val Ala Gly
35 40 45

Ile Met Tyr Tyr Ile Thr Phe Glu Ala Thr Glu Gly Gly Asn Lys Lys
50 55 60

Glu Tyr Glu Ala Lys Ile Leu Leu Arg Lys Trp Glu Asp Leu Lys Lys
65 70 75 80

Val Val Gly Phe Lys Leu Val Gly
85

<210> 291
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 291

Arg Lys Ser Leu Glu His Phe Asn Glu Ile His Ser Thr Lys Tyr Glu
1 5 10 15

Phe Val Arg Phe Ile Lys Ala Asn His Gln Val Ser Ala Gly Met Met
20 25 30

Tyr Phe Ile
35

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<210> 292
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 292

Gly Gly Trp Asn Pro Ile Pro Asp Val Ser Asp Ser His Ile Gln Glu
1 5 10 15

Leu Gly Gly Trp Ala Leu Gly Gln Ala Lys His Gln Lys Leu Ala Ala
20 25 30

Asp Gly Leu Arg Phe Arg Arg Val Val Arg Gly Glu Gln Gln Val Val
35 40 45

Ser Gly Met Asn Tyr Arg Leu Tyr Val Asp Ala Ala Asp
50 55 60

<210> 293
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 293

Gly Gly Trp Asn Pro Ile Pro Asp Val Ser Asp Ser His Ile Gln Glu
1 5 10 15

Leu Gly Gly Trp Ala Leu Gly Gln Ala Lys His Gln Lys Leu Ala Ala
20 25 30

Asp Gly Leu Arg Phe Arg Arg Val Val Arg Gly Glu Gln Gln Val Val
35 40 45

Ser Gly Met Asn Tyr Arg Leu Tyr Val Asp Ala Ala Asp
50 55 60

<210> 294
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 294

Gly Gly Trp Ser Pro Ile Arg Asn Val Ser Asp Pro His Ile Gln Glu
1 5 10 15

Leu Gly Gly Trp Ala Val Thr Glu His Val Arg Arg Ala Asn Asp Gly
20 25 30

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Leu Arg Phe Gly Glu Val Thr Gly Gly Glu Glu Gln Val Val Ser Gly
35 40 45

Met Asn Tyr Lys Leu Val Leu Asp Ala Thr Asp Ala Asp Gly Lys Val
50 55 60

<210> 295
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 295

Gly Gly Trp Lys Pro Ile Lys Asn Val Asn Asp Pro His Val Arg Glu
1 5 10 15

Ile Gly Arg Trp Ala Val Ser Glu His Ile Lys Thr Ala Asn Asp Gly
20 25 30

Leu Gly Phe Gly Arg Val Val Ser Gly Glu Glu Gln Ile Val Ala Gly
35 40 45

Lys Asn Tyr Arg Leu Arg Ile Gln Ala Thr Lys
50 55

<210> 296
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 296

Gly Gly Trp Lys Pro Ile Lys Asn Val Asn Asp Pro His Val Gln Glu
1 5 10 15

Ile Gly Arg Trp Ala Val Ser Glu His Ile Lys Thr Ala Asn Asp Gly
20 25 30

Leu Gly Phe Gly Arg Val Val Ser Gly Glu Glu Gln Ile Val Ala Gly
35 40 45

Lys Asn Tyr Arg Leu Arg Ile Gln Ala Thr Lys
50 55

<210> 297
<211> 58
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 297

Gly Trp Glu Pro Ile Gly Asn Ile Asn Asp Gln His Ile Gln Glu Leu
1 5 10 15

Gly Arg Trp Ala Val Leu Glu Phe Gly Lys His Val Asn Cys Val Leu
20 25 30

Lys Phe Asn Lys Val Val Ser Gly Arg Gln Gln Leu Val Ser Gly Met
35 40 45

Asn Tyr Glu Leu Ile Ile Glu Ala Ser Asp
50 55

<210> 298
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 298

Gly Gly Trp Ser Pro Ile Ser Asp Ala Lys Asp Pro His Val Val Glu
1 5 10 15

Ile Gly Val Phe Ala Val Ser Glu Tyr Asp Lys Gln Ser Lys Ser Gly
20 25 30

Leu Lys Phe Val Thr Val Val Ser Gly Glu Ser Gln Val Ala Ala Gly
35 40 45

Thr Asn Tyr Arg Leu Ile Val Thr Val Asp Gly Ser Ile Gly Val Ala
50 55 60

<210> 299
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 299

Gly Arg Trp Ser Pro Ile Ser Asn Val Lys Asp Pro His Val Val Glu
1 5 10 15

Val Gly Lys Phe Ala Val Ser Glu Tyr Asp Met Glu Ser Lys Ser Glu
20 25 30

Leu Lys Phe Val Val Val Val Ser Gly Glu Ser Lys Val Val Ala Gly
35 40 45

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Thr Asn Tyr Arg Leu Ile Val Ala Val Asn Asp Gly Val Ala Gly Pro
50 55 60

Gly Ala Ser Lys Asn Tyr Glu Ala Ile Val Trp Glu Lys Gln Trp Leu
65 70 75 80

Lys Ser Met Asn Leu Thr Ser Phe Lys Pro Val Val
85 90

<210> 300
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 300

Gly Gly Trp Arg Pro Leu Ser Asp Val Asn Asp Pro His Val Val Glu
1 5 10 15

Ile Gly Lys Phe Ser Val Ser Glu Tyr Asn Lys Gln Ser Lys Ala Gly
20 25 30

Leu Lys Phe Val Ala Val Val Ser Gly Glu Ser Gln Val Val Ala Gly
35 40 45

Met Asn Tyr Arg Leu Ile Val Ala Val Asn Asp Gly Val Glu Thr Ala
50 55 60

Gly Ala Gly Ala Ser Lys Asn Tyr Glu Ala Ile Val Trp Glu Arg Ala
65 70 75 80

Trp Leu Lys Ser Met Asn Leu Thr Ser Phe Lys Pro Ala Ile
85 90

<210> 301
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 301

Gly Gly Trp Ser Pro Ile Ser Asn Val Thr Asp Pro Gln Val Val Glu
1 5 10 15

Ile Gly Glu Phe Ala Val Ser Glu Tyr Asn Lys Arg Ser Glu Ser Gly
20 25 30

Leu Lys Phe Glu Thr Val Val Ser Gly Glu Thr Gln Val Val Ser Gly
35 40 45

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Thr Asn Tyr Arg Leu Lys Val Ala Ala Asn Asp Gly Asp Gly Val Ser
50 55 60

Lys Asn Tyr Leu Ala Ile Val Trp Asp Lys Pro Trp Met Lys Phe Arg
65 70 75 80

Asn Leu Thr Ser Phe Glu Pro Ala Asn
85

<210> 302
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 302

Gly Gly Trp Ser Pro Ile Ser Asn Val Thr Asp Pro Gln Val Val Glu
1 5 10 15

Ile Gly Glu Phe Ala Val Ser Glu Tyr Asn Lys Arg Ser Glu Ser Gly
20 25 30

Leu Lys Phe Glu Thr Val Val Ser Gly Glu Thr Gln Val Val Ser Gly
35 40 45

Thr Asn Tyr Arg Leu Lys Val Ala Ala Asn Asp Gly Asp Gly Val Ser
50 55 60

Lys Asn Tyr Leu Ala Ile Val Trp Asp Lys Pro Trp Met Lys Phe Arg
65 70 75 80

Asn Leu Thr Ser Phe Glu Pro Ala Asn
85

<210> 303
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 303

Gly Gly Trp Ser Pro Ile Ser Asn Val Thr Asp Pro Gln Val Val Glu
1 5 10 15

Ile Gly Glu Phe Ala Val Ser Glu Tyr Asn Lys Arg Ser Glu Ser Gly
20 25 30

Leu Lys Phe Glu Thr Val Val Ser Gly Glu Thr Gln Val Val Ser Gly
35 40 45

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Thr Asn Tyr Arg Leu Lys Val Ala Ala Asn Asp Gly Asp Gly Val Ser
50 55 60

Lys Asn Tyr Leu Ala Ile Val Trp Val Lys Pro Trp Met Lys Phe Arg
65 70 75 80

Asn Leu Thr Ser Phe Glu Pro Ala Asn
85

<210> 304
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 304

Gly Gly Trp Lys Pro Ile Glu Asp Pro Lys Glu Lys His Val Met Glu
1 5 10 15

Ile Gly Gln Phe Ala Val Thr Glu Tyr Asn Lys Gln Ser Lys Ser Ala
20 25 30

Leu Lys Phe Glu Ser Val Glu Lys Gly Glu Thr Gln Val Val Ser Gly
35 40 45

Thr Asn Tyr Arg Leu Ile Leu Val Val Lys Asp Gly Pro Ser Thr Lys
50 55 60

Lys Phe Glu Ala Val Val Trp Glu Lys Pro Trp Glu His Phe Lys Ser
65 70 75 80

Leu Thr Ser Phe Lys Pro Met Val
85

<210> 305
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 305

Gly Ser Arg Lys Pro Ile Lys Asn Val Ser Asp Pro Asp Val Val Ala
1 5 10 15

Val Ala Lys Tyr Ala Ile Glu Glu His Asn Lys Glu Ser Lys Glu Asn
20 25 30

Leu Val Phe Val Lys Val Val Glu Gly Thr Thr Gln Val Val Ser Gly
35 40 45

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Thr Lys Tyr Asp Leu Lys Ile Ala Ala Lys Asp Gly Gly Gly Lys Ile
50 55 60

Lys Asn Tyr Glu Ala Val Val Val Glu Lys Leu Trp Leu His Ser Lys
65 70 75 80

Ser Leu Glu Ser Phe Lys
85

<210> 306
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 306

Gly Ser Arg Lys Pro Ile Lys Asn Val Ser Asp Pro Asp Val Val Ala
1 5 10 15

Val Ala Lys Tyr Ala Ile Glu Glu His Asn Lys Glu Ser Lys Glu Lys
20 25 30

Leu Val Phe Val Lys Val Val Glu Gly Thr Thr Gln Val Val Ser Gly
35 40 45

Thr Lys Tyr Asp Leu Lys Ile Ala Ala Lys Asp Gly Gly Gly Lys Ile
50 55 60

Lys Asn Tyr Glu Ala Val Val Val Glu Lys Leu Trp Leu His Ser Lys
65 70 75 80

Ser Leu Glu Ser Phe Lys
85

<210> 307
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 307

Gly Gln Tyr Val Lys Ile Glu Asn Val Lys Asp Pro Tyr Val Gln Gly
1 5 10 15

Val Gly Glu Trp Ala Val Lys Glu His Asn Arg Gln Thr Gly Glu Ser
20 25 30

Leu Gln Phe Ala Glu Val Val Ser Gly Met Glu Gln Val Val Ala Gly
35 40 45

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Thr Asn Tyr Lys Leu Asn Leu Ala
50 55

<210> 308
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 308

Gly Gly Trp Arg Pro Ile Glu Ser Leu Asn Ser Ala Glu Val Gln Asp
1 5 10 15

Val Ala Gln Phe Ala Val Ser Glu His Asn Lys Gln Ala Asn Asp Glu
20 25 30

Leu Gln Tyr Gln Ser Val Val Arg Gly Tyr Thr Gln Val Val Ala Gly
35 40 45

Thr Asn Tyr Arg Leu Val Ile Ala Ala Lys Asp Gly
50 55 60

<210> 309
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 309

Gly Gly Trp Arg Pro Ile Glu Asn Leu Asn Ser Ala Glu Val Gln Asp
1 5 10 15

Val Ala Gln Phe Ala Val Ser Glu His Asn Lys Gln Ala Asn Asp Glu
20 25 30

Leu Gln Tyr Gln Ser Val Val Arg Gly Tyr Thr Gln Val Val Ser Gly
35 40 45

Thr Asn Tyr Arg Leu Val Ile Ala Ala Lys Asp Gly
50 55 60

<210> 310
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 310

Gly Gly Trp Arg Pro Ile Lys Asp Leu Asn Ser Ala Glu Val Gln Asp
1 5 10 15

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Val Ala Gln Phe Ala Val Ser Glu His Asn Lys Gln Ala Asn Asp Lys
20 25 30

Leu Gln Tyr Gln Arg Val Val Arg Gly Tyr Ser Gln Val Val Ala Gly
35 40 45

Thr Asn Tyr Arg Leu Val Ile Ala Ala Lys Asp Gly
50 55 60

<210> 311
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 311

Pro Gly Trp Gln Ser Val Pro Ala His Asp Pro Gln Val Gln Asp Ala
1 5 10 15

Ala Asn His Ala Ile Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Val
20 25 30

Pro Tyr Glu Leu His Glu Val Thr Asp Ala Lys
35 40

<210> 312
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 312

Pro Gly Trp Gln Ser Val Pro Ala His Asp Pro Gln Val Gln Asp Ala
1 5 10 15

Ala Asn His Ala Ile Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Val
20 25 30

Pro Tyr Glu Leu His Glu Val Thr Asp Ala Lys
35 40

<210> 313
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 313

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Pro Gly Trp Gln Ser Val Pro Pro His Asp Pro Gln Val Gln Asp Ala
1 5 10 15

Ala Asn His Ala Val Lys Ser Leu Gln Gln Arg Ser Asn Ser Leu Leu
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Gln
35 40

<210> 314
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 314

Pro Gly Trp Gln Asp Val His Pro Gln Asp Pro Gln Val Gln Asp Ala
1 5 10 15

Ala Asn His Ala Val Lys Ser Leu Gln Gln Lys Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Lys Ser Glu Val
35 40 45

<210> 315
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 315

Pro Gly Trp Arg Asp Val Pro Val His Asp Pro Val Val Lys Asp Ala
1 5 10 15

Ala Ser His Ala Val Lys Ser Ile Gln Gln Arg Ser Asn Ser Leu Leu
20 25 30

Pro Tyr Glu Leu Val Glu Ile Val Arg Ala Lys Ala Glu Val Val
35 40 45

<210> 316
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 316

Pro Gly Trp Arg Asp Val Pro Val His Asp Pro Val Val Lys Asp Ala
1 5 10 15

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Ala Asp His Ala Val Lys Ser Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Ile Val Arg Ala Lys Ala Glu Val Val
35 40 45

<210> 317
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 317

Pro Gly Trp Arg Glu Val Pro Val Glu Asp Pro Val Val Lys Asp Ala
1 5 10 15

Ala His His Ala Val Lys Ser Ile Gln Glu Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Ile Leu Arg Ala His Ala Gln Val Val
35 40 45

<210> 318
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 318

Pro Gly Trp Arg Glu Val Pro Val Glu Asp Pro Val Val Lys Asp Ala
1 5 10 15

Ala His His Ala Val Lys Ser Ile Gln Glu Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Ile Leu Arg Ala His Ala Gln Val Val
35 40 45

<210> 319
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 319

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Lys His Val
1 5 10 15

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Ala Glu Gln Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Val Val His Ala Lys Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Leu Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu Val His Lys Asn His Glu Gly Ala Leu
65 70 75 80

His Val Asn His Ala Glu Gln His His
85

<210> 320
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 320

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Lys His Val
1 5 10 15

Ala Glu Gln Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Val Val His Ala Lys Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Leu Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu
65 70

<210> 321
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 321

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Lys His Val
1 5 10 15

Ala Glu Gln Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

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Pro Tyr Glu Leu Leu Glu Val Val His Ala Lys Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Leu Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu
65 70

<210> 322
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 322

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Lys His Ala
1 5 10 15

Ala Glu Gln Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Leu Glu Val Val His Ala Lys Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Leu Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu
65 70

<210> 323
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 323

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Gln His Val
1 5 10 15

Ala Asp His Ala Val Lys Ser Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Asn Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Val Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

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Glu Glu Lys Phe Lys Val Glu Val His Lys Asn His Glu Gly Val Leu
65 70 75 80

His Leu Asn His Met Glu Gln Gln His
85

<210> 324
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 324

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Gln His Val
1 5 10 15

Ala Asp His Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Asn Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Val Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu Val His Lys Asn His Glu Gly Val Leu
65 70 75 80

His Leu Asn His Met Glu Gln Gln His
85

<210> 325
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 325

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Gln His Val
1 5 10 15

Ala Asp His Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Asn Ala Glu Val Thr Gly
35 40 45

Glu Ala Ala Lys Tyr Asn Met Val Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

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Glu Glu Lys Phe Lys Val Glu Val His Lys Asn His Glu Gly Val Leu
65 70 75 80

His Leu Asn His Met Glu Gln His His
85

<210> 326
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 326

Ser Gly Trp Arg Glu Val Pro Gly Asp Asp Pro Glu Val Gln His Val
1 5 10 15

Ala Glu His Ala Val Lys Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Gln Glu Val Val His Ala Asn Ala Glu Val Thr Gly
35 40 45

Glu Thr Ala Lys Phe Asn Met Leu Leu Lys Leu Lys Arg Gly Glu Lys
50 55 60

Glu Glu Lys Phe Lys Val Glu Val His Lys Asn His Glu Gly Ala Leu
65 70 75 80

His Leu Asn His Met Glu Gln His His
85

<210> 327
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 327

Ser Gly Trp Arg Pro Val Pro Val His Asp Pro Val Val Gln Asp Ala
1 5 10 15

Ala His His Ala Ile Lys Thr Ile Gln Glu Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Glu Leu Ser Glu Val Val His Ala Asn Ala Glu Val Val
35 40 45

<210> 328
<211> 47
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 328

Ala Glu Trp Lys Glu Val Ala Ala His Asp Pro Val Val Gln Asp Ala
1 5 10 15

Ala Thr His Ala Val Asn Thr Ile Gln Gln Arg Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Gln Leu Gln Glu Ile Val His Ala Lys Ala Gln Val Val
35 40 45

<210> 329
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 329

Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro Glu Val Gln Glu Ala
1 5 10 15

Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg Ala Lys Val Val Glu
35 40 45

Glu Arg Val Lys Phe Glu Leu Leu Leu Lys Leu Glu Arg Gly Asn
50 55 60

<210> 330
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 330

Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro Glu Val Gln Glu Ala
1 5 10 15

Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys Ser Asn Ser Leu Phe
20 25 30

Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg Ala Lys Val Val Glu
35 40 45

Glu Arg Val Lys Phe Glu Leu Leu Leu Lys Leu Glu Arg Gly Asn
50 55 60

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<210> 331
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 331

Leu Tyr Val Gln Val Ile Gln Ala Ile Asn Asn Ser Val Val Asn Pro
1 5 10 15

Ser Ala Arg Ile Cys Cys Pro Val Val Glu Ile Thr Leu Gly Asn Tyr
20 25 30

Lys Ser Ser Thr Lys Asn Leu Pro Met Gly Pro Asn Met Asp Trp Asn
35 40 45

Gln Val Phe Ala Phe Asp Lys Ser Lys Gly Asp Val Leu Ser Val Thr
50 55 60

Leu Lys Asp Gly Pro Thr Asn Thr Val Ile Asn Lys Arg Asn
65 70 75

<210> 332
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 332

Leu Tyr Val Asp Val Ile Arg Ala Ile Lys Asn Ser Asp Val Asp Pro
1 5 10 15

Gly Pro Cys Asp Pro Val Val Glu Ile Thr Leu Gly Asn Tyr Lys Ser
20 25 30

Ser Thr Lys Asp Leu Pro Val Gly Pro Asn Met Asp Trp Asn Gln Val
35 40 45

Phe Ala Phe Asp Lys Thr Lys Gly Asp Val Leu Ser Val Thr Leu Lys
50 55 60

Asp Arg
65

<210> 333
<211> 71
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 333

Leu Tyr Val Arg Val Val Arg Ala Arg Gly Val Ala Ala Val Gly Glu
1   5   10   15

Thr Val Ala Glu Val Lys Leu Gly Asn Tyr Arg Gly Val Thr Pro Ala
            20   25   30

Thr Ala Ala His His Trp Asp Gln Val Phe Ala Phe Ser Lys Glu Thr
        35   40   45

Ile Gln Ser Ser Phe Val Glu Val Phe Val Arg Ala Arg Gly Ser Asp
    50   55   60

Asp His Val Gly Arg Val Trp
65   70

<210> 334
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 334

Leu Tyr Val Asn Ile Val Lys Ala Lys Asp Leu Ser Val Leu Gly Glu
1   5   10   15

Val Val Ser Glu Val Lys Leu Gly Asn Tyr Arg Gly Val Thr Lys Lys
            20   25   30

Val Ser Ser Asn Ser Ser Asn Pro Glu Trp Asn Gln Val Phe Val Phe
        35   40   45

Ser Lys Glu Arg Ile Gln Ser Ser Val Val Glu Leu Phe Val Lys Glu
    50   55   60

Gly Asn Lys Asp Glu Tyr Thr Gly Arg Val Leu
65   70   75

<210> 335
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 335

Leu Tyr Val Arg Val Val Lys Ala Arg Gly Leu Lys Trp Ser Gly Glu
1   5   10   15

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Phe Asp Pro Phe Ala Glu Leu Arg Leu Gly Gly Tyr Ser Cys Ile Thr
20 25 30

Arg His Val Glu Lys Thr Ala Ser Pro Glu Trp Asp Asp Val Phe Ala
35 40 45

Phe Ser Arg Glu Arg Ile His Ala Pro Phe Leu Asp Val Leu Val Arg
50 55 60

Gly Arg Gly Phe Ala Lys Asp Asp Tyr Val Gly Ser Thr Arg
65 70 75

<210> 336
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 336

Leu Tyr Val Arg Val Val Arg Arg Leu Thr Ala Ala Ala Ser Thr Val
1 5 10 15

Ala Gly Gly Gly Gly Cys Asn Pro Tyr Val Glu Val Arg Leu Gly Asn
20 25 30

Tyr Arg Gly Thr Thr Arg His His Glu Arg Lys Ala Ala Pro Glu Trp
35 40 45

Asn Gln Val Phe Ala Phe Ser Arg Glu Arg Val Gln Ala Ser Val Leu
50 55 60

Glu Val Phe Val Arg Asp Lys Asp Ala Val Ala Ala Val Ala Arg Asp
65 70 75 80

Gly Tyr Val Gly Arg Val Ala
85

<210> 337
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 337

Leu Tyr Val Arg Val Val Lys Ala Arg Glu Leu Pro Ile Met Asp Ile
1 5 10 15

Thr Gly Ser Val Asp Pro Phe Val Glu Val Arg Val Gly Asn Tyr Lys
20 25 30

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Gly Ile Thr Arg His Phe Glu Lys Arg Gln His Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ala Lys Glu Arg Met Gln Ala Ser Val Leu Glu Val
50 55 60

Val Val Lys Asp Lys Asp Leu Leu Lys Asp Asp Tyr Val Gly Phe Val
65 70 75 80

Arg

<210> 338
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 338

Leu Tyr Val Arg Val Val Lys Ala Arg Glu Leu Pro Ile Met Asp Ile
1 5 10 15

Thr Gly Ser Val Asp Pro Phe Val Glu Val Arg Val Gly Asn Tyr Lys
20 25 30

Gly Ile Thr Arg His Phe Glu Lys Arg Gln His Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ala Lys Glu Arg Met Gln Ala Ser Val Leu Glu Val
50 55 60

Val Val Lys Asp Lys Asp Leu Leu Lys Asp Asp Tyr Val Gly Phe Val
65 70 75 80

Arg

<210> 339
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 339

Leu Phe Val Arg Val Val Lys Ala Arg Asp Leu Pro Asp Met Asp Val
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Glu Val Arg Val Gly Asn Tyr Arg
20 25 30

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Gly Ile Thr Arg His Phe Glu Lys Gln Lys Asn Pro Glu Trp Asn Ala
35 40 45

Val Phe Ala Phe Ser Arg Asp Arg Met Gln Ala Thr Ile Leu Glu Val
50 55 60

Val Val Lys Asp Lys Asp Leu Leu Lys Asp Asp Phe Val Gly Leu Val
65 70 75 80

Arg

<210> 340
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 340

Leu Phe Val Arg Val Val Lys Ala Arg Asp Leu Pro Asp Met Asp Val
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Glu Val Arg Tyr Gly Asn Tyr Arg
20 25 30

Gly Ile Thr Arg His Phe Glu Lys Gln Lys Asn Pro Glu Trp Asn Ala
35 40 45

Val Phe Ala Phe Ser Arg Asp Arg Met Gln Ala Thr Ile Leu Glu Val
50 55 60

Val Val Lys Asp Lys Asp Leu Leu Lys Asp Asp Phe Val Gly Leu Val
65 70 75 80

Arg

<210> 341
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 341

Leu Phe Val Arg Val Val Lys Ala Arg Asp Leu Pro His Met Asp Ile
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Glu Val His Leu Gly Asn Tyr Lys
20 25 30

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Met Lys Thr Arg His Phe Glu Lys Asn Gln Arg Pro Glu Trp Asp Glu
35 40 45

Val Phe Ala Phe Pro Arg Glu Val Met Gln Ser Thr Ser Leu Glu Val
50 55 60

Ile Val Lys Asp Lys Asp Phe Ile Arg Asp Asp Tyr Val Gly Arg Val
65 70 75 80

Ser

<210> 342
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 342

Leu Tyr Val Arg Val Val Lys Ala Arg Asp Leu Pro Asn Lys Asp Leu
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Val Val Lys Ile Gly Asn Phe Lys
20 25 30

Gly Val Thr Thr His Phe Asn Lys Asn Thr Asp Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ala Lys Asp Asn Leu Gln Ser Asn Phe Leu Glu Val
50 55 60

Met Val Lys Asp Lys Asp Ile Leu Leu Asp Asp Phe Val Gly Ile Val
65 70 75 80

Lys

<210> 343
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 343

Leu Tyr Val Arg Val Val Lys Ala Arg Asp Leu Pro Asn Lys Asp Leu
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Val Val Lys Ile Gly Asn Phe Lys
20 25 30

Gly Val Thr Thr His Phe Asn Lys Asn Thr Asp Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ala Lys Asp Asn Leu Gln Ser Asn Phe Leu Glu Val
50 55 60

Met Val Lys Asp Lys Asp Ile Leu Leu Asp Asp Phe Val Gly Ile Val
65 70 75 80

Lys

<210> 344
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 344

Leu Phe Ile Arg Val Val Lys Ala Arg Asp Leu Pro Arg Met Asp Leu
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Val Ile Val Lys Val Gly Asn Phe Lys
20 25 30

Gly Thr Thr Asn His Phe Glu Lys Asn Asn Ser Pro Glu Trp Asn Leu
35 40 45

Val Phe Ala Phe Ala Lys Glu Asn Gln Gln Ala Thr Thr Leu Glu Val
50 55 60

Val Ile Lys Asp Lys Asp Thr Ile His Asp Asp Phe Val Gly Thr Val
65 70 75 80

Arg

<210> 345
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 345

Leu Tyr Val Ser Val Val Lys Ala Arg Asp Leu Pro Val Met Asp Val
1 5 10 15

Ser Gly Ser Leu Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
20 25 30

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Gly Leu Thr Lys His Leu Glu Lys Asn Ser Asn Pro Ile Trp Lys Gln
35 40 45

Ile Phe Ala Phe Ser Lys Glu Arg Leu Gln Ser Asn Leu Leu Glu Val
50 55 60

Thr Val Lys Asp Lys Asp Leu Leu Thr Lys Asp Asp Phe Val Gly Arg
65 70 75 80

Val His

<210> 346
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 346

Leu Tyr Val Ser Val Val Lys Ala Arg Asp Leu Pro Val Met Asp Val
1 5 10 15

Ser Gly Ser Leu Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
20 25 30

Gly Leu Thr Lys His Leu Glu Lys Asn Ser Asn Pro Ile Trp Lys Gln
35 40 45

Ile Phe Ala Phe Ser Lys Glu Arg Leu Gln Ser Asn Leu Leu Glu Val
50 55 60

Thr Val Lys Asp Lys Asp Leu Leu Thr Lys Asp Asp Phe Val Gly Arg
65 70 75 80

Val His

<210> 347
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 347

Leu Tyr Val Ser Val Val Lys Ala Arg Asp Leu Pro Asn Met Asp Ile
1 5 10 15

Thr Gly Ala Leu Asp Pro Tyr Val Glu Val Arg Leu Gly Asn Phe Lys
20 25 30

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Gly Val Thr Arg His Leu Glu Lys Asn Pro Asn Pro Val Trp Arg Gln
35 40 45

Val Phe Ala Phe Ser Arg Asp His Leu Gln Ser Ser Gln Leu Glu Val
50 55 60

Val Val Lys Asp Lys Asp Val Leu Lys Asp Asp Phe Val Gly Arg Val
65 70 75 80

Val

<210> 348
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 348

Leu Phe Ile Lys Ile Val Lys Ala Arg Asn Leu Pro Ser Met Asp Leu
1 5 10 15

Thr Gly Ser Leu Asp Pro Tyr Ile Glu Val Lys Leu Gly Asn Tyr Thr
20 25 30

Gly Lys Thr Lys His Phe Glu Lys Asn Gln Asn Pro Val Trp Asn Glu
35 40 45

Val Phe Ala Phe Ser Lys Ser Asn Gln Gln Ser Asn Val Leu Glu Val
50 55 60

Ile Val Met Asp Lys Asp Met Val Lys Asp Asp Phe Val Gly Leu Ile
65 70 75 80

Arg

<210> 349
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 349

Leu Tyr Val Arg Val Val Lys Ala Lys Asp Leu Pro Pro Gly Thr Ile
1 5 10 15

Thr Ser Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Arg
20 25 30

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Gly Arg Thr Lys His Leu Glu Lys Lys Leu Asn Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ser Lys Asp Arg Ile Gln Ser Ser Val Leu Glu Val
50 55 60

Phe Val Lys Asp Lys Glu Met Val Gly Arg Asp Asp Tyr Leu Gly Arg
65 70 75 80

Val Ile

<210> 350
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 350

Leu Tyr Val Arg Val Val Lys Ala Lys Asn Leu Thr Leu Asn Ser Leu
1 5 10 15

Thr Ser Thr Cys Asp Pro Tyr Val Glu Val Arg Leu Gly Asn Tyr Lys
20 25 30

Gly Arg Thr Lys His Leu Asp Lys Arg Ser Asn Pro Glu Trp Asn Gln
35 40 45

Val Tyr Ala Phe Ser Lys Asp Gln Ile Gln Ser Ser Ile Val Ile Val
50 55 60

Lys Asp Lys Glu Thr Val Gly Arg Asp Asp Tyr Ile Gly Arg Val Ala
65 70 75 80

<210> 351
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 351

Leu Tyr Val Arg Val Val Lys Ala Lys Asp Leu Pro Pro Asn Pro Val
1 5 10 15

Thr Ser Asn Cys Asp Pro Tyr Val Glu Val Lys Ile Gly Asn Tyr Lys
20 25 30

Gly Lys Thr Lys His Phe Glu Lys Arg Thr Asn Pro Glu Trp Asn Gln
35 40 45

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Val Phe Ala Phe Ser Lys Asp Lys Val Gln Ser Ser Thr Val Glu Val
50 55 60

Phe Val Arg Asp Lys Glu Met Val Thr Arg Asp Glu Tyr Ile Gly Lys
65 70 75 80

Val Val

<210> 352
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 352

Leu Tyr Val Arg Val Val Lys Ala Lys Glu Leu Pro Pro Gly Ser Ile
1 5 10 15

Thr Gly Gly Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
20 25 30

Gly Arg Thr Lys Ile Phe Asp Arg Lys Thr Thr Ile Pro Glu Trp Asn
35 40 45

Gln Val Phe Ala Phe Thr Lys Glu Arg Ile Gln Ser Ser Val Leu Glu
50 55 60

Val Phe Val Lys Asp Lys Glu Thr Leu Gly Arg Asp Asp Ile Leu Gly
65 70 75 80

Lys Val Val

<210> 353
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 353

Leu Tyr Val Arg Val Val Lys Ala Lys Glu Leu Pro Gly Lys Asp Met
1 5 10 15

Thr Gly Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
20 25 30

Gly Thr Thr Arg His Phe Glu Lys Lys Ser Asn Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ser Lys Asp Arg Ile Gln Ala Ser Phe Leu Glu Ala
50 55 60

Thr Val Lys Asp Lys Asp Phe Val Lys Asp Asp Leu Ile Gly Arg Val
65 70 75 80

Val

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<210> 354
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 354

Leu Tyr Val Arg Val Val Lys Ala Lys Glu Leu Pro Gly Lys Asp Met
1 5 10 15

Thr Gly Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
20 25 30

Gly Thr Thr Arg His Phe Glu Lys Lys Ser Asn Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ser Lys Asp Arg Ile Gln Ala Ser Phe Leu Glu Ala
50 55 60

Thr Val Lys Asp Lys Asp Phe Val Lys Asp Asp Leu Ile Gly Arg Val
65 70 75 80

Val

<210> 355
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 355

Leu Tyr Val Arg Val Val Lys Ala Lys Glu Leu Pro Gly Lys Asp Leu
1 5 10 15

Thr Gly Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Arg
20 25 30

Gly Thr Thr Arg His Phe Glu Lys Lys Ser Asn Pro Glu Trp Asn Gln
35 40 45

Val Phe Ala Phe Ser Lys Asp Arg Val Gln Ala Ser Tyr Leu Glu Ala
    50   55   60

Thr Val Lys Asp Lys Asp Leu Val Lys Asp Asp Leu Ile Gly Arg Val
65   70   75   80

Val

<210> 356
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 356

Leu Tyr Val Arg Val Val Lys Ala Lys Glu Leu Pro Gly Lys Asp Val
1   5   10   15

Thr Gly Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Arg
            20   25   30

Gly Met Thr Lys His Phe Glu Lys Arg Ser Asn Pro Glu Trp Lys Gln
        35   40   45

Val Phe Ala Phe Ser Lys Glu Arg Ile Gln Ala Ser Ile Leu Glu Val
    50   55   60

Val Val Lys Asp Lys Asp Val Val Leu Asp Asp Leu Ile Gly Arg Ile
65   70   75   80

Met

<210> 357
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 357

Leu Tyr Val Arg Val Val Lys Ala Lys Asp Leu Pro Ser Lys Asp Ile
1   5   10   15

Thr Gly Ser Cys Asp Pro Tyr Val Glu Val Lys Leu Gly Asn Tyr Lys
            20   25   30

Gly Thr Thr Arg His Phe Glu Lys Lys Thr Asn Pro Glu Trp Asn Gln
        35   40   45

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Val Phe Ala Phe Ser Lys Glu Arg Ile Gln Ser Ser Val Val Glu Ile
50 55 60

Ile Val Lys Asp Lys Asp Phe Val Lys Asp Asp Phe Ile Gly Arg Val
65 70 75 80

Leu

<210> 358
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 358

Leu Tyr Val His Val Val Lys Ala Lys Asp Leu Pro Ala Val Ser Ala
1 5 10 15

Ala Gly Thr Ile Asp Pro Phe Val Glu Val Lys Leu Gly Asn Phe Lys
20 25 30

Gly Thr Thr Pro Val Leu Gly Gly Asn His Asn Pro Ser Trp Lys Gln
35 40 45

Val Phe Ala Phe Ser Ala Thr His Leu Gln Ala His Val Leu Glu Val
50 55 60

Ala Val Lys Ala Lys Asp Leu Ala Gly Gly Asp Asp Leu Ile Gly Arg
65 70 75 80

Val Gly

<210> 359
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 359

Leu Tyr Ile Arg Ile Val Lys Ala Arg Ala Leu Pro Ser Asn Asp Leu
1 5 10 15

Phe Val Glu Val Thr Ile Gly Arg Tyr Lys Gly Arg Thr Lys Arg Ser
20 25 30

Thr Asn Pro Tyr Pro Asn Leu Glu Phe Asp Glu Val Phe Ala Phe Asn
35 40 45

Ser Asp Arg Leu Gln Gly Asn Met Leu Glu Val Met Lys Lys Met Asn
    50   55   60

Glu Glu Glu Ile Ile Gly Gln Cys Arg
65   70

<210> 360
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 360

Leu Tyr Ile Arg Ile Val Lys Ala Arg Ala Leu Pro Ser Asn Asp Leu
1   5   10   15

Phe Val Glu Val Thr Ile Gly Arg Tyr Lys Gly Arg Thr Lys Arg Ser
            20   25   30

Thr Asn Pro Tyr Pro Asn Leu Glu Phe Asp Glu Val Phe Ala Phe Asn
        35   40   45

Ser Asp Arg Leu Gln Gly Asn Met Leu Glu Val Met Lys Lys Met Asn
    50   55   60

Glu Glu Glu Ile Ile Gly Gln Cys Arg
65   70

<210> 361
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 361

Leu Tyr Ala Arg Ile Val Arg Ala Arg Ala Leu Pro Val Asn Asp Ser
1   5   10   15

Phe Val Ala Val Lys Ile Gly Ser Tyr Lys Gly Arg Thr Lys Gln Ile
            20   25   30

Leu Asn Ser Asn Pro Asn Pro Glu Phe His Glu Thr Phe Ala Phe Thr
        35   40   45

Lys Thr Arg Leu Gln Gly Asp Ile Leu Glu Val Val Val Arg Asn Arg
    50   55   60

Asp Asn Pro Asn Glu Asp Asp Ile Val Gly Lys Cys Lys
65   70   75

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<210> 362
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 362

```
Leu Phe Val Arg Val Ile Lys Ala Arg Lys Leu Pro Asp Met Asp Ala
1               5                   10                  15

Asn Gly Ser Leu Asp Pro Tyr Val Glu Val Lys Phe Gly Ala Tyr Asn
            20                  25                  30

Arg Gly Val Thr Arg Cys Phe Lys Arg Asn Lys Asn Pro Glu Trp Asn
        35                  40                  45

Glu Thr Phe Ala Phe Ser Phe Gln His Asp Lys Ile Pro Ser Pro Thr
    50                  55                  60

Val Asp Ile Val Val Asn Asp Lys Asp Leu Val Arg Asp Asp Phe Val
65                  70                  75                  80

Gly Lys Leu His
```

<210> 363
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 363

```
Leu Phe Val Arg Ile Val Lys Arg Leu Pro Pro Asn Glu Ser Ala Tyr
1               5                   10                  15

Val Lys Val Arg Thr Ser Asn His Phe Val Arg Ser Lys Pro Ala Val
            20                  25                  30

Asn Arg Pro Gly Glu Ser Val Asp Ser Pro Glu Trp Asn Gln Val Phe
        35                  40                  45

Ala Leu Gly His Asn Arg Ser Asp Ser Ala Val Thr Gly Ala Thr Leu
    50                  55                  60

Glu Ile Ser Ala Trp Asp Ala Ser Ser Glu Ser Phe Leu Gly Gly Val
65                  70                  75                  80

Cys
```

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<210> 364
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 364

Leu Phe Val Arg Ile Val Lys Arg Leu Pro Pro Asn Glu Ser Ala Tyr
1 5 10 15

Val Lys Val Arg Thr Ser Asn His Phe Val Arg Ser Lys Pro Ala Val
20 25 30

Asn Arg Pro Gly Glu Ser Val Asp Ser Pro Glu Trp Asn Gln Val Phe
35 40 45

Ala Leu Gly His Asn Arg Ser Asp Ser Ala Val Thr Gly Ala Thr Leu
50 55 60

Glu Ile Ser Ala Trp Asp Ala Ser Ser Glu Ser Phe Leu Gly Gly Val
65 70 75 80

Cys

<210> 365
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 365

Leu Phe Val Arg Val Val Lys Val Arg Gly Ile Arg Ala Cys Glu Gly
1 5 10 15

Pro Tyr Val Lys Ile Gln Ala Gly Pro His Thr Leu Arg Ser Arg Pro
20 25 30

Gly Arg Asp Val Ser Gly Thr Gly Asn Pro Glu Trp Asn Gln Val Phe
35 40 45

Ala Ile Asn His Ala Lys Pro Glu Pro Thr Leu Glu Ile Ser Val Trp
50 55 60

Asp Gly Gly Ala Pro Ser Pro Ile Glu Ala Phe Leu Gly Gly Val Cys
65 70 75 80

<210> 366
<211> 85
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 366

Leu Phe Val Arg Val Val Arg Arg Leu Pro Ala Gly Ala His Pro His
1 5 10 15

Val Arg Val Ala Ala Gly Gly Arg His Ala Ser Thr Arg Glu Ala Arg
20 25 30

Arg Gly Ala Phe Phe Glu Trp Asp Gln Thr Phe Ala Phe Val Arg Asp
35 40 45

Pro Gly Ala Thr Asp Ser Pro Gly Pro Thr Leu Glu Val Ser Val Trp
50 55 60

Asp Leu Pro Pro Asp Ala Asp Val Ser Asp Ala Asp Asp Arg His Phe
65 70 75 80

Leu Gly Gly Leu Cys
85

<210> 367
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 367

Val Phe Ile Arg Val Val Lys Ala Arg Ser Leu Pro Thr Ser Gly Ser
1 5 10 15

Pro Val Thr Lys Ile Ser Leu Ser Gly Thr Met Ile Gln Ser Lys Pro
20 25 30

Ala Arg Lys Thr Ser Cys Phe Glu Trp Asp Gln Thr Phe Ala Phe Leu
35 40 45

Arg Asp Ser Pro Asp Leu Ser Ser Ser Pro Ile Leu Glu Ile Ser Val
50 55 60

Trp Asp Ser Ser Thr Gly Ile Glu Thr Ser Gln Phe Leu Gly Gly Ile
65 70 75 80

Cys

<210> 368
<211> 89
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 368

Leu Glu Val His Leu Val Asp Ala Lys Gly Leu Thr Gly Asn Asp Phe
1   5   10   15

Leu Gly Glu Ile Gly Lys Ile Asp Pro Tyr Val Val Val Gln Tyr Arg
            20   25   30

Ser Gln Glu Arg Lys Ser Ser Val Ala Arg Asp Gln Gly Lys Asn Pro
        35   40   45

Ser Trp Asn Glu Val Phe Lys Phe Gln Ile Asn Ser Thr Ala Ala Thr
    50   55   60

Gly Gln His Lys Leu Phe Leu Arg Leu Met Asp His Asp Thr Phe Ser
65   70   75   80

Arg Asp Asp Phe Leu Gly Glu Ala Thr
                85

<210> 369
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 369

Met Asp Pro Tyr Val Ile Leu Thr Cys Arg Thr Gln Glu Gln Lys Ser
1   5   10   15

Ser Val Ala Lys Gly Ala Gly Ser Glu Pro Glu Trp Asn Glu Thr Phe
            20   25   30

Val Phe Thr Val Ser Asp Asp Val Pro Gln Leu Asn Val Lys Ile Met
        35   40   45

Asp Ser Asp Ala Phe Ser Ala Asp Asp Phe Val Gly Glu Ala Asn
    50   55   60

<210> 370
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 370

Leu Glu Val Leu Leu Val Cys Ala Lys Gly Leu Glu Asp Thr Asp Phe
1   5   10   15

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Leu Asn Asp Met Asp Pro Tyr Val Ile Leu Thr Cys Arg Thr Gln Glu
20 25 30

Gln Lys Ser Ser Val Ala Lys Gly Ala Gly Ser Glu Pro Glu Trp Asn
35 40 45

Glu Thr Phe Val Phe Thr Val Ser Asp Asp Val Pro Gln Leu Asn Val
50 55 60

Lys Ile Met Asp Ser Asp Ala Phe Ser Ala Asp Asp Phe Val Gly Glu
65 70 75 80

Ala Asn

<210> 371
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 371

Leu Glu Val Leu Leu Val Ser Ala Lys Gly Leu Glu Asp Thr Asp Phe
1 5 10 15

Leu Asn Asn Met Asp Pro Phe Val Ile Leu Thr Cys Arg Thr Gln Glu
20 25 30

Gln Lys Ser Ser Val Ala Asn Gly Ala Gly Ser Glu Pro Glu Trp Asn
35 40 45

Glu Thr Phe Val Phe Thr Val Ser Asp Asp Thr Pro Gln Leu His Leu
50 55 60

Lys Ile Met Asp Ser Asp Leu Thr Asn Asp Asp Phe Val Gly Glu Arg
65 70 75 80

Thr

<210> 372
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 372

Leu Glu Val Leu Leu Val Ser Ala Lys Gly Leu Glu Asp Thr Asp Phe
1 5 10 15

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Leu Asn Asn Met Asp Pro Phe Val Ile Leu Thr Cys Arg Thr Gln Glu
20 25 30

Gln Lys Ser Ser Val Ala Asn Gly Ala Gly Ser Glu Pro Glu Trp Asn
35 40 45

Glu Thr Phe Val Phe Thr Val Ser Asp Asp Thr Pro Gln Leu His Leu
50 55 60

Lys Ile Met Asp Ser Asp Leu Thr Asn Asp Asp Phe Val Gly Glu Ala
65 70 75 80

Thr

<210> 373
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 373

Leu Glu Val Val Leu Val Ser Ala Lys Gly Leu Glu Asp Ala Asp Phe
1 5 10 15

Leu Asn Asn Met Asp Pro Tyr Val Gln Leu Thr Cys Arg Thr Gln Asp
20 25 30

Gln Lys Ser Asn Val Ala Glu Gly Met Gly Thr Thr Pro Glu Trp Asn
35 40 45

Glu Thr Phe Ile Phe Thr Val Ser Glu Gly Thr Thr Glu Leu Lys Ala
50 55 60

Lys Ile Phe Asp Lys Asp Val Gly Thr Glu Asp Asp Ala Val Gly Glu
65 70 75 80

Ala Thr

<210> 374
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 374

Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu Glu Asn Thr Asp Tyr
1 5 10 15

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Leu Cys Asn Met Asp Pro Tyr Ala Val Leu Lys Cys Arg Ser Gln Glu
20 25 30

Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Ser Asp Pro Glu Trp Asn
35 40 45

Glu Thr Phe Met Phe Ser Val Thr His Asn Ala Thr Glu Leu Ile Ile
50 55 60

Lys Leu Met Asp Ser Asp Ser Gly Thr Asp Asp Asp Phe Val Gly Glu
65 70 75 80

Ala Thr

<210> 375
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 375

Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu Glu Asn Thr Asp Tyr
1 5 10 15

Leu Cys Asn Met Asp Pro Tyr Ala Val Leu Lys Cys Arg Ser Gln Glu
20 25 30

Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Ser Asp Pro Glu Trp Asn
35 40 45

Glu Thr Phe Met Phe Ser Val Thr His Asn Ala Thr Glu Leu Ile Ile
50 55 60

Lys Leu Met Asp Ser Asp Ser Gly Thr Asp Asp Asp Phe Val Gly Glu
65 70 75 80

Ala Thr

<210> 376
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 376

Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu Glu Asn Thr Asp Tyr
1 5 10 15

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Leu Cys Asn Met Asp Pro Tyr Ala Ile Leu Lys Cys Arg Ser Gln Glu
20 25 30

Gln Arg Ser Ser Ile Ala Ser Gly Lys Gly Ser Asn Pro Glu Trp Asn
35 40 45

Glu Asn Phe Val Phe Thr Val Ser Asp Lys Ala Thr Glu Leu Leu Ile
50 55 60

Lys Leu Leu Asp Ser Asp Thr Gly Ser Ala Asp Asp Phe Val Gly Glu
65 70 75 80

Ala Thr

<210> 377
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 377

Leu Glu Val Val Leu Ile Ser Ala Lys Gly Leu Glu Asp Asn Asp Phe
1 5 10 15

Leu Ser Ser Ile Asp Pro Tyr Val Ile Leu Ser Tyr Arg Ala Gln Glu
20 25 30

His Lys Ser Thr Val Gln Glu Gly Ala Gly Ser Asn Pro Gln Trp Asn
35 40 45

Glu Thr Phe Leu Phe Thr Val Ser Asp Ser Ala Ser Glu Leu Asn Leu
50 55 60

Arg Ile Met Glu Lys Asp Asn Phe Asn Asn Asp Asp Asn Leu Gly Glu
65 70 75 80

Ala Ile

<210> 378
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 378

Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

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Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asn Pro Leu Trp
35 40 45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 379
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 379

Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asn Pro Leu Trp
35 40 45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 380
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 380

Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

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```
Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
            20                  25                  30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asn Pro Leu Trp
        35                  40                  45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
    50                  55                  60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65                  70                  75                  80

Asp Tyr Ile Gly Asp Val Lys
                85
```

<210> 381
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 381

```
Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1               5                   10                  15

Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
            20                  25                  30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Ile Trp
        35                  40                  45

Asn Glu Lys Phe Lys Phe Leu Val Glu Tyr Pro Gly Ser Gly Gly Asp
    50                  55                  60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65                  70                  75                  80

Asp Tyr Ile Gly Asp Val Lys
                85
```

<210> 382
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 382

```
Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1               5                   10                  15
```

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Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Ile Trp
35 40 45

Asn Glu Lys Phe Lys Phe Leu Val Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 383
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 383

Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Ile Trp
35 40 45

Asn Glu Lys Phe Lys Phe Leu Val Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 384
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 384

Met Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala Leu Asp Pro
1 5 10 15

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Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Phe Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Ile Trp
35 40 45

Asn Glu Lys Phe Lys Phe Leu Val Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Ile
85

<210> 385
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 385

Leu Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

Leu Asn Lys Pro Ile Asp Pro Tyr Val Glu Ile Asn Tyr Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Leu Trp
35 40 45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Val Leu Phe Lys Val Met Asp His Asp Ala Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 386
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 386

Leu Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

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Leu Asn Lys Pro Ile Asp Pro Tyr Val Glu Ile Asn Tyr Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Leu Trp
35 40 45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Leu Phe Lys Val Met Asp His Asp Val Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Lys
85

<210> 387
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 387

Leu Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile Asn Tyr Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Leu Trp
35 40 45

Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe His Ile Phe Phe Lys Val Met Asp His Asp Ala Ile Asp Asp Asp
65 70 75 80

Asp Leu Ile Gly Glu Val Lys
85

<210> 388
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 388

Leu Glu Val His Leu Ile Ser Gly Lys Gly Leu Gln Ala His Asp Pro
1 5 10 15

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Leu Asn Lys Pro Ile Asp Pro Tyr Val Glu Ile Asn Tyr Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Val Trp
35 40 45

Asn Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe Leu Ile Leu Phe Lys Val Met Asp His Asp Val Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Ser
85

<210> 389
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 389

Leu Glu Val His Leu Ile Ser Gly Lys Gly Leu Arg Ala His Asp Pro
1 5 10 15

Leu Asn Lys Pro Ile Asp Pro Tyr Val Glu Ile Asn Tyr Lys Gly Gln
20 25 30

Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly Pro Asp Pro Val Trp
35 40 45

Asn Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro Gly Ser Gly Gly Asp
50 55 60

Phe Leu Ile Leu Phe Lys Val Met Asp His Asp Val Ile Asp Gly Asp
65 70 75 80

Asp Tyr Ile Gly Asp Val Ser
85

<210> 390
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 390

Leu Glu Val Ser Leu Ile Ser Gly Lys Gly Leu Lys Arg Ser Asp Phe
1 5 10 15

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```
Leu Gly Lys Ile Asp Pro Tyr Val Glu Ile Gln Tyr Lys Gly Gln Thr
            20                  25                  30

Arg Lys Ser Ser Val Ala Lys Glu Asp Gly Gly Arg Asn Pro Thr Trp
        35                  40                  45

Asn Asp Lys Leu Lys Trp Arg Ala Glu Phe Pro Gly Ser Gly Ala Asp
    50                  55                  60

Tyr Lys Leu Ile Val Lys Val Met Asp His Asp Thr Phe Ser Ser Asp
65                  70                  75                  80

Asp Phe Ile Gly Glu Ala Thr
                85
```

<210> 391
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 391

```
Val Gly Cys Gln Lys Leu Lys Asp Thr Glu Trp Phe Ser Arg Gln Asp
1               5                   10                  15

Pro Tyr Val Val Leu Glu Tyr Gly Gly Arg Ser His Arg Thr Arg Thr
            20                  25                  30

Cys Thr Asp Gly Gly Lys Asn Ala Val Phe Gln Glu Lys Phe Ile Phe
        35                  40                  45

Thr Leu Ile Glu Gly Leu Arg Asp Leu Lys Val Ala Val Trp Asn Ser
    50                  55                  60

Asn Thr Leu Ser Thr Asp Asp Phe Ile Gly Asn Ala Thr
65                  70                  75
```

<210> 392
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 392

```
Leu Glu Val Thr Val Val Gly Cys Gln Lys Leu Lys Asp Thr Glu Trp
1               5                   10                  15

Phe Ser Arg Gln Asp Pro Tyr Val Val Leu Glu Tyr Gly Gly Arg Ser
            20                  25                  30
```

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His Arg Thr Arg Thr Cys Thr Asp Gly Gly Lys Asn Ala Val Phe Gln
35 40 45

Glu Lys Phe Ile Phe Thr Leu Ile Glu Gly Leu Arg Asp Leu Lys Val
50 55 60

Ala Val Trp Asn Ser Asn Thr Leu Ser Thr Asp Asp Phe Ile Gly Asn
65 70 75 80

Ala Thr

<210> 393
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 393

Val Asp Cys Thr Leu Val Ser Ala Arg Gly Ile Lys Asp Val Glu Ile
1 5 10 15

Val Gly Lys Gln Ser Pro Tyr Ala Val Leu Thr Val Gly Pro Lys Thr
20 25 30

Phe Lys Ser Gly Thr Ala Asn Gly Gly Gly Ser Asp Pro Val Trp Asn
35 40 45

Gln Thr Phe Ser Phe Thr Asn Val Thr Pro Asp Ser Ser Val Lys Leu
50 55 60

Glu Ile Phe Asn Ser Asn Val Val Leu Arg Asp Val Ala Ile Gly Gly
65 70 75 80

Cys Lys

<210> 394
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 394

Leu Arg Ala Ser Val Ile Glu Ala His Asp Leu Arg Val Pro Ala Pro
1 5 10 15

Ser Pro Gly Leu Pro Phe Asp Val Arg Val Lys Ile Lys Ile Gly Phe
20 25 30

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Gln Ser Ala Arg Thr Gln Arg Ser Val Ala Ser Thr Ser Ser Gly Ser
35 40 45

Ala Phe Ala Trp Glu Trp Glu Glu Asp Leu Met Phe Val Val Ser Glu
50 55 60

Pro Leu Asp Glu Ser Leu Ile Val Leu Val Lys Asp Arg Thr Met Ile
65 70 75 80

Lys Glu Pro Ala Arg Arg Gly Ala Arg Pro Thr Ser Ala Leu Leu Pro
85 90 95

Ala Lys Glu Ala Ala His Val Cys
100

<210> 395
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 395

Leu Arg Ala Ser Val Ile Glu Ala Gln Asp Leu Arg Val Pro Ala Pro
1 5 10 15

Pro Pro Gly Leu Pro Phe Asp Val Arg Val Lys Ile Gln Val Gly Phe
20 25 30

Gln Ser Ala Arg Thr Arg Arg Ser Val Ala Ser Arg Ser Ser Gly Ser
35 40 45

Ala Phe Ala Trp Glu Glu Asp Leu Met Phe Val Val Ser Glu Pro Leu
50 55 60

Asp Glu Ser Leu Val Val Leu Val Glu Asp Arg Ser Met Ile Lys Glu
65 70 75 80

Pro Ala Leu Leu Gly His Ala Thr
85

<210> 396
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 396

Leu Arg Val Thr Val Leu Glu Ala Gln Asp Leu His Ile Ala Pro Asn
1 5 10 15

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Leu Pro Pro Leu Thr Ala Pro Glu Ile Arg Val Lys Ala Gln Leu Gly
20 25 30

Phe Gln Ser Ala Arg Thr Arg Arg Gly Ser Met Asn Asn His Ser Gly
35 40 45

Ser Phe His Trp His Glu Asp Met Ile Phe Val Ala Gly Glu Pro Leu
50 55 60

Glu Asp Cys Leu Val Leu Met Val Glu Asp Arg Thr Thr Lys Glu Ala
65 70 75 80

Thr Leu Leu Gly His Ala Met
85

<210> 397
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 397

Leu Arg Val Thr Val Leu Glu Ala Gln Asp Leu His Ile Ala Pro Asn
1 5 10 15

Leu Pro Pro Leu Thr Ala Pro Glu Ile Arg Val Lys Ala Gln Leu Gly
20 25 30

Phe Gln Ser Ala Arg Thr Arg Arg Gly Ser Met Asn Asn His Ser Gly
35 40 45

Ser Phe His Trp His Glu Asp Met Ile Phe Val Ala Gly Glu Pro Leu
50 55 60

Glu Asp Cys Leu Val Leu Met Val Glu Asp Arg Thr Thr Lys Glu Ala
65 70 75 80

Thr Leu Leu Gly His Ala Met
85

<210> 398
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 398

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Val Leu Leu His Pro
1 5 10 15

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Asn Arg Ile Asn Pro Glu Ile Leu Ile Lys Gly Phe Leu Gly Asn Val
20 25 30

Val Val Arg Ser Arg Ile Ser Gln Thr Lys Ser Val Ser Pro Val Trp
35 40 45

Asn Glu Asp Met Met Phe Val Ala Val Glu Pro Phe Asp Asp Ser Leu
50 55 60

Ile Leu Ser Val Glu Asp Lys Val Gly Pro Arg Glu Glu Cys Leu Gly
65 70 75 80

Arg Cys Glu

<210> 399
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 399

Leu Arg Leu Ser Val Ile Gln Ala Gln Asp Leu Arg Leu Pro Ala Pro
1 5 10 15

Pro Asp Ala Lys Ala Lys Pro Met Gly Pro Ala Phe Pro Glu Leu Tyr
20 25 30

Val Lys Ala Gln Leu Gly Ala Gln Val Phe Lys Thr Cys Arg Val Ala
35 40 45

Leu Gly Ser Ala Ala Thr Gly Thr Ser Asn Pro Ser Trp Asn Glu Asp
50 55 60

Leu Leu Phe Val Ala Ala Glu Pro Phe Asp Pro Phe Leu Thr Val Val
65 70 75 80

Val Glu Asp Ile Phe Ser Gly Gln Pro Val Gly Gln Ala Arg
85 90

<210> 400
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 400

Leu Arg Leu Thr Val Ile Gln Thr Gln Asp Leu Gln Leu Gly Leu Gly
1 5 10 15

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Ser Glu Ala Lys Ser Lys Ile Pro Thr Thr Glu Leu Tyr Val Lys Ala
20 25 30

Gln Leu Gly Pro Gln Val Phe Lys Thr Ala Arg Thr Ser Ile Gly Pro
35 40 45

Ser Ala Ser Ser Ser Gly Ser Gly Asn Pro Thr Trp Asn Glu Asp Leu
50 55 60

Val Phe Val Ala Ser Glu Pro Phe Glu Pro Phe Leu Ile Val Thr Val
65 70 75 80

Glu Asp Ile Thr Asn Gly Gln Ser Ile Gly Gln Thr Lys
85 90

<210> 401
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 401

Leu Arg Ala Thr Val Ile Glu Ala Gln Asp Leu Leu Pro Pro Gln Leu
1 5 10 15

Thr Ala Phe Lys Glu Ala Ser Phe Gln Leu Lys Ala Gln Leu Gly Ser
20 25 30

Gln Val Gln Lys Thr Lys Ser Ala Val Thr Arg Asn Gly Ala Pro Ser
35 40 45

Trp Asn Glu Asp Leu Leu Phe Val Ala Ala Glu Pro Phe Ser Asp Gln
50 55 60

Leu Val Phe Thr Leu Glu Tyr Arg Thr Ser Lys Gly Pro Val Thr Val
65 70 75 80

Gly Met Ala Arg

<210> 402
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 402

Leu Arg Ile Ser Val Leu Glu Ala Gln Asp Val Val Pro Gly Ala Val
1 5 10 15

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Ala Gly Ala Gly Gly Asp Lys Gly Arg His Gly Glu Ala Phe Val Val
20 25 30

Val Lys Val Gln Val Gly Gly Val Thr Leu Arg Thr Lys Pro Cys Cys
35 40 45

Arg Pro Thr Ser Pro Ser Trp Asn Glu Glu Leu Val Phe Val Val Ala
50 55 60

Glu Pro Phe Asp Glu Pro Ala Val Leu Val Ile Glu
65 70 75

<210> 403
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 403

Leu Arg Ile Ser Val Ile Glu Ala Gln Asp Val Ala Ile Met Asp Lys
1 5 10 15

Gly Ser Ser Leu Met Arg Phe Pro Glu Leu Ser Ala Lys Leu Gln Val
20 25 30

Gly Ser Gln Ile Leu Arg Thr Ala Ile Ala Ser Ala Ile Pro Thr Lys
35 40 45

Ser Phe Ser Asn Pro Tyr Trp Asn Glu Asp Leu Met Phe Val Val Ala
50 55 60

Glu Pro Phe Glu Asp Cys Val Thr Val Val Val Glu Asp Arg Leu Asn
65 70 75 80

Gly Gly Ala Ile Gly Gly Gln Asn Asp Val Ala Val Gly Arg Val Gln
85 90 95

<210> 404
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 404

Val Arg Val Asn Val Ile Gly Ala Gln Asp Ile Phe Pro Met Glu Asn
1 5 10 15

His Ile Pro Asp Val Phe Val Lys Val Arg Leu Gly His Gln Met Leu
20 25 30

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Lys Thr Arg Pro Ala Arg Ser Pro Thr Arg Asn Phe Met Trp Asn Glu
35 40 45

Glu Met Met Phe Val Ala Ala Glu Pro Phe Glu Glu Asp Leu Ile Ile
50 55 60

Gln Ile Glu Asp Arg Val Ala Gln Asn Lys Asp Glu Val Ile Gly Glu
65 70 75 80

Thr Met

<210> 405
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 405

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Val Ile Val Pro Asp
1 5 10 15

Arg Thr Arg Leu Pro Asn Pro Tyr Val Lys Ile Arg Leu Asn Asn Gln
20 25 30

Val Val Arg Thr Lys Pro Ser His Ser Leu Asn Pro Arg Trp Asn Glu
35 40 45

Glu Phe Thr Leu Val Ala Ala Glu Pro Phe Glu Asp Leu Ile Ile Ser
50 55 60

Ile Glu Asp Arg Val Ala Pro Asn Arg Glu Glu Thr Leu Gly Glu Val
65 70 75 80

His

<210> 406
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 406

Leu Arg Val Lys Val Ile Glu Ala His Asp Leu Val Ser His Asp Asn
1 5 10 15

Lys Ser Arg Ala Pro Asp Ala Phe Val Lys Val Gln His Gly Asn Gln
20 25 30

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Ile Phe Lys Thr Lys Pro Val Gln Ser Arg Ile Asn Asn Pro Arg Trp
35 40 45

Asp Gln Gly Thr Leu Phe Val Ala Ala Glu Pro Phe Glu Glu Pro Leu
50 55 60

Ile Ile Thr Val Glu Asp Lys Asp
65 70

<210> 407
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 407

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Val Ile Ser Ser Asp Arg
1 5 10 15

Asn Arg Val Pro Glu Val Phe Ile Lys Ala Gln Met Gly Ser Gln Val
20 25 30

Leu Arg Thr Lys Val Cys Pro Thr Arg Ser Thr Thr Gln Ile Trp Asn
35 40 45

Glu Asp Leu Val Phe Val Ala Ala Glu Pro Phe Glu Glu Gln Leu Thr
50 55 60

Ile Thr Val Glu Asp Arg Val His Gly Ser Lys Asp Glu Val Leu Gly
65 70 75 80

Lys Ile Met

<210> 408
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 408

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Val Ile Pro Ser Asp Arg
1 5 10 15

Asn Arg Leu Pro Glu Val Ser Val Lys Ala His Leu Gly Cys Gln Val
20 25 30

Leu Lys Thr Lys Ile Cys Ser Thr Arg Thr Thr Ser Pro Leu Trp Asn
35 40 45

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Glu Asp Leu Val Phe Val Ala Ala Glu Pro Phe Glu Glu Gln Leu Thr
    50   55   60

Ile Thr Val Glu Asp His Val Gln Pro Ser Lys Asp Glu Val Leu Gly
65   70   75   80

Arg Ile Ser

<210> 409
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 409

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Met Ile Pro Ser Asp Arg
1   5   10   15

Asn Arg Leu Pro Asp Val Phe Val Lys Ala Ser Val Gly Met Gln Thr
            20   25   30

Leu Lys Thr Ser Ile Cys Ser Ile Lys Thr Thr Asn Pro Leu Trp Lys
        35   40   45

Glu Asp Leu Val Phe Val Val Ala Glu Pro Phe Glu Glu Gln Leu Val
    50   55   60

Ile Ser Val Glu Asp Arg Val His Thr Ser Lys Asp Glu Val Ile Gly
65   70   75   80

Lys Ile Thr

<210> 410
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 410

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Val Glu Pro Ser Asp Arg
1   5   10   15

Ser Gln Pro Pro Gln Ala Phe Val Lys Val Gln Val Gly Asn Gln Ile
            20   25   30

Leu Lys Thr Lys Leu Cys Pro Asn Lys Thr Thr Asn Pro Met Trp Asn
        35   40   45

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Glu Asp Leu Val Phe Val Ala Ala Glu Pro Phe Glu Glu Gln Phe Phe
50 55 60

Leu Thr Val Glu Asn Lys Val Thr Pro Ala Lys Asp Glu Val Met Gly
65 70 75 80

Arg Leu Ile

<210> 411
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 411

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Val Glu Pro Ser Asp Arg
1 5 10 15

Ser Gln Pro Pro Gln Ala Phe Val Lys Val Gln Val Gly Asn Gln Ile
20 25 30

Leu Lys Thr Lys Leu Cys Pro Asn Lys Thr Thr Asn Pro Met Trp Asn
35 40 45

Glu Asp Leu Val Phe Val Ala Ala Glu Pro Phe Glu Glu Gln Phe Phe
50 55 60

Leu Thr Val Glu Asn Lys Val Thr Pro Ala Lys Asp Glu Val Met Gly
65 70 75 80

Arg Leu Ile

<210> 412
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 412

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Val Gln Pro Gln Ala Arg
1 5 10 15

Gly Arg Ala Pro Glu Val Phe Val Lys Ala Gln Val Gly Asn Gln Ile
20 25 30

Leu Lys Thr Ser Val Val Ala Ala Pro Thr Leu Asn Pro Arg Trp Asn
35 40 45

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Glu Asp Leu Val Phe Val Val Ala Glu Pro Phe Glu Glu Gln Leu Leu
    50   55   60

Leu Thr Val Glu Asp Arg Val Thr Pro Arg Lys Asp Asp Leu Leu Gly
65   70   75   80

Arg Ala Ala

<210> 413
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 413

Leu Arg Val Asn Ile Ile Glu Ala Gln Asp Ile Ala Ile Thr Asp Lys
1   5   10   15

Thr Arg Tyr Pro Asp Val Phe Val Arg Ala Gln Val Gly His Gln His
            20   25   30

Gly Arg Thr Lys Pro Val Gln Ala Arg Asn Phe Asn Pro Phe Trp Asn
        35   40   45

Glu Asp Leu Met Phe Val Ala Ala Glu Pro Phe Glu Asp His Leu Ile
    50   55   60

Leu Ser Leu Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Val Leu Gly
65   70   75   80

Arg Val Ile

<210> 414
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 414

Leu Arg Val Asn Ile Ile Glu Ala Gln Asp Ile Ala Ile Thr Asp Lys
1   5   10   15

Thr Arg Tyr Pro Asp Val Phe Val Arg Ala Gln Val Gly His Gln His
            20   25   30

Gly Arg Thr Lys Pro Val Gln Ala Arg Asn Phe Asn Pro Phe Trp Asn
        35   40   45

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Glu Asp Leu Met Phe Val Ala Ala Glu Pro Phe Glu Asp His Leu Ile
50 55 60

Leu Ser Leu Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Val Leu Gly
65 70 75 80

Arg Val Ile

<210> 415
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 415

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Thr Asp Lys
1 5 10 15

Gln Arg Tyr Pro Glu Val Tyr Val Lys Ala Ile Val Gly Asn Gln Ala
20 25 30

Leu Arg Thr Arg Val Ser Gln Ser Arg Thr Ile Asn Pro Met Trp Asn
35 40 45

Glu Asp Leu Met Phe Val Ala Ala Glu Pro Phe Glu Glu Pro Leu Ile
50 55 60

Leu Ser Val Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Val Leu Gly
65 70 75 80

Arg Cys Ala

<210> 416
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 416

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Thr Asp Lys
1 5 10 15

Gln Arg Tyr Pro Glu Val Tyr Val Lys Ala Ile Val Gly Asn Gln Ala
20 25 30

Leu Arg Thr Arg Val Ser Gln Ser Arg Thr Ile Asn Pro Met Trp Asn
35 40 45

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Glu Asp Leu Met Phe Val Ala Ala Glu Pro Phe Glu Glu Pro Leu Ile
    50   55   60

Leu Ser Val Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Val Leu Gly
65   70   75   80

Arg Cys Ala

<210> 417
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 417

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Ser Asp Lys
1   5   10   15

Gly Arg Tyr Pro Glu Val Phe Val Lys Val Ile Met Gly Asn Gln Ala
            20   25   30

Leu Arg Thr Arg Val Ser Gln Ser Arg Ser Ile Asn Pro Met Trp Asn
        35   40   45

Glu Asp Leu Met Phe Val Val Ala Glu Pro Phe Glu Glu Pro Leu Ile
    50   55   60

Leu Ser Val Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Val Leu Gly
65   70   75   80

Arg Cys Ala

<210> 418
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 418

Val Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro His Asp Lys
1   5   10   15

Thr Lys Phe Pro Glu Val Tyr Val Lys Ala Met Leu Gly Asn Gln Thr
            20   25   30

Leu Arg Thr Arg Ile Ser Gln Thr Lys Thr Leu Asn Pro Met Trp Asn
        35   40   45

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Glu Asp Leu Met Phe Val Val Ala Glu Pro Phe Glu Glu Ala Leu Ile
50 55 60

Leu Ala Val Glu Asp Arg Val Ala Pro Asn Lys Asp Glu Thr Leu Gly
65 70 75 80

Arg Cys Ala

<210> 419
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 419

Leu Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Asn Asp Arg
1 5 10 15

Thr Arg Phe Pro Asp Val Tyr Val Lys Ala Met Leu Gly Asn Gln Ala
20 25 30

Leu Arg Thr Arg Val Ser Pro Ser Arg Thr Leu Asn Pro Met Trp Asn
35 40 45

Glu Asp Leu Met Phe Val Ala Ala Glu Pro Phe Glu Glu His Leu Ile
50 55 60

Leu Ser Val Glu Asp Arg Ile Ala Pro Gly Lys Asp Asp Val Leu Gly
65 70 75 80

Arg Thr Ile

<210> 420
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 420

Val Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Thr Asp Lys
1 5 10 15

Thr Arg Phe Pro Asp Val Tyr Val Lys Ala Gln Leu Gly Asn Gln Val
20 25 30

Met Lys Trp Cys Gln Ala Arg Thr Leu Gly Ala Val Trp Asn Glu Asp
35 40 45

Phe Leu Phe Val Val Ala Glu Pro Phe Glu Asp His Leu Val Leu Thr
    50   55   60

Val Glu Asp Arg Val Ala Pro Gly Lys Asp Glu Ile Val Gly Arg Thr
65   70   75   80

Tyr

<210> 421
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 421

Val Arg Val Asn Val Ile Glu Ala Gln Asp Leu Ile Pro Thr Asp Lys
1   5   10   15

Thr Arg Phe Pro Asp Val Tyr Val Lys Ala Gln Leu Gly Asn Gln Val
            20   25   30

Met Lys Trp Cys Gln Ala Arg Thr Leu Gly Ala Val Trp Asn Glu Asp
        35   40   45

Phe Leu Phe Val Val Ala Glu Pro Phe Glu Asp His Leu Val Leu Thr
    50   55   60

Val Glu Asp Arg Val Ala Pro Gly Lys Asp Glu Ile Val Gly Arg Thr
65   70   75   80

Tyr

<210> 422
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 422

Leu Arg Val Ser Val Ile Glu Ala Gln Asp Leu Ile Pro Met Asp Lys
1   5   10   15

Gly Pro Met Ala Ile Gly Arg Tyr Pro Glu Leu Phe Val Arg Ala Gln
            20   25   30

Val Gly Ser Gln Met Leu Arg Thr Arg Pro Ala Pro Val Ala Ala Asn
        35   40   45

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Arg Gly Pro Ser Ser Pro Phe Trp Asn Glu Asp Leu Met Phe Val Val
    50   55   60

Ala Glu Pro Phe Glu Glu Phe Leu Val Leu Ser Leu Glu Asp His Val
65   70   75   80

Ser Pro Gly Arg Asp Asp Val Leu Gly Arg Leu Val
                85   90

<210> 423
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 423

Asp Lys Ser Arg Val Pro Glu Val Phe Val Arg Val Lys Val Gly Asn
1   5   10   15

Gln Met Leu Arg Thr Lys Phe Pro Gln Arg Ser Asn Asn Pro Lys Trp
            20   25   30

Gly Asp Glu Phe Thr Phe Val Val Ala Glu Pro Phe Glu Asp Asn Leu
        35   40   45

Val Leu Ser Val Glu Asp His Thr Ala Pro Asn Arg Asp Glu Pro Val
    50   55   60

Gly Lys Ala Val
65

<210> 424
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 424

Leu Arg Val Gln Ile Leu Glu Ala Gln Asp Val Ile Ile Val Ser Asp
1   5   10   15

Lys Ser Arg Val Pro Glu Val Phe Val Arg Val Lys Val Gly Asn Gln
            20   25   30

Met Leu Arg Thr Lys Phe Pro Gln Arg Ser Asn Asn Pro Lys Trp Gly
        35   40   45

Asp Glu Phe Thr Phe Val Val Ala Glu Pro Phe Glu Asp Asn Leu Val
    50   55   60

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Leu Ser Val Glu Asp His Thr Ala Pro Asn Arg Asp Glu Pro Val Gly
65   70   75   80

Lys Ala Val

<210> 425
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 425

Leu Arg Ile His Val Met Glu Ala Gln Asp Leu Val Pro Ser Asp Lys
1   5   10   15

Gly Arg Val Pro Asp Ala Ile Val Lys Ile Gln Ala Gly Asn Gln Met
            20   25   30

Arg Ala Thr Arg Thr Pro Gln Met Arg Thr Met Asn Pro Gln Trp His
        35   40   45

Glu Glu Leu Met Phe Val Val Ser Glu Pro Phe Glu Asp Met Val Ile
    50   55   60

Val Ser Val Asp Asp Arg Ile Gly Pro Gly Lys Asp Glu Ile Leu Gly
65   70   75   80

Arg Val Phe

<210> 426
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 426

Leu Arg Ile His Val Met Glu Ala Gln Asp Leu Val Pro Ser Asp Lys
1   5   10   15

Gly Arg Val Pro Asp Ala Ile Val Lys Ile Gln Ala Gly Asn Gln Met
            20   25   30

Arg Ala Thr Arg Thr Pro Gln Met Arg Thr Met Asn Pro Gln Trp His
        35   40   45

Glu Glu Leu Met Phe Val Val Ser Glu Pro Phe Glu Asp Met Val Ile
    50   55   60

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Val Ser Val Asp Asp Arg Ile Gly Pro Gly Lys Asp Glu Ile Leu Gly
65 70 75 80

Arg Val Phe

<210> 427
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 427

Leu Lys Val Val Ala Ile Ala Ala Gln Asp Leu Ile Pro Ala Glu Lys
1 5 10 15

Gly Arg Pro Leu Ala Pro Ser Ile Val Lys Ile Gln Leu Gly Gly Gln
20 25 30

Thr Arg Arg Thr Arg Ser Gln Gly Ser Ala Asn Pro Met Trp Asn Glu
35 40 45

Glu Phe Leu Phe Val Ala Ala Glu Pro Phe Asp Glu Pro Leu Val Val
50 55 60

Thr Val Glu Glu Arg Val Ala Ala Gly Arg Asp Glu Pro Val Gly Arg
65 70 75 80

Val Ile

<210> 428
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 428

Leu Arg Val Ala Ala Ile Gly Ala Gln Asp Leu Val Pro Leu Asp Ala
1 5 10 15

Ser Arg Pro Ala Asn Phe Cys Val Lys Leu Gln Leu Ala Gly Gln Val
20 25 30

Arg Arg Thr Arg Pro Gly Ala Pro Pro Gly Thr Leu Asn Pro Ile Trp
35 40 45

Asn Glu Glu Phe Met Phe Val Val Ser Glu Pro Phe Asp Glu Pro Leu
50 55 60

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Phe Val Thr Val Glu Asp Arg Val Gly Pro Gly Arg Asp Glu Pro Leu
65 70 75 80

Gly Arg Ile Met

<210> 429
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 429

Val Arg Val Thr Ile Val Ser Gly His Asp Leu Ile Ser Thr Asp Arg
1 5 10 15

Asn Arg Thr Pro Ser Val Tyr Val Thr Ala Thr Leu Gly Gln Val Thr
20 25 30

Leu Lys Thr Glu Val Ser Ser Gly Thr Asn Pro Ser Trp Asn Lys Asp
35 40 45

Leu Ile Phe Val Ala Ser Glu Pro Leu Glu Gly Thr Val Tyr Ile Arg
50 55 60

Leu Ile Asp Arg Val Asp Asp Gln His Glu Glu Arg Ile Ile Gly Lys
65 70 75 80

Leu Glu

<210> 430
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 430

Val Arg Val Thr Ile Val Ser Gly His Asp Leu Ile Ser Lys Asp Lys
1 5 10 15

Asn Lys Thr Pro Ser Val Tyr Val Thr Ala Thr Leu Gly Lys Val Ala
20 25 30

Leu Lys Thr Lys Val Ser Ser Gly Thr Asn Pro Ser Trp Asn Gln Asp
35 40 45

Leu Ile Phe Val Ala Ser Glu Pro Leu Glu Gly Thr Val Tyr Ile Arg
50 55 60

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Leu Ile Asp Arg Glu Asp Glu Gln His Glu Gly Cys Ile Gly Thr Leu
65 70 75 80

Lys

<210> 431
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 431

Ile Ile Val Thr Val Leu Ala Gly Lys Asn Leu Val Ser Lys Asp Lys
1 5 10 15

Ser Gly Lys Cys Asp Ala Ser Val Lys Leu Gln Tyr Gly Lys Ile Ile
20 25 30

Gln Lys Thr Lys Ile Val Asn Ala Ala Glu Cys Val Trp Asn Gln Lys
35 40 45

Phe Glu Phe Glu Glu Leu Ala Gly Glu Glu Tyr Leu Lys Val Lys Cys
50 55 60

Tyr Arg Glu Glu Met Leu Gly Thr Asp Asn Ile Gly Thr Ala Thr
65 70 75

<210> 432
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 432

Ile Ile Val Thr Val Leu Ala Gly Lys Asn Leu Val Ser Lys Asp Lys
1 5 10 15

Ser Gly Lys Cys Asp Ala Ser Val Lys Leu Gln Tyr Gly Lys Ile Ile
20 25 30

Gln Lys Thr Lys Ile Val Asn Ala Ala Glu Cys Val Trp Asn Gln Lys
35 40 45

Phe Glu Phe Glu Glu Leu Ala Gly Glu Glu Tyr Leu Lys Val Lys Cys
50 55 60

Tyr Arg Glu Glu Met Leu Gly Thr Asp Asn Ile Gly Thr Ala Thr
65 70 75

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<210> 433
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 433

Ile Tyr Val Thr Val Val Ser Gly Asn Asn Leu Asn Arg Arg Ile Leu
1 5 10 15

Arg Gly Ser Pro Ser Lys Ser Ser Glu Ile Gly Glu Gly Ser Ser Gly
20 25 30

Asn Ser Ser Ser Lys Pro Val Gln Thr Phe Val Glu Val Glu Leu Glu
35 40 45

Gln Leu Ser Arg Arg Thr Glu Met Lys Ser Gly Pro Asn Pro Ala Tyr
50 55 60

Gln Ser Thr Phe Asn Met Ile Leu His Asp Asn Thr Gly Thr Leu Lys
65 70 75 80

Phe Asn Leu Tyr Glu Asn Asn Pro Gly Ser Val Arg Tyr Asp Ser Leu
85 90 95

Ala Ser Cys Glu
100

<210> 434
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 434

Ile Tyr Val Thr Val Val Ser Gly Asn Asn Leu Asn Arg Arg Ile Leu
1 5 10 15

Arg Gly Ser Pro Ser Lys Ser Ser Glu Ile Gly Glu Gly Ser Ser Gly
20 25 30

Asn Ser Ser Ser Lys Pro Val Gln Thr Phe Val Glu Val Glu Leu Glu
35 40 45

Gln Leu Ser Arg Arg Thr Glu Met Lys Ser Gly Pro Asn Pro Ala Tyr
50 55 60

Gln Ser Thr Phe Asn Met Ile Leu His Asp Asn Thr Gly Thr Leu Lys
65 70 75 80

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Phe Asn Leu Tyr Glu Asn Asn Pro Gly Ser Val Arg Tyr Asp Ser Leu
85 90 95

Ala Ser Cys Glu
100

<210> 435
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 435

Val Lys Leu Glu Ile Leu Glu Gly Ser Asp Met Lys Pro Ser Asp Met
1 5 10 15

Asn Gly Leu Ser Asp Pro Tyr Val Lys Gly Arg Leu Gly Pro Phe Lys
20 25 30

Phe Gln Thr Gln Ile Gln Lys Lys Thr Leu Ser Pro Lys Trp Phe Glu
35 40 45

Glu Phe Lys Ile Pro Ile Thr Ser Trp Glu Ser Leu Asn Glu Leu Ala
50 55 60

Met Glu Val Cys Asp Lys Asp His Met Phe Asp Asp Ser Leu Gly Thr
65 70 75 80

Cys Thr

<210> 436
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 436

Ala Lys Val Glu Ile Leu Glu Gly Ala Asp Met Lys Pro Ser Asp Pro
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly His Leu Gly Pro Tyr Arg
20 25 30

Phe Gln Thr Lys Ile His Lys Lys Thr Leu Asn Pro Lys Trp Met Glu
35 40 45

Glu Phe Lys Ile Pro Val Thr Ser Trp Ala Ala Leu Asn Leu Leu Ser
50 55 60

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Leu Gln Val Arg Asp Lys Asp Pro Ile Phe Asp Asp Thr Leu Gly Asp
65 70 75 80

Cys Ser

<210> 437
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 437

Ala Leu Val Glu Val Val Glu Ala Cys Asp Val Lys Pro Ser Asp Leu
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly Gln Leu Gly Ala Tyr Arg
20 25 30

Phe Lys Thr Lys Ile Leu Trp Lys Thr Leu Ala Pro Lys Trp Gln Glu
35 40 45

Glu Phe Lys Ile Pro Ile Cys Thr Trp Asp Ser Ala Asn Ile Leu Asn
50 55 60

Ile Glu Val Gln Asp Lys Asp Arg Phe Ser Asp Asp Ser Leu Gly Asp
65 70 75 80

Cys Ser

<210> 438
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 438

Ala Leu Val Glu Val Val Glu Ala Cys Asp Val Lys Pro Ser Asp Leu
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly Gln Leu Gly Ala Tyr Arg
20 25 30

Phe Lys Thr Lys Ile Leu Trp Lys Thr Leu Ala Pro Lys Trp Gln Glu
35 40 45

Glu Phe Lys Ile Pro Ile Cys Thr Trp Asp Ser Ala Asn Ile Leu Asn
50 55 60

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Ile Glu Val Gln Asp Lys Asp Arg Phe Ser Asp Asp Ser Leu Gly Asp
65 70 75 80

Cys Ser

<210> 439
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 439

Val Leu Val Glu Val Phe Glu Ala Ser Asp Leu Lys Pro Ser Asp Leu
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly Lys Leu Gly Ala Tyr Arg
20 25 30

Phe Lys Thr Lys Ile Gln Lys Lys Thr Leu Ser Pro Lys Trp His Glu
35 40 45

Glu Phe Lys Ile Pro Ile Phe Thr Trp Asp Ser Pro Ser Ile Leu Asn
50 55 60

Ile Glu Val Gly Asp Lys Asp Arg Phe Val Asp Asp Thr Leu Gly Glu
65 70 75 80

Cys Ser

<210> 440
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 440

Val Leu Val Glu Val Phe Glu Ala Ser Asp Leu Lys Pro Ser Asp Leu
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly Lys Leu Gly Ala Tyr Arg
20 25 30

Phe Lys Thr Lys Ile Gln Lys Lys Thr Leu Ser Pro Lys Trp His Glu
35 40 45

Glu Phe Lys Ile Pro Ile Phe Thr Trp Asp Ser Pro Ser Ile Leu Asn
50 55 60

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Ile Glu Val Gly Asp Lys Asp Arg Phe Val Asp Asp Thr Leu Gly Glu
65 70 75 80

Cys Ser

<210> 441
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 441

Val Leu Val Glu Val Phe Glu Ala Ser Asp Leu Lys Pro Ser Asp Leu
1 5 10 15

Asn Gly Leu Ala Asp Pro Tyr Val Lys Gly Lys Leu Gly Ala Tyr Arg
20 25 30

Phe Lys Thr Lys Ile Gln Lys Lys Thr Leu Ser Pro Lys Trp His Glu
35 40 45

Glu Phe Lys Ile Pro Ile Phe Thr Trp Asp Ser Pro Ser Ile Leu Asn
50 55 60

Ile Glu Val Gly Asp Lys Asp Arg Phe Val Asp Asp Thr Leu Gly Phe
65 70 75 80

Ala Pro

<210> 442
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 442

Leu Cys Val His Val Leu Glu Ala Arg Leu Gln Ala Ala Tyr Leu Thr
1 5 10 15

Gly His Ser Asp Pro Tyr Val Arg Leu Gln Met Gly Arg Arg Arg Ala
20 25 30

Lys Thr Thr Val Val Lys Arg Cys Leu Ser Pro Leu Trp Asp Glu Glu
35 40 45

Phe Gly Phe Ala Val Gly Asp Ala Glu Glu Glu Leu Val Val Ser Val
50 55 60

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Leu Asn Glu Glu Gly Tyr Phe Gly Gly Gly Phe Leu Gly Arg Val Lys
65 70 75 80

<210> 443
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 443

Leu Gln Val Arg Val Val Glu Ala Arg Gly Leu Pro Ala Val Arg Val
1 5 10 15

Asp Gly Thr Ser Asp Pro Phe Val Lys Leu Gln Leu Gly Lys Arg Arg
20 25 30

Ala Lys Thr Ala Val Ala Arg Arg Thr Leu Ala Pro Ala Trp Asp Glu
35 40 45

Glu Phe Ser Phe Leu Val Gly Asp Ile Ala Glu Glu Leu Val Val Ser
50 55 60

Val Leu Asn Glu Asp Lys Tyr Phe Ser Asn Asp Leu Leu Gly Lys Val
65 70 75 80

Arg

<210> 444
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 444

Leu Gln Val Arg Val Val Glu Ala Arg Asn Leu Pro Ala Met Asp Leu
1 5 10 15

Asn Gly Phe Ser Asp Pro Tyr Val Arg Leu Gln Leu Gly Lys Gln Arg
20 25 30

Ser Arg Thr Lys Val Val Lys Lys Asn Leu Asn Pro Lys Trp Thr Glu
35 40 45

Asp Phe Ser Phe Gly Val Asp Asp Leu Asn Asp Glu Leu Val Val Ser
50 55 60

Val Leu Asp Glu Asp Lys Tyr Phe Asn Asp Asp Phe Val Gly Gln Val
65 70 75 80

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Arg

<210> 445
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 445

Leu Asn Val Arg Val Ile Glu Ala Arg Asn Leu Arg Ala Met Asp Ser
1   5   10   15

Asn Gly Phe Ser Asp Pro Tyr Val Lys Leu Gln Leu Gly Lys Gln Arg
            20   25   30

Phe Lys Thr Lys Val Val Lys Lys Asn Leu Asn Pro Ala Trp Asp Gln
        35   40   45

Glu Phe Ser Phe Ser Val Gly Asp Val Arg Asp Val Leu Lys Leu Tyr
    50   55   60

Val Tyr Asp Glu Asp Met Ile Gly Ile Asp Asp Phe Leu Gly Gln Val
65   70   75   80

Lys

<210> 446
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 446

Leu Leu Val Gln Val Ser Glu Ala Arg Asn Leu Pro Ala Ile Asp Gly
1   5   10   15

Gly Gly Gly Leu Ser Asp Pro Tyr Ala Lys Leu Gln Leu Gly Arg Gln
            20   25   30

Arg Gly Lys Thr Arg Val Ala Lys Arg Thr Leu Ser Pro Thr Trp Asp
        35   40   45

Glu Glu Phe Ala Phe Arg Val Val Asp Leu Lys Asp Glu Leu Val Val
    50   55   60

Val Val Val Asp Glu Asp Arg Tyr Phe Ser Asp Asp Phe Leu Gly Gln
65   70   75   80

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Val Arg

<210> 447
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 447

Leu Cys Val Ser Val Ile Glu Ala Arg Asn Val Gln Ala Asp Asp Phe
1 5 10 15

Ala Gly Lys Asn Phe Tyr Val Lys Leu Arg Val Gly Ser Asn Glu Val
20 25 30

Lys Thr Asp Val Val Lys Gly Ser Leu Ala Pro Lys Phe Leu Lys Asp
35 40 45

Cys Arg Leu Ala Val Pro Thr Pro Glu Ser Asp Tyr Leu Arg Ile Glu
50 55 60

Leu
65

<210> 448
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 448

Val Lys Val Glu Leu Leu Ala Ala Lys Asn Leu Ile Gly Ala Asn Leu
1 5 10 15

Asn Gly Thr Ser Asp Pro Tyr Ala Ile Val Asn Cys Gly Ser Glu Lys
20 25 30

Arg Phe Ser Ser Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu
35 40 45

Glu Phe Asn Phe Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn Val Thr
50 55 60

Ile His Asp Trp Asp Ile Ile Trp Lys Ser Thr Val Leu Gly Ser Val
65 70 75 80

Thr

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<210> 449
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 449

Val Lys Val Glu Leu Leu Ala Ala Lys Asn Leu Ile Gly Ala Asn Leu
1 5 10 15

Asn Gly Thr Ser Asp Pro Tyr Ala Ile Val Asn Cys Gly Ser Glu Lys
20 25 30

Arg Phe Ser Ser Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu
35 40 45

Glu Phe Asn Phe Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn Val Thr
50 55 60

Ile His Asp Trp Asp Ile Ile Trp Lys Ser Thr Val Leu Gly Ser Val
65 70 75 80

Thr

<210> 450
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 450

Val Lys Leu Glu Leu Leu Ala Ala Lys Asn Leu Ile Ala Ala Asn Leu
1 5 10 15

Asn Gly Thr Ser Asp Pro Tyr Ala Leu Ile Thr Cys Gly Glu Glu Lys
20 25 30

Arg Phe Ser Ser Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu
35 40 45

Glu Phe Asn Phe Phe Val Asp Ser Leu Pro Val Lys Ile Asn Val Thr
50 55 60

Ile Tyr Asp Trp Asp Ile Val Trp Lys Ser Thr Val Leu Gly Ser Val
65 70 75 80

Ile

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<210> 451
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 451

Ile Lys Leu Glu Leu Leu Cys Ala Lys Tyr Leu Ile Gly Ala Asn Leu
1   5   10   15

Asn Gly Ser Ser Asp Pro Tyr Ala Val Ile Ser Cys Gly Glu Gln Arg
            20   25   30

Arg Phe Ser Ser Met Val Pro Ser Ser Arg Asn Pro Leu Trp Gly Glu
        35   40   45

Glu Phe Asn Phe Leu Val Arg Glu Leu Pro Val Glu Phe Cys Thr Ala
    50   55   60

Pro Val Asn Asp Ser Lys Val Thr Ile Thr Met Tyr Asp Trp Asp Thr
65   70   75   80

Val Cys Lys Cys Lys Val Ile Gly Ser Val Thr
                85   90

<210> 452
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 452

Leu Glu Val His Leu Leu Glu Ala His Gly Leu Leu Asp Thr Asp Thr
1   5   10   15

Phe Gly Lys Ser Asp Pro Tyr Ala Ile Val Tyr Cys Gln Lys Glu
            20   25   30

<210> 453
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 453

Ile Glu Leu Val Leu Val Glu Ala Arg Asp Leu Val Ala Ala Asp Ile
1   5   10   15

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Arg Gly Thr Ser Asp Pro Tyr Val Arg Val Gln Tyr Gly Glu Lys Lys
            20   25   30

Gln Arg Thr Lys Val Ile Tyr Lys Thr Leu Gln Pro Lys Trp Asn Gln
        35   40   45

Thr Met Glu Phe Pro Asp Asp Gly Ser Ser Leu Glu Leu His Val Lys
    50   55   60

Asp Tyr Asn Thr Leu Leu Pro Thr Ser Ser Ile Gly Asn Cys Val
65   70   75

<210> 454
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 454

Ile Glu Leu Val Leu Val Glu Ala Arg Asp Leu Val Ala Ala Asp Ile
1   5   10   15

Arg Gly Thr Ser Asp Pro Tyr Val Arg Val Gln Tyr Gly Glu Lys Lys
            20   25   30

Gln Arg Thr Lys Val Ile Tyr Lys Thr Leu Gln Pro Lys Trp Asn Gln
        35   40   45

Thr Met Glu Phe Pro Asp Asp Gly Ser Ser Leu Glu Leu His Val Lys
    50   55   60

Asp Tyr Asn Thr Leu Leu Pro Thr Ser Ser Ile Gly Asn Cys Val
65   70   75

<210> 455
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 455

Leu Val Val Ile Val His Glu Ala Gln Asp Val Glu Gly Lys His His
1   5   10   15

Thr Asn Pro Gln Ala Arg Leu Ile Phe Arg Gly Glu Glu Lys Lys Thr
            20   25   30

Lys Arg Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp Glu Phe Gln
        35   40   45

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Phe Ile Ala Glu Glu Pro Pro Thr Asn Asp Lys Leu His Val Glu Val
    50   55   60

Val Ser Ser Ser Ser Arg Thr Leu Leu His Gln Lys Glu Ser Leu Gly
65   70   75   80

Tyr Val Asp

<210> 456
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 456

Leu Val Val Ile Val His Glu Ala Gln Asp Val Glu Gly Lys His His
1   5   10   15

Thr Asn Pro Tyr Val Arg Ile Val Phe Arg Gly Glu Glu Arg Lys Thr
            20   25   30

Lys His Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Gln Glu Phe Gln
        35   40   45

Phe Val Cys Glu Glu Pro Pro Ile Asn Asp Lys Met Gln Ile Glu Val
    50   55   60

Ile Ser Arg Pro Pro Ser Ile Gly Ile His Ser Lys Glu Asn Leu Gly
65   70   75   80

Tyr Val Val

<210> 457
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 457

Leu Val Val Ile Val His Glu Ala Glu Asp Leu Glu Gly Lys Tyr His
1   5   10   15

Thr Asn Pro Ser Val Arg Leu Leu Phe Arg Gly Glu Glu Arg Lys Thr
            20   25   30

Lys Arg Val Lys Lys Asn Arg Glu Pro Arg Trp Asp Glu Asp Phe Gln
        35   40   45

Phe Pro Leu Asp Glu Pro Pro Ile Asn Asp Lys Leu His Val Glu Val
50 55 60

Ile Ser Ser Ser Ser Arg Leu Ile His Pro Lys Glu Thr Leu Gly Tyr
65 70 75 80

Val Val

<210> 458
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 458

Phe Val Val Ile Val His Ser Ala Glu Asp Val Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Val His Ile Tyr Phe Lys Gly Glu Glu Arg Lys Thr
20 25 30

Lys His Val Lys Lys Asn Lys Asp Pro Lys Trp Asn Glu Glu Phe Ser
35 40 45

Phe Met Leu Glu Glu Pro Pro Ile His Glu Lys Met His Val Lys Val
50 55 60

Phe
65

<210> 459
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 459

Phe Val Val Ile Val His Ser Ala Glu Asp Val Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Val His Ile Tyr Phe Lys Gly Glu Glu Arg Lys Thr
20 25 30

Lys His Val Lys Lys Asn Lys Asp Pro Lys Trp Asn Glu Glu Phe Ser
35 40 45

Phe Met Leu Glu Glu Pro Pro Ile His Glu Lys Met His Val Lys Val
50 55 60

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Phe
65

<210> 460
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 460

Leu Val Val Ile Val His Ser Ala Glu Asp Val Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Val His Ile Tyr Phe Lys Gly Glu Glu Arg Lys Thr
20 25 30

Lys Asn Val Lys Lys Asn Lys Asp Pro Lys Trp Asn Glu Glu Phe Ser
35 40 45

Phe Met Leu Glu Glu Pro Pro Val His Glu Lys Leu His Val Glu Val
50 55 60

Phe
65

<210> 461
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
<221> misc_feature
<222> (58)..(58)
<223> Xaa can be any naturally occurring amino acid

<400> 461

Leu Ala Val Ile Val His Ser Ala Glu Asp Val Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Val Arg Ile Tyr Phe Lys Gly Glu Glu Arg Lys Thr
20 25 30

Lys His Val Lys Lys Asn Arg Asp Pro Arg Trp Glu Glu Glu Phe Thr
35 40 45

Phe Met Leu Glu Glu Pro Pro Val Arg Xaa Lys Leu His Val Glu Val
50 55 60

Leu Ser Thr Ser Ser Arg Ile Gly Leu Leu His Pro Lys Glu Thr Leu
65 70 75 80

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Gly Tyr Val Asp

<210> 462
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 462

Leu Val Val Ile Val His Ser Ala Glu Asp Val Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Val Arg Ile Tyr Phe Lys Gly Glu Glu Arg Lys Thr
20 25 30

Lys His Val Lys Lys Asn Arg Asp Pro Arg Trp Asn Glu Glu Phe Thr
35 40 45

Phe Met Leu Glu Glu Pro Pro Val Arg Glu Lys Leu His Val Glu Val
50 55 60

Leu Ser Thr Ser Ser Arg Ile Gly Leu Leu His Pro Lys Glu Thr Leu
65 70 75 80

Gly Tyr Val Asp

<210> 463
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 463

Leu Tyr Val Val Val His Glu Ala Gln Asp Leu Glu Gly Lys His His
1 5 10 15

Thr Asn Pro Tyr Ala Lys Ile Ile Phe Lys Gly Glu Glu Lys Lys Thr
20 25 30

Lys Val Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp Glu Phe Glu
35 40 45

Phe Val Cys Glu Glu Pro Pro Val Asn Asp Lys Leu His Ile Glu Val
50 55 60

Leu Ser Lys Ala Ser Lys Lys Gly Leu Ile His Gly Lys Glu Thr Leu
65 70 75 80

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Gly Tyr Ile Asp

<210> 464
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 464

Leu Tyr Val Val Val His Glu Ala Lys Glu Leu Glu Gly Lys Cys Asn
1 5 10 15

Thr Asn Pro Tyr Val Lys Leu Thr Phe Lys Gly Val Glu Lys Lys Thr
20 25 30

Lys Val Val Lys Glu Asn Arg Asn Pro Arg Trp Lys Glu Glu Phe Glu
35 40 45

Phe Glu Cys Glu Glu Thr Pro Ala Asn Asp Lys Leu His Val Glu Val
50 55 60

<210> 465
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 465

Leu Ser Val Ala Val Gln Ser Ala Lys Asp Val Glu Gly Lys Lys Lys
1 5 10 15

His Ser Asn Pro Tyr Ala Val Val Leu Phe Arg Gly Glu Lys Lys Lys
20 25 30

Thr Lys Met Leu Lys Lys Thr Arg Asp Pro Arg Trp Asn Glu Glu Phe
35 40 45

Gln Phe Thr Leu Glu Glu Pro Pro Val Lys Glu Ser Ile Arg Val Glu
50 55 60

Val Met Ser Lys Gly Thr Gly Phe His Phe Arg Ser Lys Glu Glu Leu
65 70 75 80

Gly His Val Asp

<210> 466
<211> 84

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 466

Leu Ser Val Ala Val Gln Ser Ala Lys Asp Val Glu Gly Lys Lys Lys
1 5 10 15

His Ser Asn Pro Tyr Ala Val Val Leu Phe Arg Gly Glu Lys Lys Lys
20 25 30

Thr Lys Met Leu Lys Lys Thr Arg Asp Pro Arg Trp Asn Glu Glu Phe
35 40 45

Gln Phe Thr Leu Glu Glu Pro Pro Val Lys Glu Ser Ile Arg Val Glu
50 55 60

Val Met Ser Lys Gly Thr Gly Phe His Phe Arg Ser Lys Glu Glu Leu
65 70 75 80

Gly His Val Asp

<210> 467
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 467

Leu Ser Val Ala Val Gln Ser Ala Lys Asp Val Glu Gly Lys Lys Lys
1 5 10 15

His Ser Asn Pro Tyr Ala Val Val Leu Phe Arg Gly Glu Lys Lys Lys
20 25 30

Thr Lys Met Leu Lys Lys Thr Arg Asp Pro Arg Trp Asn Glu Glu Phe
35 40 45

Gln Phe Thr Leu Glu Glu Pro Pro Val Lys Glu Ser Ile Arg Val Glu
50 55 60

Val Met Ser Lys Gly Thr Gly Phe His Phe Arg Ser Lys Glu Glu Leu
65 70 75 80

Gly His Val Asp

<210> 468
<211> 85

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 468

Leu Leu Val Ser Val Glu Asn Ala Glu Asp Val Glu Gly Lys Arg His
1 5 10 15

Thr Asn Pro Tyr Ala Val Val His Phe Arg Gly Glu Arg Lys Glu Thr
20 25 30

Lys Ile Ile Lys Lys Thr Arg Asp Pro Arg Trp Asn Glu Glu Phe Gln
35 40 45

Phe Met Val Asp Glu Ala Pro Val Asp Asp Lys Ile His Ile Glu Val
50 55 60

Val Ser Lys Arg Arg Gly Leu Arg Leu Pro Phe Arg Asn Lys Glu Ser
65 70 75 80

Leu Gly His Val Asp
85

<210> 469
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 469

Leu Gly Val Glu Val Ala Ser Ala His Asp Leu Met Pro Lys Asp Gly
1 5 10 15

Gln Gly Ser Ala Ser Ala Cys Val Glu Leu Thr Phe Asp Gly Gln Arg
20 25 30

Phe Arg Thr Ala Ile Lys Asp Lys Asp Leu Asn Pro Val Trp Asn Glu
35 40 45

Arg Phe Tyr Phe Asn Val Ser Asp Pro Ser Asn Leu Pro Glu Leu Ala
50 55 60

Leu Glu Ala Tyr Val Tyr Asn Ile Asn Arg Ser Ile Asp Gly Ser Arg
65 70 75 80

Ser Phe Leu Gly Lys Val Arg
85

<210> 470
<211> 87

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 470

Leu Gly Val Glu Val Ala Ser Ala His Asp Leu Met Pro Lys Asp Gly
1 5 10 15

Gln Gly Ser Ala Ser Ala Cys Val Glu Leu Thr Phe Asp Gly Gln Arg
20 25 30

Phe Arg Thr Ala Ile Lys Asp Lys Asp Leu Asn Pro Val Trp Asn Glu
35 40 45

Arg Phe Tyr Phe Asn Val Ser Asp Pro Ser Asn Leu Pro Glu Leu Ala
50 55 60

Leu Glu Ala Tyr Val Tyr Asn Ile Asn Arg Ser Val Asp Gly Ser Arg
65 70 75 80

Ser Phe Leu Gly Lys Val Arg
85

<210> 471
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 471

Leu Gly Val Asp Val Ile Gly Ala His Asn Leu Phe Pro Lys Asp Gly
1 5 10 15

Gln Gly Thr Ser Asn Ala Tyr Val Glu Leu Tyr Phe Asp Gly Gln Lys
20 25 30

His Arg Thr Thr Ile Lys Asp Arg Asp Leu Asn Pro Val Trp Asn Glu
35 40 45

Ser Phe Phe Phe Asn Ile Ser Asp Pro Ser Arg Leu His Tyr Leu Asn
50 55 60

Leu Glu Ala Gln Ala Tyr Ser His Asn Arg Ser Thr Asn Gly Arg Ser
65 70 75 80

Phe Leu Gly Lys Val Ser
85

<210> 472
<211> 86

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 472

Leu Gly Val Asp Val Ile Gly Ala His Asn Leu Phe Pro Lys Asp Gly
1 5 10 15

Gln Gly Thr Ser Asn Ala Tyr Val Glu Leu Tyr Phe Asp Gly Gln Lys
20 25 30

His Arg Thr Thr Ile Lys Asp Arg Asp Leu Asn Pro Val Trp Asn Glu
35 40 45

Ser Phe Phe Phe Asn Ile Ser Asp Pro Ser Arg Leu His Tyr Leu Asn
50 55 60

Leu Glu Ala Gln Ala Tyr Ser His Asn Arg Ser Thr Asn Gly Arg Ser
65 70 75 80

Phe Leu Gly Lys Val Ser
85

<210> 473
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 473

Leu Gly Val Glu Val Thr Ser Ala His Asp Leu Leu Pro Lys Glu Gln
1 5 10 15

Gly Thr Cys Asn Pro Tyr Val Glu Ile Glu Phe Asp Asp Gln Lys Phe
20 25 30

Arg Thr Ala Ile Lys Glu Arg Asp Ile Asn Pro Val Trp Asn Glu Gln
35 40 45

Phe Tyr Phe Asn Ile Ser Asp Pro Ser Arg Leu Thr Glu Lys Asp Leu
50 55 60

Glu Ala Tyr Val Tyr His Ala Asn Arg Ala Ser Asn Ser Lys Thr Cys
65 70 75 80

Leu Gly Lys Val Arg
85

<210> 474
<211> 86

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 474

Leu Cys Val Glu Val Val Gly Ala His Asp Leu Val Ala Lys Asp Gly
1 5 10 15

Glu Gly Ser Ser Thr Thr Phe Val Glu Leu Glu Phe Asp Asp Gln Lys
20 25 30

Phe Arg Thr Thr Thr Lys Asp Lys Asp Leu Ser Pro Tyr Trp Asn Glu
35 40 45

Ile Phe Tyr Phe Asn Ile Thr Asp Pro Ser Lys Leu Ser Asn Leu Asn
50 55 60

Leu Glu Ala Cys Ile Asn His Tyr Asn Lys Thr Asn Gly Ser Lys Ile
65 70 75 80

Pro Leu Gly Lys Val Lys
85

<210> 475
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 475

Leu Gly Val Glu Val Ile Ser Ala Gln Gly Leu Leu Gln Arg Asp Lys
1 5 10 15

His Asn Ser Cys Ser Pro Phe Val Glu Leu Lys Phe Asp Asn Gln Ile
20 25 30

Phe Arg Ala Thr Thr Lys His Asn Asp Pro Asn Pro Val Trp His Glu
35 40 45

Cys Phe Tyr Phe Val Val Ser Asp Pro Ser Val
50 55

<210> 476
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 476

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Leu Gly Val Glu Val Ile Ser Ala Gln Gly Leu Leu Gln Arg Asp Lys
1   5   10   15

His Asn Ser Cys Ser Pro Phe Val Glu Leu Lys Phe Asp Asn Gln Ile
            20   25   30

Phe Arg Ala Thr Thr Lys His Asn Asp Pro Asn Pro Val Trp His Glu
        35   40   45

Cys Phe Tyr Phe Val Val Ser Asp Pro Ser Val Leu Ser Thr Arg Thr
    50   55   60

Leu Glu Ala His Val Tyr Ser Tyr Gln Asn Glu Phe Asp Ala Lys Pro
65   70   75   80

Phe Leu Gly Lys Val Arg
                85

<210> 477
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 477

Leu Gly Val Glu Val Ile Ser Ala Arg Leu Lys Pro Arg Glu Asp Tyr
1   5   10   15

Gly Gly Val Asn Ala Tyr Val Glu Leu Arg Phe Asp Asp Gln Lys Val
            20   25   30

Ile Thr Met Thr Lys Ile Asp Asp Ser Ser Pro Val Trp Asn Glu Lys
        35   40   45

Phe Phe Phe Asn Ile Ser Asp Thr Glu Asp Leu Ser Asn Gln Phe Leu
    50   55   60

Asp Ala Tyr Val Tyr Asn Lys Thr Ser Ser Ile Thr Lys Ser Cys Leu
65   70   75   80

Gly Lys Ile Arg

<210> 478
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 478

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Leu Val Val Glu Val Ile Ser Ala Asp Ile Pro Ser Ser Ser Asn Thr
1   5   10   15

Ser Gln Thr Asn Tyr Ser Val Glu Leu His Phe Asn Ser Gln Ser Lys
            20   25   30

Ser Thr Thr Ile Lys Glu Asn Val Ala Val Trp Asn Glu Arg Phe Ser
        35   40   45

Phe Asp Met Arg Gln Arg Glu Asp Pro Ser Gly Asn Leu Ile Leu Glu
    50   55   60

Ala Ala Val Tyr Cys Phe Asp Gln Met Ser Asn Ser Lys Ser Leu Leu
65   70   75   80

Gly Lys Val Leu

<210> 479
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 479

Val Val Val Glu Val Cys Asn Ala Arg Asn Leu Met Pro Lys Asp Gly
1   5   10   15

Gln Gly Thr Ala Ser Ala Tyr Ala Val Val Asp Phe Asp Gly Gln Arg
            20   25   30

Arg Arg Thr Ala Thr Arg Pro Arg Asp Leu Asn Pro Gln Trp Gly Glu
        35   40   45

Arg Leu Glu Phe Leu Val His Asp Pro Asp Ala Met Cys Ala Glu Thr
    50   55   60

Leu Glu Leu Asn Leu Tyr Asn Asp Lys Lys Ala Ile Ala Ala Thr Gly
65   70   75   80

Gly Gly Gly Arg Arg Gly Gly Thr Phe Leu Gly Lys Val Lys
                85   90

<210> 480
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 480

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Leu Ile Val Glu Ile Cys Ser Ala Arg Asn Leu Met Pro Lys Asp Gly
1   5   10   15

Gln Gly Thr Ala Ser Ala Tyr Ala Ile Val Asp Phe Asp Gly Gln Arg
            20   25   30

Arg Arg Thr Lys Thr Lys Phe Arg Asp Leu Asn Pro Gln Trp Asp Glu
        35   40   45

Lys Leu Glu Phe Phe Val His Asp Val Ala Thr Met Gly Glu Glu Ile
    50   55   60

Leu Glu Ile Asn Leu Cys Asn Asp Lys Lys Thr Gly Lys Arg Ser Thr
65   70   75   80

Phe Leu Gly Lys Val Lys
                85

<210> 481
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 481

Leu Val Val Glu Val Val Glu Ala Arg Asn Ile Leu Pro Lys Asp Gly
1   5   10   15

Gln Gly Ser Ser Ser Ala Tyr Val Val Val Asp Phe Asp Ala Gln Lys
            20   25   30

Lys Arg Thr Ser Thr Lys Phe Arg Asp Leu Asn Pro Ile Trp Asn Glu
        35   40   45

Met Leu Asp Phe Ala Val Ser Asp Pro Lys Asn Met Asp Tyr Asp Glu
    50   55   60

Leu Asp Ile Glu Val Tyr Asn Asp Lys Arg Phe Gly Asn Gly Gly Gly
65   70   75   80

Arg Lys Asn His Phe Leu Gly Arg Val Lys
                85   90

<210> 482
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 482

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Leu Val Val Glu Val Val Glu Ala Arg Asn Ile Leu Pro Lys Asp Gly
1   5   10   15

Gln Gly Ser Ser Ser Ala Tyr Val Val Val Asp Phe Asp Ala Gln Lys
            20   25   30

Lys Arg Thr Ser Thr Lys Phe Arg Asp Leu Asn Pro Ile Trp Asn Glu
        35   40   45

Met Leu Asp Phe Ala Val Ser Asp Pro Lys Asn Met Asp Tyr Asp Glu
    50   55   60

Leu Asp Ile Glu Val Tyr Asn Asp Lys Arg Phe Gly Asn Gly Gly Gly
65   70   75   80

Arg Lys Asn His Phe Leu Gly Arg Val Lys
                85   90

<210> 483
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 483

Leu Ala Val Glu Val Val Asp Ala Arg Asp Leu Val Pro Lys Asp Gly
1   5   10   15

Leu Gly Thr Ser Ser Ala Phe Ala Val Val Asp Phe Asp Gly Gln Arg
            20   25   30

Lys Arg Thr Arg Thr Val Pro Arg Asp Leu Ser Pro Gln Trp His Glu
        35   40   45

Arg Leu Glu Phe Ala Val His Asp Pro Ala Ala Met His Ala Glu Ala
    50   55   60

Leu Asp Val Ser Leu Tyr His Asp Arg Arg Phe Asn Pro Ser Gly Gly
65   70   75   80

Gly Gly Gly Gly Gly Gly Lys Asn His Phe Leu Gly Arg Val Arg
                85   90   95

<210> 484
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 484

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```
Leu Ile Val Glu Val Ile Asn Ala His Asp Leu Met Pro Lys Asp Gly
1               5                   10                  15

Glu Gly Ser Ala Ser Thr Phe Val Glu Val Asp Phe Glu Asn Gln Leu
            20                  25                  30

Ser Arg Thr Arg Thr Val Pro Lys Asn Leu Asn Pro Thr Trp Asn Gln
        35                  40                  45

Lys Leu Val Phe Asn Leu Asp Thr Thr Lys Pro Tyr His His Lys Thr
    50                  55                  60

Ile Glu Val Ser Val Tyr Asn Asp Arg Arg Gln Pro Asn Pro Gly Arg
65                  70                  75                  80

Asn Phe Leu Gly Arg Val Arg
                85
```

<210> 485
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 485

```
Leu Val Val His Val Val Asp Ala Gln Tyr Leu Met Pro Arg Asp Gly
1               5                   10                  15

Gln Gly Ser Ala Ser Pro Phe Val Glu Val Asp Phe Leu Asn Gln Leu
            20                  25                  30

Ser Lys Thr Arg Thr Val Pro Lys Ser Leu Asn Pro Val Trp Asn Gln
        35                  40                  45

Lys Leu Tyr Phe Asp Tyr Asp Gln Ser Val Ile Asn Gln His Asn Gln
    50                  55                  60

His Ile Glu Val Ser Val Tyr His Glu Arg Arg Pro Ile Pro Gly Arg
65                  70                  75                  80

Ser Phe Leu Gly Arg Val Lys
                85
```

<210> 486
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 486

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Leu Val Val Glu Val Val Ala Ala His Asn Leu Met Pro Lys Asp Gly
1 5 10 15

Gln Gly Ser Ser Ser Ala Tyr Val Glu Val Glu Phe Glu His Gln Arg
20 25 30

Arg Arg Thr Arg Ala Arg Pro Lys Glu Leu Asn Pro Val Trp Asn Glu
35 40 45

Arg Leu Val Phe Ala Val Ala Asp Pro Asp Asp Leu Pro Tyr Arg Ala
50 55 60

Ile Asp Val Gly Val Tyr Asn Asp Arg Ala Ala Ser Gly Gly Val Ala
65 70 75 80

Gly Gly Gly Gly Ala Ala Pro His Gly Arg Asn Phe Leu Gly Lys Val
85 90 95

Arg

<210> 487
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 487

Leu Val Val Glu Ile Val Gly Ala His Asn Leu Met Pro Lys Asp Gly
1 5 10 15

Glu Asp Ser Ser Ser Pro Phe Val Glu Val Gln Phe Glu Asn Gln Arg
20 25 30

Leu Arg Thr Lys Val Lys Pro Lys Asp Leu Asn Pro Ile Trp Asn Glu
35 40 45

Lys Leu Val Phe His Val Ile Asp Val Asn Asp Leu Arg His Lys Ala
50 55 60

Leu Glu Ile Asn Val Tyr Asn Glu Lys Arg Ser Ser Asn Ser Arg Asn
65 70 75 80

Phe Leu Gly Lys Val Arg
85

<210> 488
<211> 86
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 488

Leu Val Val Glu Ile Val Asp Ala Ser Asp Leu Met Pro Lys Asp Gly
1 5 10 15

Gln Gly Ser Ala Ser Pro Phe Val Glu Val Glu Phe Asp Glu Gln Arg
20 25 30

Gln Arg Thr Gln Thr Arg Phe Lys Asp Leu Asn Pro Gln Trp Asn Glu
35 40 45

Lys Leu Val Phe Asn Val Gly Asp Leu Lys Arg Leu Asn Asn Lys Thr
50 55 60

Val Asp Val Thr Val Tyr Asp Asp Arg Arg Asp Asn Gln Pro Gly Lys
65 70 75 80

Phe Leu Gly Arg Val Lys
85

<210> 489
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 489

Val Gly Val Glu Ile Leu Asp Ala Ser Glu Leu Ala Pro Lys Asp Gly
1 5 10 15

Ala Gly Ala Cys Asn Ala Phe Val Glu Val Glu Phe Asp Gly Gln Lys
20 25 30

Gln Arg Thr Pro Thr Lys Pro Ala Asp Arg Ser Pro Gln Trp Asn His
35 40 45

Thr Leu Val Phe Asp Val Arg Asp Pro Ser Arg Leu Pro Ser Leu Pro
50 55 60

Val Asp Val Ser Val His His Asp Arg Ser Leu Thr Asp His His Ala
65 70 75 80

Thr Arg Leu His Thr Phe Leu Gly Arg Val Arg
85 90

<210> 490
<211> 90
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 490

Leu Val Val Glu Val Val Asp Ala Lys Asp Leu Thr Pro Lys Asp Gly
1 5 10 15

His Gly Thr Ser Ser Pro Tyr Val Val Leu Asp Tyr Tyr Gly Gln Arg
20 25 30

Arg Arg Thr Arg Thr Ile Val Arg Asp Leu Asn Pro Val Trp Asn Glu
35 40 45

Thr Leu Glu Phe Ser Leu Ala Lys Arg Pro Ser His Gln Leu Phe Thr
50 55 60

Asp Val Leu Glu Leu Asp Met Tyr His Asp Lys Asn Phe Gly Gln Thr
65 70 75 80

Arg Arg Asn Asn Phe Leu Gly Arg Ile Arg
85 90

<210> 491
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 491

Leu Asn Val Arg Val Val Arg Gly Ser Asn Leu Ala Ile Cys Asp Pro
1 5 10 15

Leu Thr His Thr Ser Asp Pro Tyr Val Val Leu His Tyr Gly Ala Gln
20 25 30

Lys Val Lys Thr Ser Val Gln Lys Lys Asn Pro Asn Pro Val Trp Asn
35 40 45

Glu Val Leu Gln Leu Ser Val Thr Asn Pro Thr Lys Pro Val His Leu
50 55 60

Glu Val Phe Asp Glu Asp Lys Phe Thr Ala Asp Asp Ser Met Gly Val
65 70 75 80

Ala Glu

<210> 492
<211> 82
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 492

Leu Asn Val Arg Val Val Arg Gly Ser Asn Leu Ile Ile Ala Asp Pro
1 5 10 15

Leu Thr His Thr Ser Asp Pro Tyr Val Val Leu Ser Tyr Gly Pro Gln
20 25 30

Lys Val Lys Thr Ser Val Gln Lys Lys Asn Ser Asn Pro Val Trp Asn
35 40 45

Glu Val Leu Gln Leu Ala Val Thr Asn Pro Thr Lys Pro Val Lys Leu
50 55 60

Glu Val Phe Asp Glu Asp Lys Phe Thr Ala Asp Asp Ser Met Gly Val
65 70 75 80

Ala Glu

<210> 493
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 493

Leu Lys Val Arg Val Met Arg Gly Leu Asn Leu Ala Ile Cys Asp Pro
1 5 10 15

Leu Thr His Ser Ser Asp Pro Tyr Val Val Leu Arg His Gly Ser Gln
20 25 30

Lys Val Lys Ser Ser Ile Arg Tyr His Ser Ile Asn Pro Glu Trp Asn
35 40 45

Glu Glu Leu Thr Leu Ser Ile Thr Asn Met Met Leu Pro Val Lys Ile
50 55 60

Glu Val Phe Asp Lys Asp Thr Phe Thr Lys Asp Asp Ser Met Gly Asp
65 70 75 80

Ala Glu

<210> 494
<211> 80
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 494

Leu Lys Ile Arg Val Val Arg Gly Ile Asn Leu Ala Tyr Arg Asp Thr
1 5 10 15

Arg Gly Ser Asp Pro Tyr Val Val Leu Arg Leu Gly Lys Gln Lys Val
20 25 30

Lys Thr Ser Val Lys Lys Lys Ser Val Asn Pro Ile Trp His Glu Glu
35 40 45

Leu Thr Leu Ser Ile Met Asn Pro Ile Ala Pro Ile Lys Leu Gly Val
50 55 60

Phe Asp Lys Asp Thr Phe Ser Arg Asp Asp Pro Met Gly Asp Ala Glu
65 70 75 80

<210> 495
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 495

Leu Ser Val Arg Val Leu Arg Gly Val Asn Leu Val Ser Arg Asp Ala
1 5 10 15

Gly Gly Ser Asp Pro Tyr Val Val Leu His Leu Asp Asn Gln Lys Leu
20 25 30

Lys Thr Gly Val Val Lys Lys Thr Thr Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Thr Leu Ala Val Arg Asn Pro Glu Thr Pro Ile Gln Leu Glu Val
50 55 60

Phe Asp Lys Asp Thr Phe Ser Lys Asp Asp Gln Met Gly Asp Ala Glu
65 70 75 80

<210> 496
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 496

Val Lys Val Arg Val Val Arg Gly Val Asn Leu Ala Val Arg Asp Leu
1 5 10 15

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Arg Ser Ser Asp Pro Tyr Val Ile Val Arg Met Gly Lys Gln Lys Leu
20 25 30

Lys Thr Arg Val Ile Lys Lys Thr Thr Asn Pro Glu Trp Asn Asp Glu
35 40 45

Leu Thr Leu Ser Ile Glu Asp Pro Ala Val Pro Val Arg Leu Glu Val
50 55 60

Tyr Asp Lys Asp Thr Phe Ile Asp Asp Ala Met Gly Asn Ala Glu
65 70 75

<210> 497
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 497

Leu Arg Ile Arg Val Lys Arg Gly Ile Asn Leu Ala Gln Arg Asp Thr
1 5 10 15

Leu Gly Ser Asp Pro Phe Val Val Ile Thr Met Gly Ser Gln Lys Leu
20 25 30

Lys Thr Arg Val Val Glu Asn Asn Cys Asn Pro Glu Trp Asn Glu Glu
35 40 45

Leu Thr Leu Ala Leu Arg His Pro Asp Glu Pro Val Asn Leu Ile Val
50 55 60

Tyr Asp Lys Asp Thr Phe Thr Ser His Asp Lys Met Gly Asp Ala Lys
65 70 75 80

<210> 498
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 498

Leu Arg Ile Arg Val Lys Arg Gly Ile Asn Leu Ala Gln Arg Asp Thr
1 5 10 15

Leu Ser Ser Asp Pro Phe Val Val Ile Thr Met Gly Ser Gln Lys Leu
20 25 30

Lys Thr Arg Val Val Glu Asn Asn Cys Asn Pro Glu Trp Asn Glu Glu
35 40 45

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Leu Thr Leu Ala Leu Arg His Pro Asp Glu Pro Val Asn Leu Ile Val
50 55 60

Tyr Asp Lys Asp Thr Phe Thr Ser His Asp Lys Met Gly Asp Ala Lys
65 70 75 80

<210> 499
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 499

Leu Arg Ile Arg Val Lys Arg Gly Ile Asn Leu Ala Gln Arg Asp Thr
1 5 10 15

Leu Ser Ser Asp Pro Phe Val Val Ile Thr Met Gly Ser Gln Val Phe
20 25 30

<210> 500
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 500

Val Arg Ile Leu Val Lys Arg Gly Ile Asp Leu Ala Arg Arg Asp Ala
1 5 10 15

Leu Ser Ser Asp Pro Phe Val Val Ile Thr Met Gly Pro Gln Lys Leu
20 25 30

Lys Ser Phe Thr Val Lys Asn Asn Cys Asn Pro Glu Trp Asn Glu Glu
35 40 45

Leu Thr Leu Ala Ile Glu Asp Pro Asn Glu Pro Val Lys Leu Met Val
50 55 60

Tyr Asp Lys Asp Thr Phe Thr Ala Asp Asp Lys Met Gly Asp Ala Gln
65 70 75 80

<210> 501
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 501

Leu Arg Ile Arg Val Lys Arg Gly Ile Asn Leu Val Ser Arg Asp Ser
1 5 10 15

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Asn Thr Ser Asp Pro Phe Val Val Val Thr Met Gly Ser Gln Lys Leu
20 25 30

Lys Thr Arg Gly Val Glu Asn Ser Cys Asn Pro Glu Trp Asp Asp Glu
35 40 45

Leu Thr Leu Gly Ile Asn Asp Pro Asn Gln His Val Thr Leu Glu Val
50 55 60

Tyr Asp Lys Asp Thr Phe Thr Ser His Asp Pro Met Gly Asp Ala Glu
65 70 75 80

<210> 502
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 502

Leu Arg Val His Val Lys Arg Gly Ile Asn Leu Ala Ile Arg Asp Ala
1 5 10 15

Thr Thr Ser Asp Pro Tyr Val Val Ile Thr Leu Ala Asn Gln Lys Leu
20 25 30

Lys Thr Arg Val Ile Asn Asn Asn Cys Asn Pro Val Trp Asn Glu Gln
35 40 45

Leu Thr Leu Ser Ile Lys Asp Val Asn Asp Pro Ile Arg Leu Thr Val
50 55 60

Phe Asp Lys Asp Arg Phe Ser Gly Asp Asp Lys Met Gly Asp Ala Glu
65 70 75 80

<210> 503
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 503

Leu Thr Ile His Val Lys Arg Gly Ile Asn Leu Ala Ile Arg Asp His
1 5 10 15

Arg Ser Ser Asp Pro Tyr Ile Val Leu Asn Val Ala Asp Gln Thr Leu
20 25 30

Lys Thr Arg Val Val Lys Lys Asn Cys Asn Pro Val Trp Asn Glu Glu
35 40 45

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Met Thr Val Ala Ile Lys Asp Pro Asn Val Pro Ile Arg Leu Thr Val
    50   55   60

Phe Asp Trp Asp Lys Phe Thr Gly Asp Asp Lys Met Gly Asp Ala Asn
65   70   75   80

<210> 504
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 504

Leu Lys Leu Arg Ile Lys Arg Gly Ile Asn Leu Ala Ile Arg Asp Ser
1   5   10   15

Asn Ser Ser Asp Pro Tyr Val Val Val Asn Ile Gly His Glu Gln Lys
            20   25   30

Leu Lys Thr Arg Val Val Lys Asn Asn Cys Asn Pro Glu Trp Asn Glu
        35   40   45

Glu Leu Thr Leu Ser Ile Arg Asp Val Arg Val Pro Ile Cys Leu Thr
    50   55   60

Val Phe Asp Lys Asp Thr Phe Phe Val Asp Asp Lys Met Gly Asp Ala
65   70   75   80

Glu

<210> 505
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 505

Leu Arg Ile Arg Ile Lys Arg Gly Val Asn Leu Ala Val Arg Asp Ile
1   5   10   15

Ser Ser Ser Asp Pro Tyr Val Val Val Lys Met Gly Lys Gln Lys Leu
            20   25   30

Lys Thr Arg Val Ile Asn Lys Asp Val Asn Pro Glu Trp Asn Glu Asp
        35   40   45

Leu Thr Leu Ser Val Thr Asp Ser Asn Leu Thr Val Leu Leu Thr Val
    50   55   60

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Tyr Asp His Asp Met Phe Ser Lys Asp Asp Lys Met Gly Asp Ala Glu
65 70 75 80

<210> 506
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 506

Leu Arg Ile Arg Ile Lys Arg Gly Val Asn Leu Ala Val Arg Asp Leu
1 5 10 15

Asn Ser Ser Asp Pro Tyr Val Val Val Lys Met Ala Lys Gln Lys Leu
20 25 30

Lys Thr Arg Val Ile Tyr Lys Asn Val Asn Pro Glu Trp Asn Glu Asp
35 40 45

Leu Thr Leu Ser Val Ser Asp Pro Asn Leu Thr Val Leu Leu Thr Val
50 55 60

Tyr Asp Tyr Asp Thr Phe Thr Lys Asp Asp Lys Met Gly Asp Ala Glu
65 70 75 80

<210> 507
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 507

Leu Arg Ile Arg Ile Lys Arg Gly Val Asn Leu Ala Val Arg Asp Val
1 5 10 15

Asn Thr Ser Asp Pro Tyr Ala Val Val Lys Met Gly Lys Gln Arg Leu
20 25 30

Lys Thr His Val Ile Lys Lys Asp Val Asn Pro Glu Trp Asn Glu Asp
35 40 45

Leu Thr Leu Ser Ile Thr Asp Pro Val Val Pro Phe Lys Leu Thr Val
50 55 60

Tyr Asp Tyr Asp Thr Phe Ser Lys Asp Asp Lys Met Gly Asp Ala Glu
65 70 75 80

<210> 508
<211> 80

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 508

Leu Arg Ile His Val Lys Arg Gly Val Asn Leu Ala Ile Arg Asp Ile
1   5   10   15

Ser Ser Ser Asp Pro Tyr Ile Val Val His Cys Gly Lys Gln Lys Leu
            20   25   30

Lys Thr Arg Val Val Lys His Ser Val Asn Pro Glu Trp Asn Asp Asp
        35   40   45

Leu Thr Leu Ser Val Thr Asp Pro Asn Leu Pro Ile Lys Leu Thr Val
    50   55   60

Tyr Asp Tyr Asp Leu Leu Ser Ala Asp Asp Lys Met Gly Glu Ala Glu
65   70   75   80

<210> 509
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 509

Leu Arg Leu His Val Ile Arg Gly Val Asn Leu Ala Ile Arg Asp Ser
1   5   10   15

Gln Ser Ser Asp Pro Tyr Val Ile Val Arg Met Gly Lys Gln Lys Leu
            20   25   30

Arg Thr Arg Val Met Lys Lys Asn Leu Asn Thr Glu Trp Asn Glu Asp
        35   40   45

Leu Thr Leu Ser Val Thr Asp Pro Thr Leu Pro Val Lys Ile Met Val
    50   55   60

Tyr Asp Arg Asp Arg Phe Ser Arg Asp Asp Lys Met Gly Asp Ala Ile
65   70   75   80

<210> 510
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 510

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Leu Arg Val Arg Val Gln Arg Gly Val Asn Leu Ala Val Arg Asp Val
1 5 10 15

Ser Ser Ser Asp Pro Tyr Val Val Leu Lys Leu Gly Arg Gln Lys Leu
20 25 30

Lys Thr Lys Val Val Lys Gln Asn Val Asn Pro Gln Trp Gln Glu Asp
35 40 45

Leu Ser Phe Thr Val Thr Asp Pro Asn Leu Pro Leu Thr Leu Ile Val
50 55 60

Tyr Asp His Asp Phe Phe Ser Lys Asp Asp Lys Met Gly Asp Ala Glu
65 70 75 80

<210> 511
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 511

Leu Lys Val Thr Ile Lys Lys Gly Thr Asn Leu Ala Ile Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Val Leu Asn Leu Gly Lys Gln Lys Leu
20 25 30

Gln Thr Thr Val Met Asn Ser Asn Leu Asn Pro Val Trp Asn Gln Glu
35 40 45

Leu Met Leu Ser Val Pro Glu Ser Tyr Gly Pro Val Lys Leu Gln Val
50 55 60

Tyr Asp Tyr Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Asp
65 70 75 80

<210> 512
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 512

Leu Lys Val Thr Ile Lys Lys Gly Thr Asn Leu Ala Ile Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Val Leu Asn Leu Gly Lys Gln Lys Leu
20 25 30

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Gln Thr Thr Val Met Asn Ser Asn Leu Asn Pro Val Trp Asn Gln Glu
35 40 45

Leu Met Leu Ser Val Pro Glu Ser Tyr Gly Pro Val Lys Leu Gln Val
50 55 60

Tyr Asp Tyr Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Asp
65 70 75 80

<210> 513
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 513

Leu Lys Val Thr Ile Lys Lys Gly Thr Asn Met Ala Ile Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
20 25 30

Gln Ser Thr Val Val Lys Ser Asn Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Met Leu Ser Val Pro His Asn Tyr Gly Ser Val Lys Leu Gln Val
50 55 60

Phe Asp Tyr Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Glu
65 70 75 80

<210> 514
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 514

Leu Lys Val Thr Ile Lys Lys Gly Thr Asn Met Ala Ile Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
20 25 30

Gln Ser Thr Val Val Lys Ser Asn Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Met Leu Ser Val Pro His Asn Tyr Gly Ser Val Lys Leu Gln Val
50 55 60

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Phe Asp Tyr Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Glu
65 70 75 80

<210> 515
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 515

Leu Lys Val Thr Ile Lys Lys Gly Thr Asn Met Ala Ile Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
20 25 30

Gln Ser Thr Val Val Lys Ser Asn Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Met Leu Ser Val Pro His Asn Tyr Gly Ser Val Lys Leu Gln Val
50 55 60

Phe Asp Tyr Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Glu
65 70 75 80

<210> 516
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 516

Leu Lys Val Lys Val Val Lys Gly Thr Asn Leu Ala Ile Arg Asp Met
1 5 10 15

Arg Thr Ser Asp Pro Tyr Val Val Leu Lys Leu Gly Gln Gln Thr Val
20 25 30

Gln Thr Thr Val Ile Arg Ser Asn Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Met Leu Ser Val Pro Gln Gln Phe Gly Pro Ile Ser Leu Glu Val
50 55 60

Phe Asp His Asp Leu Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Gln
65 70 75 80

<210> 517
<211> 80
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 517

```
Leu Asn Val Lys Val Lys Gly Gly Thr Asn Leu Ala Ile Arg Asp Met
1               5                   10                  15

Ser Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
            20                  25                  30

Gln Thr Ser Val Ile Lys Ala Asn Leu Asn Pro Val Trp Asn Glu Glu
        35                  40                  45

Leu Lys Leu Ser Val Pro Gln Gln Tyr Gly Pro Leu Lys Leu Gln Ala
    50                  55                  60

Phe Asp His Asp Met Leu Ser Lys Asp Asp Leu Met Gly Glu Ala Glu
65                  70                  75                  80
```

<210> 518
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 518

```
Leu Asn Val Lys Val Lys Gly Gly Thr Asn Leu Ala Ile Arg Asp Met
1               5                   10                  15

Ser Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
            20                  25                  30

Gln Thr Ser Val Ile Lys Ala Asn Leu Asn Pro Val Trp Asn Glu Glu
        35                  40                  45

Leu Lys Leu Ser Val Pro Gln Gln Tyr Gly Pro Leu Lys Leu Gln Val
    50                  55                  60

Phe Asp His Asp Met Leu Ser Lys Asp Asp Leu Met Gly Glu Ala Glu
65                  70                  75                  80
```

<210> 519
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 519

```
Ile Lys Val Lys Val Ile Arg Gly Thr Lys Leu Ala Val Arg Asp Ile
1               5                   10                  15
```

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Leu Ser Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Gln Gln Lys Ala
20 25 30

Lys Thr Lys Val Ile Lys Ser Asn Leu Asn Pro Val Trp Asn Glu Val
35 40 45

Leu Thr Leu Ser Val Pro Gln Lys Tyr Gly Pro Leu Lys Leu Gln Val
50 55 60

Tyr Asp His Asp Val Leu Ser Arg Asp Asp Ile Met Gly Glu Ala Glu
65 70 75 80

<210> 520
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 520

Leu Asn Ile Thr Val Val Arg Gly Ile Gln Leu Ala Val Arg Asp Met
1 5 10 15

Leu Thr Ser Asp Pro Tyr Val Val Leu Thr Leu Gly Glu Gln Lys Ala
20 25 30

Gln Thr Thr Val Lys Pro Ser Asp Leu Asn Pro Val Trp Asn Glu Val
35 40 45

Leu Lys Ile Ser Ile Pro Arg Asn Tyr Gly Pro Leu Lys Leu Glu Val
50 55 60

Tyr Asp His Asp Thr Phe Ser Ala Asp Asp Ile Met Gly Glu Ala Glu
65 70 75 80

<210> 521
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 521

Ile Lys Val Asp Ile Arg Arg Gly Thr Asn Leu Ala Val Arg Asp Val
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Met Leu Asn Leu Gly His Gln Thr Met
20 25 30

Lys Thr Lys Val Ile Lys Asn Thr Leu Asn Pro Val Trp Asn Glu Arg
35 40 45

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Leu Met Leu Ser Ile Pro His Pro Val Pro Pro Leu Lys Leu Gln Val
50 55 60

Phe Asp Lys Asp Thr Phe Ser Ser Asp Asp Arg Met Gly Asp Val Glu
65 70 75 80

<210> 522
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 522

Ile Lys Val Asn Val Ile Arg Gly Thr Asn Leu Ala Val Arg Asp Met
1 5 10 15

Met Ser Ser Asp Pro Tyr Val Ile Leu Asn Leu Gly His Gln Ser Met
20 25 30

Lys Thr Lys Val Ile Lys Ser Ser Leu Asn Pro Val Trp Asn Glu Arg
35 40 45

Ile Leu Leu Ser Ile Pro Asp Pro Ile Pro Met Leu Lys Leu Gln Val
50 55 60

Tyr Asp Lys Asp Thr Phe Thr Thr Asp Asp Arg Met Gly Glu Ala Glu
65 70 75 80

<210> 523
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 523

Ile Lys Val Asn Val Val Lys Gly Thr Asn Leu Ala Val Arg Asp Val
1 5 10 15

Met Thr Ser Asp Pro Tyr Val Ile Leu Ala Leu Gly Gln Gln Ser Val
20 25 30

Lys Thr Arg Val Ile Lys Asn Asn Leu Asn Pro Val Trp Asn Glu Thr
35 40 45

Leu Met Leu Ser Ile Pro Glu Pro Met Pro Pro Leu Lys Val Leu Val
50 55 60

Tyr Asp Lys Asp Thr Phe Ser Thr Asp Asp Phe Met Gly Glu Ala Glu
65 70 75 80

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<210> 524
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 524

Ile Lys Val Asn Val Val Lys Gly Thr Asn Leu Ala Val Arg Asp Val
1 5 10 15

Met Thr Ser Asp Pro Tyr Val Ile Leu Ala Leu Gly Gln Gln Ser Val
20 25 30

Lys Thr Arg Val Ile Lys Asn Asn Leu Asn Pro Val Trp Asn Glu Thr
35 40 45

Leu Met Leu Ser Ile Pro Glu Pro Met Pro Pro Leu Lys Val Leu Val
50 55 60

Tyr Asp Lys Asp Thr Phe Ser Thr Asp Asp Phe Met Gly Glu Ala Glu
65 70 75 80

<210> 525
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 525

Ile Lys Val Asn Val Arg Lys Gly Thr His Leu Ala Ile Arg Asp Val
1 5 10 15

Val Thr Ser Asp Pro Tyr Val Ile Leu Ser Leu Gly His Gln Ser Val
20 25 30

Lys Thr Arg Val Ile Arg Asn Asn Leu Asn Pro Val Trp Asn Glu Ser
35 40 45

Leu Met Leu Ser Ile Pro Glu Asn Ile Pro Pro Leu Lys Val Leu Val
50 55 60

Tyr Asp Lys Asp Thr Phe Ser Thr Asp Asp Phe Met Gly Glu Ala Glu
65 70 75 80

<210> 526
<211> 80
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 526

Leu Gln Val Thr Val Ile Gln Gly Lys Lys Leu Val Ile Arg Asp Phe
1   5   10   15

Lys Ser Ser Asp Pro Tyr Val Ile Val Lys Leu Gly Asn Glu Ser Ala
            20   25   30

Lys Thr Lys Val Ile Asn Asn Cys Leu Asn Pro Val Trp Asn Glu Glu
        35   40   45

Leu Asn Phe Thr Leu Lys Asp Pro Ala Ala Val Leu Ala Leu Glu Val
    50   55   60

Phe Asp Lys Asp Arg Phe Lys Ala Asp Asp Lys Met Gly His Ala Ser
65   70   75   80

<210> 527
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 527

Leu Gln Val Thr Val Ile Arg Gly Lys Lys Leu Ala Ile Arg Asp Phe
1   5   10   15

Lys Ser Ser Asp Pro Tyr Val Ile Val Lys Leu Gly Asn Glu Ser Ala
            20   25   30

Lys Thr Lys Val Ile Asn Asn Cys Leu Asn Pro Val Trp Asp Glu Glu
        35   40   45

Leu Ser Phe Thr Leu Lys Asp Pro Ala Ala Val Leu Ser Leu Glu Val
    50   55   60

Phe Asp Lys Asp Arg Phe Lys Ala Asp Asp Lys Met Gly His Ala Thr
65   70   75   80

<210> 528
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 528

Leu Lys Val Ile Val Val Gln Gly Lys Arg Leu Val Ile Arg Asp Phe
1   5   10   15

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Lys Thr Ser Asp Pro Tyr Val Val Leu Lys Leu Gly Asn Gln Thr Ala
20 25 30

Lys Thr Lys Val Ile Asn Ser Cys Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Leu Asn Phe Thr Leu Thr Glu Pro Leu Gly Val Leu Asn Leu Glu Val
50 55 60

Phe Asp Lys Asp Leu Leu Lys Ala Asp Asp Lys Met Gly Asn Ala Phe
65 70 75 80

<210> 529
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 529

Leu Lys Val Val Val Ala Ser Gly Thr Asn Leu Ala Val Arg Asp Phe
1 5 10 15

Thr Ser Ser Asp Pro Tyr Val Val Val Arg Leu Ala Ala Met Asn Lys
20 25 30

Lys Thr Lys Val Ile Asn Ser Cys Leu Asn Pro Val Trp Asn Glu Glu
35 40 45

Met Ser Phe Ser Ile Glu Glu Pro Ala Gly Val Ile Lys Phe Glu Val
50 55 60

Phe Asp Trp Asp Arg Phe Lys Tyr Asp Asp Lys Met Gly His Ala Phe
65 70 75 80

<210> 530
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 530

Val Lys Val Lys Val Val Arg Gly Thr Asn Leu Ala Val Arg Asp Val
1 5 10 15

Phe Ser Ser Asp Pro Tyr Val Val Leu Lys Leu Gly Asn Gln Glu Val
20 25 30

Arg Thr Arg Thr Val Arg Lys Asn Thr Asn Pro Val Trp Asn Glu Asp
35 40 45

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Leu Thr Leu Ile Val Gln Asp Leu Asn His Leu Leu Val Thr Leu Glu
50 55 60

Val Tyr Asp Arg Asp Pro Phe Val Asp Asp Pro Met Gly Ala Ala Phe
65 70 75 80

<210> 531
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 531

Leu Glu Leu Gly Ile Leu Gly Ala Gln Gly Ile Val Pro Met Lys Thr
1 5 10 15

Arg Asp Gly Lys Gly Ser Ser Asp Thr Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Ser Lys Trp Val Arg Thr Arg Thr Ile Val Asn Asn Pro Gly Pro Lys
35 40 45

Phe Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Ala Thr Val Leu
50 55 60

Thr Val Gly Val Phe Asp Asn Gly Gln Leu Gly Glu Lys Gly Gly Glu
65 70 75 80

Lys Thr Ser Ser Ser Lys Asp Ala Lys Ile Gly Lys Val Arg
85 90

<210> 532
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 532

Leu Glu Leu Gly Ile Leu Gly Ala Gln Gly Ile Val Pro Met Lys Thr
1 5 10 15

Arg Asp Gly Lys Gly Ser Ser Asp Thr Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Ser Lys Trp Val Arg Thr Arg Thr Ile Val Asn Asn Pro Gly Pro Lys
35 40 45

Phe Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Ala Thr Val Leu
50 55 60

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Thr Val Gly Val Phe Asp Asn Gly Gln Leu Gly Glu Lys Gly Gly Glu
65 70 75 80

Lys Thr Ser Ser Ser Lys Asp Ala Lys Ile Gly Lys Val Arg
85 90

<210> 533
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 533

Leu Glu Leu Gly Ile Leu Asn Ala Val Gly Leu His Pro Met Lys Thr
1 5 10 15

Arg Glu Gly Arg Gly Thr Ser Asp Thr Phe Cys Val Gly Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Met Val Asp Asn Leu Cys Pro Lys
35 40 45

Tyr Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Ala Thr Val Leu
50 55 60

Thr Val Gly Val Phe Asp Asn Gly Gln Leu Gly Glu Lys Gly Asn Arg
65 70 75 80

Asp Val Lys Ile Gly Lys Ile Arg
85

<210> 534
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 534

Leu Glu Leu Gly Ile Leu Asn Ala Val Gly Leu His Pro Met Lys Thr
1 5 10 15

Arg Glu Gly Arg Gly Thr Ser Asp Thr Phe Cys Val Gly Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Met Val Asp Asn Leu Cys Pro Lys
35 40 45

Tyr Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Ala Thr Val Leu
50 55 60

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Thr Val Gly Val Phe Asp Asn Gly Gln Leu Gly Glu Lys Gly Asn Arg
65 70 75 80

Asp Val Lys Ile Gly Lys Ile Arg
85

<210> 535
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 535

Arg Thr Ile Ser Asn Ser Leu Asp Pro Lys Tyr His Glu Gln Tyr Thr
1 5 10 15

Trp Glu Val Phe Asp Pro Ala Thr Val Leu Thr Val Gly Val Phe Asp
20 25 30

Asn Cys Gln Val Asn Gly Pro Asp Asn Lys Asp Leu Leu Ile Gly Lys
35 40 45

Val Arg
50

<210> 536
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 536

Arg Asp Gly Arg Gly Ala Ala Asp Val Tyr Cys Val Ala Lys Tyr Gly
1 5 10 15

His Lys Trp Val Arg Thr Arg Thr Ile Val Gly Ser Leu Ser Pro Lys
20 25 30

Phe His Glu Gln Tyr Tyr Trp Glu Val Tyr Asp Pro Ser Thr Val Leu
35 40 45

Thr Leu Gly Val Phe Asn Asn Gly Gln Leu Asn Asp Ser Asn Asp Ser
50 55 60

Asn Asp Ser Lys Ile Gly Lys Val Arg
65 70

<210> 537
<211> 91
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 537

Leu Glu Ile Gly Ile Leu Ser Ala Thr Gly Leu Met Pro Met Lys Val
1 5 10 15

Arg Asp Gly Lys Cys Gly Gly Ile Ala Asp Ser Tyr Cys Val Ala Lys
20 25 30

Tyr Gly Pro Lys Trp Val Arg Thr Arg Thr Val Val Asp Ser Leu Cys
35 40 45

Pro Lys Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr
50 55 60

Val Val Thr Val Gly Val Phe Asp Asn Ala Arg Val Asn Glu Asn Asn
65 70 75 80

Asn Ser Arg Asp Val Arg Ile Gly Lys Val Arg
85 90

<210> 538
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 538

Leu Val Leu Gly Val Ile Ser Ala Ser Gly Ser Ile Pro Met Lys Ser
1 5 10 15

Arg Asp Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Ile Val Asp Ser Leu Ser Pro Lys
35 40 45

Trp Ser Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Tyr Thr Val Ile
50 55 60

Thr Val Ala Val Phe Asp Asn
65 70

<210> 539
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 539

Leu Glu Leu Gly Val Leu Asn Ala Thr Gly Leu Met Pro Met Lys Ser
1 5 10 15

Arg Gly Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Thr Lys Trp Val Arg Thr Arg Thr Ile Val Asp Thr Phe Asp Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Tyr Thr Val Ile
50 55 60

Thr Ile Gly Val Phe Asp Asn Leu Lys Leu Phe Gly Ala Gly Asn Glu
65 70 75 80

Asn Arg Leu Ile Asn Asp Ser Arg Ile Gly Lys Ile Arg
85 90

<210> 540
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 540

Leu Glu Leu Gly Ile Leu Asn Ala Thr Gly Leu Met Pro Met Lys Thr
1 5 10 15

Lys Asp Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Ile Arg Thr Arg Thr Ile Ile Asp Ser Phe Thr Pro Arg
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val Val
50 55 60

Thr Val Gly Val Phe Asp Asn Cys His Leu His Gly Gly Glu Lys Ile
65 70 75 80

Gly Gly Ala Lys Asp Ser Arg Ile Gly Lys Val Arg
85 90

<210> 541
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 541

Leu Glu Leu Gly Ile Leu Asn Ala Thr Gly Leu Met Pro Met Lys Thr
1 5 10 15

Lys Asp Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Ile Arg Thr Arg Thr Ile Ile Asp Ser Phe Thr Pro Arg
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val Val
50 55 60

Thr Val Gly Val Phe Asp Asn Cys His Leu His Gly Gly Glu Lys Ile
65 70 75 80

Gly Gly Ala Lys Asp Ser Arg Ile Gly Lys Val Arg
85 90

<210> 542
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 542

Leu Glu Leu Gly Val Leu Asn Ala Thr Gly Leu Met Pro Met Lys Ala
1 5 10 15

Lys Glu Gly Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr
20 25 30

Gly Gln Lys Trp Ile Arg Thr Arg Thr Ile Ile Asp Ser Phe Thr Pro
35 40 45

Arg Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val
50 55 60

Val Thr Val Gly Val Phe Asp Asn Cys His Leu His Gly Gly Asp Lys
65 70 75 80

Asn Asn Gly Gly Gly Lys Asp Ser Arg Ile Gly Lys Val Arg
85 90

<210> 543
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 543

Leu Glu Leu Gly Ile Leu Thr Ala Gln Gly Leu Leu Pro Met Lys Thr
1 5 10 15

Lys Asp Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Ile Ile Asp Ser Phe Thr Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
50 55 60

Thr Ile Gly Val Phe Asp Asn Cys His Leu Asn Gly Gly Glu Lys Ala
65 70 75 80

Asn Gly Ala Arg Asp Thr Arg Ile Gly Lys Val Arg
85 90

<210> 544
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 544

Leu Glu Val Gly Ile Leu Ser Ala Gln Gly Leu Ser Pro Met Lys Thr
1 5 10 15

Lys Asp Gly Lys Ala Thr Thr Asp Pro Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Ile Ile Asp Ser Ser Ser Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
50 55 60

Thr Leu Gly Val Phe Asp Asn Cys His Leu Gly Gly Ser Glu Lys Ser
65 70 75 80

Asn Ser Gly Ala Lys Val Asp Ser Arg Ile Gly Lys Val Arg
85 90

<210> 545
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 545

Leu Glu Val Gly Ile Leu Ser Ala Gln Gly Leu Ser Pro Met Lys Thr
1 5 10 15

Lys Asp Gly Lys Ala Thr Thr Asp Pro Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Val Arg Thr Arg Thr Ile Ile Asp Ser Ser Ser Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
50 55 60

Thr Leu Gly Val Phe Asp Asn Cys His Leu Gly Gly Ser Glu Lys Ser
65 70 75 80

Asn Ser Gly Ala Lys Val Asp Ser Arg Ile Gly Lys Val Arg
85 90

<210> 546
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 546

Leu Glu Val Gly Ile Ile Ser Ala His Gly Leu Met Pro Met Lys Ser
1 5 10 15

Lys Asp Gly Lys Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
20 25 30

Gln Lys Trp Ile Arg Thr Arg Thr Ile Val Asp Ser Phe Thr Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Thr Cys Thr Val Ile
50 55 60

Thr Phe Gly Ala Phe Asp Asn Gly His Ile Pro Gly Gly Ser Gly Lys
65 70 75 80

Asp Leu Arg Ile Gly Lys Val Arg
85

<210> 547
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 547

Leu Glu Met Gly Ile Leu Gly Ala Lys Gly Leu Leu Pro Met Lys Met
1   5   10   15

Lys Asp Gly His Gly Ser Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
            20   25   30

Gln Lys Trp Ile Arg Thr Arg Thr Leu Leu Asp Thr Phe Ser Pro Lys
        35   40   45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
    50   55   60

Thr Leu Gly Val Phe Asp Asn Cys His Leu Gly Glu Lys Ala Pro Ser
65   70   75   80

Gly Ser Ser Ile Lys Asp Ser Arg Ile Gly Lys Val Arg
                85   90

<210> 548
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 548

Leu Glu Val Gly Ile Leu Gly Ala Gln Lys Leu Leu Pro Met Lys Met
1   5   10   15

Asn Asn Ser Arg Gly Ser Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
            20   25   30

Gln Lys Trp Ile Arg Thr Arg Thr Ile Leu Asp Thr Phe Ser Pro Lys
        35   40   45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
    50   55   60

Thr Leu Gly Val Phe Asp Asn Cys His Leu Gly Gly Gly Gly Glu Lys
65   70   75   80

Ala Pro Ser Gly Gly Ser Asn Ala Ala Arg Asp Ser Arg Ile Gly Lys
                85   90   95

Val Arg

<210> 549
<211> 93
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 549

Leu Glu Ile Gly Ile Leu Gly Ala Asn Gly Leu Val Pro Met Lys Leu
1   5   10   15

Lys Asp Gly Arg Gly Ser Thr Asn Ala Tyr Cys Val Ala Lys Tyr Gly
            20   25   30

Gln Lys Trp Val Arg Thr Arg Thr Ile Leu Asp Thr Leu Ser Pro Arg
        35   40   45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr Val Ile
    50   55   60

Thr Leu Gly Val Phe Asp Asn Ser His Leu Gly Ser Ala Gln Ser Gly
65   70   75   80

Thr Ala Asp Ser Arg Asp Ala Arg Ile Gly Lys Val Arg
                85   90

<210> 550
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 550

Leu Glu Val Gly Ile Leu Gly Ala Ala Gly Leu Gln Pro Met Lys Asn
1   5   10   15

Arg Asp Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly
            20   25   30

Gln Lys Trp Val Arg Thr Arg Thr Met Leu Gly Thr Phe Ser Pro Thr
        35   40   45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val Ile
    50   55   60

Thr Ile Gly Val Phe Asp Asn Asn His Leu Gly Asn Gly Asn Gly Asn
65   70   75   80

Gly Asn Asn Ala Gly Gly Gly Gly Gly Gly Ser Pro Pro Ala Arg Asp
                85   90   95

Ala Arg Val Gly Lys Ile Arg
            100

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<210> 551
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 551

Leu Glu Met Gly Ile Leu Gly Ala His Gly Leu Pro Pro Met Lys Ser
1 5 10 15

Lys Asp Gly Trp Thr Thr Thr Asp Ala Tyr Cys Val Ala Lys Phe Gly
20 25 30

Thr Lys Trp Val Arg Thr Arg Thr Ile Thr Asn Asn Phe His Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Ser Ile Ile
50 55 60

Thr Ile Gly Val Phe Asp Asn Asn Phe His Leu Gln Gly Gly Asp Lys
65 70 75 80

Arg Ile Gly Lys Val Arg
85

<210> 552
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 552

Leu Glu Val Gly Val Leu Gly Ala Gln Gly Leu Pro Pro Met Lys Thr
1 5 10 15

Ala Ala Asp Gly Gly Arg Gly Thr Thr Asp Ala Tyr Cys Val Ala Lys
20 25 30

Tyr Gly His Lys Trp Val Arg Thr Arg Thr Val Val Asp Ser Ser Thr
35 40 45

Pro Arg Trp Asn Glu Gln Tyr Thr Trp Glu Val Tyr Asp Pro Cys Thr
50 55 60

Val Leu Thr Leu Ala Val Phe Asp Asn Cys Asn Leu Gly Asn Gly Gly
65 70 75 80

Gly Gly Gly Lys Asp Gln Arg Ile Gly Lys Val Arg
85 90

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<210> 553
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 553

Leu Glu Leu Gly Val Leu Gly Ala Thr Gly Leu Ile Pro Met Lys Ala
1 5 10 15

Arg Asp Gly Arg Gly Ala Thr Ser Asp Ala Tyr Cys Val Ala Lys Tyr
20 25 30

Gly Gln Lys Trp Ile Arg Thr Arg Thr Val Val Asp Ser Val Cys Pro
35 40 45

Arg Trp Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val
50 55 60

Ile Thr Val Gly Val Phe Asp Asn Cys His Val Asp Lys Pro Ala Ser
65 70 75 80

Gly Asn Thr Thr Leu Ala Val Arg Asp Asn Cys Ile Gly Lys Val Arg
85 90 95

<210> 554
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 554

Leu Glu Leu Gly Ile Leu Ser Ala Arg Asn Leu Met Pro Met Lys Gly
1 5 10 15

Lys Asp Gly Arg Met Thr Asp Pro Tyr Cys Val Ala Lys Tyr Gly Asn
20 25 30

Lys Trp Val Arg Thr Arg Thr Leu Leu Asp Ala Leu Ala Pro Lys Trp
35 40 45

Asn Glu Gln Tyr Thr Trp Glu Val His Asp Pro Cys Thr Val Ile Thr
50 55 60

Ile Gly Val Phe Asp Asn Ser His Val Asn Asp Gly Gly Asp Phe Lys
65 70 75 80

Asp Gln Arg Ile Gly Lys Val Arg
85

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<210> 555
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 555

Leu Glu Leu Gly Ile Leu Ser Ala Arg Asn Leu Met Pro Met Lys Gly
1   5   10   15

Lys Asp Gly Arg Met Thr Asp Pro Tyr Cys Val Ala Lys Tyr Gly Asn
            20   25   30

Lys Trp Val Arg Thr Arg Thr Leu Leu Asp Ala Leu Ala Pro Lys Trp
        35   40   45

Asn Glu Gln Tyr Thr Trp Glu Val His Asp Pro Cys Thr Val Ile Thr
    50   55   60

Ile Gly Val Phe Asp Asn Ser His Val Asn Asp Gly Gly Asp Phe Lys
65   70   75   80

Asp Gln Arg Ile Gly Lys Val Arg
                85

<210> 556
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 556

Leu Glu Leu Gly Ile Leu Gly Ala Arg Asn Leu Ile Pro Met Lys Gly
1   5   10   15

Lys Asp Gly Arg Thr Thr Asp Ala Tyr Cys Val Ala Lys Tyr Gly Pro
            20   25   30

Lys Trp Val Arg Thr Arg Thr Ile Leu Asn Thr Leu Asn Pro Gln Trp
        35   40   45

Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Cys Thr Val Ile Thr
    50   55   60

Val Val Val Phe Asp Asn Asn Gln Ile Gly Lys Asn Gly Asp Ala Arg
65   70   75   80

Asp Glu Ser Ile Gly Lys Val Arg
                85

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<210> 557
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 557

Leu Glu Leu Gly Ile Leu Gly Ala Arg Asn Leu Ala Gly Gly Lys Ser
1 5 10 15

Pro Tyr Cys Val Ala Lys Tyr Gly Ala Lys Trp Val Arg Thr Arg Thr
20 25 30

Leu Val Gly Thr Ala Ala Pro Arg Trp Asn Glu Gln Tyr Thr Trp Glu
35 40 45

Val Phe Asp Leu Cys Thr Val Val Thr Val Ala Val Phe Asp Asn Cys
50 55 60

His Leu Thr Gly Gly Gly Asp Ala Lys Asp Gln Arg Ile Gly Lys Val
65 70 75 80

Arg

<210> 558
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 558

Arg Lys Gly Thr Ser Asp Thr Tyr Val Val Ala Lys Tyr Gly His Lys
1 5 10 15

Trp Val Arg Ser Arg Thr Val Ile Asn Ser Met Asn Pro Lys Tyr Asn
20 25 30

Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Ala Thr Val Leu Thr Ile
35 40 45

Cys Val Phe Asp Asn Ala His Phe Ala Ala Gly Asp Gly Gly Asn Lys
50 55 60

Arg Asp Gln Pro Ile Gly Lys Val Arg
65 70

<210> 559
<211> 91
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 559

Leu Glu Leu Gly Ile Leu Asn Ala Asn Val Phe His Ser Met Lys Thr
1   5   10   15

Arg Glu Gly Lys Gly Thr Ser Asp Thr Tyr Val Val Ala Lys Tyr Gly
            20   25   30

His Lys Trp Val Arg Ser Arg Thr Val Ile Asn Ser Met Asn Pro Lys
        35   40   45

Tyr Asn Glu Gln Tyr Thr Trp Glu Val Phe Asp Pro Ala Thr Val Leu
    50   55   60

Thr Ile Cys Val Phe Asp Asn Ala His Phe Ala Ala Gly Asp Gly Gly
65   70   75   80

Asn Lys Arg Asp Gln Pro Ile Gly Lys Val Arg
                85   90

<210> 560
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 560

Leu Glu Leu Gly Ile Leu Arg Ile Glu Gly Leu Asn Leu Ser Gln Glu
1   5   10   15

Gly Lys Lys Glu Thr Val Asp Ala Tyr Cys Val Ala Lys Tyr Gly Thr
            20   25   30

Lys Trp Val Arg Thr Arg Thr Val Thr Asn Cys Leu Asn Pro Arg Phe
        35   40   45

Asn Glu Gln Tyr Thr Trp Glu Val Tyr Glu Pro Ala Thr Val Ile Thr
    50   55   60

Ile Gly Val Phe Asp Asn Asn Gln Ile Asn Ser Gly Asn Gly Asn Lys
65   70   75   80

Gly Asp Gly Lys Ile Gly Lys Ile Arg
                85

<210> 561
<211> 95
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 561

Leu Glu Val Gly Ile Leu Ser Ala Asn Gly Leu Asn Pro Thr Lys Thr
1   5   10   15

Lys His Glu Arg Gly Ser Cys Asp Ala Tyr Cys Val Ala Lys Tyr Gly
            20   25   30

Gln Lys Trp Val Arg Thr Arg Thr Ile Val Asp Asn Leu Asn Pro Arg
        35   40   45

Phe Asn Glu Gln Tyr Thr Trp Asp Val Phe Asp His Gly Thr Val Leu
    50   55   60

Thr Ile Gly Leu Phe Asp Asn Cys His Ile Ser Ala Asp Ser Asn His
65   70   75   80

Ser Ser Ser Pro Gly His Met Asp Lys Pro Ile Gly Lys Val Arg
                85   90   95

<210> 562
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 562

Arg Asp Gly Arg Gly Ser Cys Asp Ala Tyr Cys Val Ala Lys Tyr Gly
1   5   10   15

Val Lys Trp Tyr Arg Thr Arg Thr Val Thr Asp Ser Ile Ser Pro Arg
            20   25   30

Phe His Gln Gln Tyr His Trp Glu Val His Asp His Cys Thr Val Leu
        35   40   45

Thr Val Ala Val Phe His Asn Ser Gln Ile Gly Asp Lys Gly Gly Leu
    50   55   60

Val Ala Gly Asp Pro Val Lys Asp Val Leu Leu Gly Lys Val Arg
65   70   75

<210> 563
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

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<400> 563

Val Glu Leu Gly Ile Ile Gly Cys Lys Asn Leu Leu Pro Met Lys Thr
1 5 10 15

Val Asn Gly Lys Gly Ser Thr Asp Ala Tyr Thr Val Ala Lys Tyr Gly
20 25 30

Ser Lys Trp Val Arg Thr Arg Thr Val Ser Asp Ser Leu Asp Pro Lys
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Lys Val Tyr Asp Pro Cys Thr Val Leu
50 55 60

Thr Ile Gly Val Phe Asp Ser Trp Gly Val Tyr Glu Val Asp Gly Gly
65 70 75 80

Lys Glu Ala Thr Arg Gln Asp Leu Arg Ile Gly Lys Val Arg
85 90

<210> 564
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 564

Val Glu Leu Gly Ile Val Gly Cys Lys Gly Leu Leu Pro Met Arg Thr
1 5 10 15

Ala Asp Gly Lys Gly Cys Thr Asp Ala Tyr Ala Val Ala Lys Tyr Gly
20 25 30

Pro Lys Trp Ala Arg Thr Arg Thr Ile Ser Asp Ser Phe Asp Pro Ala
35 40 45

Trp Asn Glu Gln Tyr Thr Trp Pro Val Tyr Asp Pro Cys Thr Val Leu
50 55 60

Thr Val Gly Val Phe Asp Asp Pro Pro Pro Pro Ser Pro Ser Gln Leu
65 70 75 80

Pro Asp Gly Ala Lys Asp Ala Ala Ala Phe Ser Arg Pro Met Gly Lys
85 90 95

Val Arg

<210> 565
<211> 92
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 565

Leu Glu Leu Gly Ile Leu Gly Ala Arg Gly Leu Leu Pro Met Lys Ala
1 5 10 15

Lys Asn Gly Gly Lys Gly Ser Thr Asp Ala Tyr Cys Val Ala Lys Tyr
20 25 30

Gly Lys Lys Trp Val Arg Thr Arg Thr Ile Thr Asp Ser Phe Asp Pro
35 40 45

Arg Trp His Glu Gln Tyr Thr Trp Gln Val Tyr Asp Pro Cys Thr Val
50 55 60

Leu Thr Val Gly Val Phe Asp Asn Trp Arg Met Phe Ser Asp Ala Ser
65 70 75 80

Asp Asp Arg Pro Asp Thr Arg Ile Gly Lys Ile Arg
85 90

<210> 566
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 566

Leu Glu Leu Gly Ile Leu Gly Ala Arg Gly Leu Leu Pro Met Lys Ala
1 5 10 15

Lys Asn Gly Gly Lys Gly Ser Thr Asp Ala Tyr Cys Val Ala Lys Tyr
20 25 30

Gly Lys Lys Trp Val Arg Thr Arg Thr Ile Thr Asp Ser Phe Asp Pro
35 40 45

Arg Trp His Glu Gln Tyr Thr Trp Gln Val Tyr Asp Pro Cys Thr Val
50 55 60

Leu Thr Val Gly Val Phe Asp Asn Trp Arg Met Phe Ser Asp Ala Ser
65 70 75 80

Asp Asp Arg Pro Asp Thr Arg Ile Gly Lys Ile Arg
85 90

<210> 567
<211> 95
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 567

Leu Glu Leu Gly Ile Ile Gly Ala Cys Gly Leu Leu Pro Met Lys Thr
1 5 10 15

Lys Gly Gly Ala Lys Gly Ser Thr Asp Ala Tyr Cys Val Ala Lys Tyr
20 25 30

Gly Lys Lys Trp Val Arg Thr Arg Thr Val Thr Asp Ser Leu Asn Pro
35 40 45

Arg Trp Asn Glu Gln Tyr Thr Trp Gln Val Tyr Asp Pro Cys Thr Val
50 55 60

Leu Thr Val Ala Val Phe Asp Asn Trp Arg Met Phe Ala Phe Ala Gly
65 70 75 80

Ala Gly Asp Glu Gln Arg Gln Asp Tyr Arg Ile Gly Lys Val Arg
85 90 95

<210> 568
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 568

Leu Glu Val Gly Ile Arg Gly Ala Ala Asn Leu Val Pro Met Lys Ile
1 5 10 15

Ala Lys Asp Gly Ala Ser Gly Ser Thr Asp Ala Tyr Val Val Leu Lys
20 25 30

Tyr Gly Pro Lys Trp Ala Arg Thr Arg Thr Ile Leu Asp Gln Phe Asn
35 40 45

Pro Arg Trp Asn Glu Gln Tyr Ala Trp Asp Val Phe Asp Pro Cys Thr
50 55 60

Val Leu Thr Ile Ala Val Phe Asp Asn Val Arg Tyr Arg Ser Ala Glu
65 70 75 80

Ala Ser Gly Asp Ala Gly Lys Leu Pro Lys Asp Ala Arg Ile Gly Lys
85 90 95

Leu Arg

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<210> 569
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 569

Leu Glu Val Gly Ile Arg Gly Ala Thr Asn Leu Leu Pro Val Lys Thr
1 5 10 15

Arg Asp Gly Thr Arg Gly Thr Thr Asp Ala Tyr Val Val Ala Lys Tyr
20 25 30

Gly Pro Lys Trp Ile Arg Thr Arg Thr Ile Leu Asp Arg Phe Asn Pro
35 40 45

Arg Trp Asn Glu Gln Tyr Thr Trp Asp Val Tyr Asp Pro Cys Thr Val
50 55 60

Leu Thr Ile Gly Val Phe Asp Asn Gly Arg Tyr Lys Arg Asp Glu Ser
65 70 75 80

Gly Lys Gln Gly Arg Asp Val Arg Val Gly Lys Ile Arg
85 90

<210> 570
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 570

Leu Glu Ile Gly Ile Leu Gly Ala Thr Gly Leu Lys Gly Ser Asp Glu
1 5 10 15

Arg Lys Gln Gly Ile Asp Ser Tyr Val Val Ala Lys Tyr Gly Asn Lys
20 25 30

Trp Ala Arg Thr Arg Thr Val Val Asn Ser Val Thr Pro Lys Trp Asn
35 40 45

Glu Gln Tyr Ser Trp Asp Asp Tyr Glu Lys Cys Thr Val Leu Thr Leu
50 55 60

Gly Ile Tyr Asp Asn Arg Gln Ile Phe Lys Glu Asp Gln Ala Asn Asp
65 70 75 80

Val Pro Ile Gly Lys Val Arg
85

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<210> 571
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 571

Leu Glu Ile Gly Ile Leu Gly Ala Thr Gly Leu Lys Gly Ser Asp Glu
1 5 10 15

Lys Lys Gln Thr Ile Asp Ser Tyr Val Val Ala Lys Tyr Gly Asn Lys
20 25 30

Trp Ala Arg Thr Arg Thr Val Val Asn Ser Val Ser Pro Lys Trp Asn
35 40 45

Glu Gln Tyr Ser Trp Asp Val Tyr Glu Lys Cys Thr Val Leu Thr Leu
50 55 60

Gly Ile Tyr Asp Asn Arg Gln Ile Leu Glu Asp Lys Asn Lys Ala Asn
65 70 75 80

Asp Val Pro Ile Gly Lys Val Arg
85

<210> 572
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 572

Val His Leu Gly Ile Leu Arg Ala Thr Gly Leu Pro Leu Arg Met Gly
1 5 10 15

Lys Ser Thr Val Asn Pro Tyr Cys Val Ala Lys Tyr Gly Asp Lys Trp
20 25 30

Val Arg Thr Arg Thr Ile Leu Asp Gly Pro Glu His Val Phe Asn Glu
35 40 45

Gln His Thr Trp Ser Val Tyr Asp Ile Ala Thr Val Leu Thr Ala Gly
50 55 60

Val Phe Asp His Phe Pro His Thr Arg Lys Ala His Arg Glu Ile Gly
65 70 75 80

Lys Val Gln

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<210> 573
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 573

Leu Ser Val Thr Val Ile Ser Gly Glu Asp Leu Pro Ala Met Asp Met
1 5 10 15

Asn Gly Lys Ser Asp Pro Tyr Val Val Leu Ser Leu Lys Lys Ser Lys
20 25 30

Thr Lys Tyr Lys Thr Arg Val Val Ser Glu Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Met Leu Glu Val Tyr Asp His Asp Thr Phe Ser Arg Asp Tyr Met Gly
65 70 75 80

Arg Cys Ile

<210> 574
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 574

Leu Ser Val Thr Val Ile Ser Gly Glu Asp Leu Pro Ala Met Asp Met
1 5 10 15

Asn Gly Lys Ser Asp Pro Tyr Val Val Leu Ser Leu Lys Lys Ser Lys
20 25 30

Thr Lys Tyr Lys Thr Arg Val Val Ser Glu Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Met Leu Glu Val Tyr Asp His Asp Thr Phe Ser Arg Asp Tyr Met Gly
65 70 75 80

Arg Cys Ile

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<210> 575
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 575

Arg Val Val Asn Glu Ser Leu Asn Pro Val Trp Asn Gln Thr Phe Asp
1 5 10 15

Phe Val Val Glu Asp Gly Leu His Asp Met Leu Val Leu Glu Val Tyr
20 25 30

Asp His Asp Thr Phe Ser Arg Asp Tyr Met Gly Arg Cys Ile
35 40 45

<210> 576
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 576

Leu Ser Val Thr Val Ile Ser Ala Glu Glu Ile Pro Ile Gln Asp Leu
1 5 10 15

Met Gly Lys Ala Asp Pro Tyr Val Val Leu Ser Met Lys Lys Ser Gly
20 25 30

Ala Lys Ser Lys Thr Arg Val Val Asn Asp Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Val Leu Glu Val Trp Asp His Asp Thr Phe Gly Lys Asp Tyr Ile Gly
65 70 75 80

Arg Cys Ile

<210> 577
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 577

Leu Ser Val Thr Val Ile Ser Ala Glu Glu Ile Pro Ile Gln Asp Leu
1 5 10 15

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Met Gly Lys Ala Asp Pro Tyr Val Val Leu Ser Met Lys Lys Ser Gly
20 25 30

Ala Lys Ser Lys Thr Arg Val Val Asn Asp Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Val Leu Glu Val Trp Asp His Asp Thr Phe Gly Lys Asp Tyr Ile Gly
65 70 75 80

Arg Cys Ile

<210> 578
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 578

Leu Ser Val Thr Val Ile Ser Ala Glu Asp Leu Pro Ile Val Asp Phe
1 5 10 15

Met Gly Lys Ala Asp Pro Phe Val Val Leu Ala Leu Lys Lys Ser Glu
20 25 30

Lys Lys Gln Lys Thr Arg Val Val Asn Glu Thr Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Ile Val Glu Leu Trp Asp His Asp Thr Phe Gly Lys Glu Lys Met Gly
65 70 75 80

Lys Val Ile

<210> 579
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 579

Leu Ser Val Thr Val Ile Ser Ala Glu Asp Leu Pro Ala Val Asp Phe
1 5 10 15

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Met Gly Lys Ser Asp Pro Phe Val Val Leu Thr Leu Lys Lys Ala Glu
20 25 30

Thr Lys Asn Lys Thr Arg Val Val Asn Asn Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Gly Leu His Asp Met Leu
50 55 60

Leu Val Glu Val Tyr Asp His Asp Thr Phe Gly Lys Asp Tyr Met Gly
65 70 75 80

Arg Val Ile

<210> 580
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 580

Leu Ser Val Thr Val Ile Ser Ala Glu Asp Leu Pro Pro Met Asp Val
1 5 10 15

Met Gly Lys Ala Asp Pro Phe Val Val Leu Tyr Leu Lys Lys Gly Glu
20 25 30

Thr Lys Lys Lys Thr Arg Val Val Thr Glu Thr Leu Asn Pro Ile Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Ala Leu His Asp Leu Leu
50 55 60

Met Val Glu Val Trp Asp His Asp Thr Phe Gly Lys Asp Tyr Ile Gly
65 70 75 80

Arg Cys Ile

<210> 581
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 581

Leu Ser Val Thr Val Ile Ser Ala Glu Asp Leu Pro Pro Met Asp Val
1 5 10 15

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Met Gly Lys Ala Asp Pro Phe Val Val Leu Tyr Leu Lys Lys Gly Glu
20 25 30

Thr Lys Lys Lys Thr Arg Val Val Thr Glu Thr Leu Asn Pro Ile Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Ala Leu His Asp Leu Leu
50 55 60

Met Val Glu Val Trp Asp His Asp Thr Phe Gly Lys Asp Tyr Ile Gly
65 70 75 80

Arg Cys Ile

<210> 582
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 582

Leu Ser Val Thr Val Val Ala Ala Glu Asp Leu Pro Ala Val Asp Phe
1 5 10 15

Met Gly Lys Ala Asp Ala Phe Val Val Ile Thr Leu Lys Lys Ser Glu
20 25 30

Thr Lys Ser Lys Thr Arg Val Val Pro Asp Ser Leu Asn Pro Val Trp
35 40 45

Asn Gln Thr Phe Asp Phe Val Val Glu Asp Ala Leu His Asp Leu Leu
50 55 60

Thr Leu Glu Val Trp Asp His Asp Lys Phe Gly Lys Asp Lys Ile Gly
65 70 75 80

Arg Val Ile

<210> 583
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 583

Leu Ile Val Thr Val Val Lys Ala Thr Asn Leu Lys Asn Lys Glu Leu
1 5 10 15

Ile Gly Lys Ser Asp Pro Tyr Ala Thr Ile Tyr Ile Arg Pro Val Phe
20 25 30

Lys Tyr Lys Thr Asn Ala Ile Asp Asn Asn Leu Asn Pro Val Trp Asp
35 40 45

Gln Thr Phe Glu Leu Ile Ala Glu Asp Lys Glu Thr Gln Ser Leu Thr
50 55 60

Val Glu Val Phe Asp Lys Asp Val Gly Gln Asp Glu Arg Leu Gly Leu
65 70 75 80

Val Lys

<210> 584
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 584

Leu Ile Val Thr Val Val Lys Ala Thr Asn Leu Lys Asn Lys Glu Leu
1 5 10 15

Ile Gly Lys Ser Asp Pro Tyr Ala Thr Ile Tyr Ile Arg Pro Val Phe
20 25 30

Lys Tyr Lys Thr Lys Ala Ile Glu Asn Asn Leu Asn Pro Val Trp Asp
35 40 45

Gln Thr Phe Glu Leu Ile Ala Glu Asp Lys Glu Thr Gln Ser Leu Thr
50 55 60

Val Glu Val Phe Asp Lys Asp Val Gly Gln Asp Glu Arg Leu Gly Leu
65 70 75 80

Val Lys

<210> 585
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 585

Ile Glu Asn Asn Leu Asn Pro Val Trp Asp Gln Thr Phe Glu Leu Ile
1 5 10 15

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Val Glu Asp Lys Glu Thr Gln Ser Leu Thr Val Glu Val Phe Asp Lys
20 25 30

Asp Val Gly Gln Asp Glu Arg Leu Gly Leu Val Lys
35 40

<210> 586
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 586

Thr Val Val Lys Ala Thr Asn Leu Lys Asn Lys Glu Phe Ile Gly Lys
1 5 10 15

Ser Asp Pro Tyr Ala Thr Ile His Ile Arg Pro Val Phe Lys Tyr Asn
20 25 30

Thr Lys Ala Ile Glu Asn Asn Leu Asn Pro Val Trp Asp Gln Thr Phe
35 40 45

Asp Leu Ile Ala Glu Asp Lys Glu Thr Gln Ser Leu Thr Ile Glu Val
50 55 60

Phe Asp Lys Asp Val Gly Gln Asp Glu Arg Leu Gly Leu Val Lys
65 70 75

<210> 587
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 587

Leu Thr Val Thr Ile Val Lys Ala Asn Gly Leu Lys Asn His Glu Met
1 5 10 15

Ile Gly Lys Ser Asp Pro Tyr Ala Val Val His Ile Arg Pro Leu Phe
20 25 30

Lys Val Lys Thr Lys Thr Ile Asp Asn Asn Leu Asn Pro Val Trp Asp
35 40 45

Gln Thr Phe Glu Leu Ile Ala Glu Asp Lys Glu Thr Gln Ser Leu Phe
50 55 60

Ile Glu Val Phe Asp Lys Asp Asn Ile Gly Gln Asp Gln Arg Met Gly
65 70 75 80

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Val Ala Lys

<210> 588
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 588

Leu Thr Val Thr Val Val Lys Ala Thr Ser Leu Lys Asn Lys Glu Leu
1   5   10   15

Ile Gly Lys Ser Asp Pro Tyr Val Ile Leu Tyr Val Arg Pro Met Phe
            20   25   30

Lys Val Lys Thr Lys Val Ile Asp Asp Asn Leu Asn Pro Glu Trp Asn
        35   40   45

Glu Thr Phe Pro Leu Ile Val Glu Asp Lys Glu Thr Gln Ser Val Ile
    50   55   60

Phe Glu Val Tyr Asp Glu Asp Arg Leu Gln Gln Asp Lys Lys Leu Gly
65   70   75   80

Val Ala Lys

<210> 589
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 589

Leu Glu Val Lys Leu Val Glu Ala Arg Asp Leu Thr Asn Lys Asp Leu
1   5   10   15

Val Gly Lys Ser Asp Pro Phe Ala Val Leu Tyr Ile Arg Pro Leu Gln
            20   25   30

Asp Lys Met Lys Lys Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
        35   40   45

Trp Asn Glu His Tyr Glu Phe Val Val Glu Asp Thr Ser Thr Gln Arg
    50   55   60

Leu Thr Val Lys Ile Tyr Asp Asp Glu Gly Leu Gln Ala Ser Glu Leu
65   70   75   80

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Ile Gly Cys Ala Arg
85

<210> 590
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 590

Leu Glu Val Lys Leu Val Glu Ala Arg Asp Leu Thr Asn Lys Asp Leu
1 5 10 15

Val Gly Lys Ser Asp Pro Phe Ala Val Leu Tyr Ile Arg Pro Leu Gln
20 25 30

Asp Lys Met Lys Lys Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Tyr Glu Phe Val Val Glu Asp Thr Ser Thr Gln Arg
50 55 60

Leu Thr Val Lys Ile Tyr Asp Asp Glu Gly Leu Gln Ala Ser Glu Leu
65 70 75 80

Ile Gly Cys Ala Arg
85

<210> 591
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 591

Leu Glu Val Lys Leu Val Gln Ala Lys Asn Leu Thr Asn Lys Asp Leu
1 5 10 15

Val Gly Lys Ser Asp Pro Phe Ala Lys Met Phe Ile Arg Pro Leu Arg
20 25 30

Glu Lys Thr Lys Arg Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Val Val Glu Asp Ala Ser Thr Gln His
50 55 60

Leu Val Val Arg Ile Tyr Asp Asp Glu Gly Val Gln Ala Ser Glu Leu
65 70 75 80

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Ile Gly Cys Ala Gln
85

<210> 592
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 592

Leu Glu Val Lys Leu Val Gln Ala Lys Asn Leu Thr Asn Lys Asp Leu
1 5 10 15

Val Gly Lys Ser Asp Pro Phe Ala Lys Met Phe Ile Arg Pro Leu Arg
20 25 30

Glu Lys Thr Lys Arg Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Val Val Glu Asp Ala Ser Thr Gln His
50 55 60

Leu Val Val Arg Ile Tyr Asp Asp Glu Gly Val Gln Ala Ser Glu Leu
65 70 75 80

Ile Gly Cys Ala Gln
85

<210> 593
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 593

Leu Glu Val Lys Leu Val Gln Ala Arg Asp Leu Thr Asn Lys Asp Leu
1 5 10 15

Ile Gly Lys Ser Asp Pro Phe Ala Ile Val Tyr Val Arg Pro Leu Pro
20 25 30

Asp Lys Met Lys Arg Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Ile Val Glu Asp Ala Asp Thr Gln Thr
50 55 60

Val Thr Val Lys Ile Tyr Asp Asp Asp Gly Ile Gln Glu Ser Glu Leu
65 70 75 80

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Ile Gly Cys Ala Gln
85

<210> 594
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 594

Leu Glu Val Lys Leu Val Gln Ala Arg Asp Leu Thr Asn Lys Asp Leu
1 5 10 15

Ile Gly Lys Ser Asp Pro Phe Ala Ile Val Tyr Val Arg Pro Leu Pro
20 25 30

Asp Lys Met Lys Arg Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Ile Val Glu Asp Ala Asp Thr Gln Thr
50 55 60

Val Thr Val Lys Ile Tyr Asp Asp Asp Gly Ile Gln Glu Ser Glu Leu
65 70 75 80

Ile Gly Cys Ala Gln
85

<210> 595
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 595

Leu Glu Val Lys Leu Val Gln Ala Lys Glu Leu Thr Asn Lys Asp Ile
1 5 10 15

Ile Gly Lys Ser Asp Pro Tyr Ala Val Leu Tyr Ile Arg Pro Leu Arg
20 25 30

Asn Arg Thr Lys Lys Ser Lys Thr Ile Asn Asn Asp Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Ile Val Glu Asp Ala Ser Thr Gln His
50 55 60

Leu Phe Val Lys Val Tyr Asp Asp Glu Gly Leu Gln Ser Ser Glu Leu
65 70 75 80

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Ile Gly Cys Thr Asp
85

<210> 596
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 596

Leu Asp Val Lys Leu Val Gln Ala Lys Asn Leu Ser Asn Lys Asp Ile
1 5 10 15

Ile Gly Lys Ser Asp Pro Phe Ala Val Val Phe Val Arg Pro Leu Arg
20 25 30

Asp Lys Thr Lys Thr Ser Lys Ile Ile Asn Asn Gln Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Ile Ile Glu Asp Glu Ser Thr Gln His
50 55 60

Leu Thr Ile Arg Ile Phe Asp Asp Glu Gly Ile Gln Ala Ala Glu Leu
65 70 75 80

Ile Gly Cys Ala Gln
85

<210> 597
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 597

Leu Asp Val Lys Val Val Gln Ala Lys Asp Leu Ala Asn Lys Asp Met
1 5 10 15

Ile Gly Lys Ser Asp Pro Tyr Ala Ile Val Phe Ile Arg Pro Leu Pro
20 25 30

Asp Arg Thr Lys Lys Thr Lys Thr Ile Ser Asn Ser Leu Asn Pro Ile
35 40 45

Trp Asn Glu His Phe Glu Phe Ile Val Glu Asp Val Ser Thr Gln His
50 55 60

Leu Thr Val Arg Val Phe Asp Asp Glu Gly Val Gly Ser Ser Gln Leu
65 70 75 80

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Ile Gly Ala Ala Gln
85

<210> 598
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 598

Lys Val Val Arg Ala Val Gly Leu Arg Lys Lys Asp Met Met Gly Gly
1 5 10 15

Ala Asp Pro Tyr Val Lys Ile Lys Leu Ser Glu Asp Lys Ile Pro Ser
20 25 30

Lys Lys Thr Thr Val Lys His Lys Asn Leu Asn Pro Glu Trp Asn Glu
35 40 45

Glu His Lys Phe Ser Val Arg Asp Pro Gln Thr Gln Val Leu Glu Phe
50 55 60

Ser Val Tyr Asp Trp Gly Gln Leu Gly Lys His Asp Lys Met Gly Met
65 70 75 80

Asn Val

<210> 599
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 599

Val His Val Lys Val Val Arg Ala Val Gly Leu Arg Lys Lys Asp Leu
1 5 10 15

Met Gly Gly Ala Asp Pro Phe Val Lys Ile Lys Leu Ser Glu Asp Lys
20 25 30

Ile Pro Ser Lys Lys Thr Thr Val Lys His Lys Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu Glu Phe Lys Phe Ser Val Arg Asp Pro Gln Thr Gln Val
50 55 60

Leu Glu Phe Ser Val Tyr Asp Trp Glu Gln Val Gly Asn Pro Glu Lys
65 70 75 80

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Met Gly Met Asn Val
85

<210> 600
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 600

Gly Met Ile Asn Pro Tyr Val Gln Ile Glu Leu Ser Glu Asp Lys Ile
1 5 10 15

Ser Ser Lys Lys Thr Thr Val Lys His Lys Asn Leu Asn Pro Glu Trp
20 25 30

Asn Glu Glu Phe Lys Phe Ser Val Arg Asp Pro Lys Thr Gln Val Leu
35 40 45

Glu Phe Asn Val Tyr Asp Trp Glu Lys Ile Gly Lys His Asp Lys Met
50 55 60

Gly Met Asn Val
65

<210> 601
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 601

Leu His Val Lys Val Leu His Ala Met Lys Leu Lys Lys Lys Asp Leu
1 5 10 15

Leu Gly Ala Ser Asp Pro Tyr Val Lys Leu Lys Leu Thr Asp Asp Lys
20 25 30

Met Pro Ser Lys Lys Thr Thr Val Lys His Lys Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu Glu Phe Asn Leu Val Val Lys Asp Pro Glu Thr Gln Val
50 55 60

Leu Gln Leu Asn Val Tyr Asp Trp Glu Gln Val Gly Lys His Asp Lys
65 70 75 80

Met Gly Met Asn Val
85

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<210> 602
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 602

Leu Ser Val Lys Val Ile Lys Ala Ile Lys Leu Lys Lys Lys Asp Leu
1 5 10 15

Leu Gly Gly Ser Asp Pro Tyr Val Lys Leu Thr Leu Ser Gly Asp Lys
20 25 30

Val Pro Gly Lys Lys Thr Val Val Lys His Ser Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu Glu Phe Asp Leu Val Val Lys Glu Pro Glu Ser Gln Glu
50 55 60

Leu Gln Leu Ile Val Tyr Asp Trp Glu Gln Val Gly Lys His Asp Lys
65 70 75 80

Ile Gly Met Asn Val
85

<210> 603
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 603

Leu His Val Asn Ile Val Arg Ala Val Lys Leu Thr Lys Lys Asp Phe
1 5 10 15

Leu Gly Lys Ser Asp Pro Tyr Val Lys Leu Lys Leu Thr Glu Glu Lys
20 25 30

Leu Pro Ser Lys Lys Thr Ser Val Lys Arg Ser Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu Asp Phe Lys Leu Val Val Lys Asp Pro Glu Ser Gln Ala
50 55 60

Leu Glu Leu Thr Val Tyr Asp Trp Glu Gln Val Gly Lys His Asp Lys
65 70 75 80

Ile Gly Met Ser Val
85

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<210> 604
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 604

Leu His Val Ser Ile Leu Arg Ala Arg Asn Leu Leu Lys Lys Asp Leu
1 5 10 15

Leu Gly Thr Ser Asp Pro Tyr Val Lys Leu Ser Leu Thr Gly Glu Lys
20 25 30

Leu Pro Ala Lys Lys Thr Thr Ile Lys Lys Arg Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu His Phe Lys Leu Ile Val Lys Asp Pro Asn Ser Gln Val
50 55 60

Leu Gln Leu Glu Val Phe Asp Trp Asp Lys Val Gly Gly His Asp Arg
65 70 75 80

Leu Gly Met Gln Met
85

<210> 605
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 605

Leu His Val Ser Ile Leu Arg Ala Arg Asn Leu Leu Lys Lys Asp Leu
1 5 10 15

Leu Gly Thr Ser Asp Pro Tyr Val Lys Leu Ser Leu Thr Gly Glu Lys
20 25 30

Leu Pro Ala Lys Lys Thr Thr Ile Lys Lys Arg Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu His Phe Lys Leu Ile Val Lys Asp Pro Asn Ser Gln Val
50 55 60

Leu Gln Leu Glu Val Phe Asp Trp Asp Lys Val Gly Gly His Asp Arg
65 70 75 80

Leu Gly Met Gln Met
85

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<210> 606
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 606

Leu His Val Ser Ile Leu Arg Ala Arg Asn Leu Leu Lys Lys Asp Leu
1 5 10 15

Leu Gly Thr Ser Asp Pro Tyr Val Lys Leu Ser Leu Thr Gly Glu Lys
20 25 30

Leu Pro Ala Lys Lys Thr Thr Ile Lys Lys Arg Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu His Phe Lys Leu Ile Val Lys Asp Pro Asn Ser Gln Val
50 55 60

Leu Gln Leu Glu Val Phe Asp Trp Asp Lys Val Gly Gly His Asp Arg
65 70 75 80

Leu Gly Met Gln Met
85

<210> 607
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 607

Leu His Val Lys Val Ile Arg Ala Met Asn Leu Leu Lys Met Asp Leu
1 5 10 15

Leu Gly Lys Ser Asp Pro Tyr Val Lys Leu Arg Leu Ser Gly Glu Lys
20 25 30

Leu Pro Ser Lys Lys Thr Ser Ile Lys Met Ser Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu His Phe Arg Phe Ile Val Lys Asp Pro Glu Thr Gln Ile
50 55 60

Leu Glu Leu Arg Met Phe Asp Trp Glu Lys Val Lys Met His Asp Lys
65 70 75 80

Leu Gly Met Gln Val
85

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<210> 608
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 608

Leu Leu Val Lys Val Leu Arg Ala Gln Asn Leu Arg Glu Lys Gly Pro
1 5 10 15

Leu Gly Lys Arg Asp Pro Tyr Val Lys Leu Lys Met Ser Gly Ser Lys
20 25 30

Leu Pro Ser Lys Lys Thr Ala Val Lys His Ser Asn Leu Asn Pro Glu
35 40 45

Trp Asn Gln Glu Phe Lys Phe Val Ile Arg Asp Pro Glu Thr Gln Glu
50 55 60

Leu Asp Ile Asn Phe Gly Lys Asp Glu Lys Leu Gly Met Cys Lys
65 70 75

<210> 609
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 609

Leu Leu Val Lys Val Leu Arg Ala Gln Asn Leu Arg Lys Lys Asp Leu
1 5 10 15

Leu Gly Lys Ser Asp Pro Tyr Val Lys Leu Lys Met Ser Asp Asp Lys
20 25 30

Leu Pro Ser Lys Lys Thr Thr Val Lys Arg Ser Asn Leu Asn Pro Glu
35 40 45

Trp Asn Glu Asp Phe Lys Phe Val Val Thr Asp Pro Glu Thr Gln Ala
50 55 60

Leu Glu Ile Asn Val Phe Asp Trp Glu Gln Val Gly Lys His Glu Lys
65 70 75 80

Met Gly Met Asn Asn
85

<210> 610
<211> 86

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 610

Leu Ser Val Thr Leu Val Asp Ala Gln Lys Leu Arg Tyr Met Phe Phe
1 5 10 15

Gly Lys Thr Asp Pro Tyr Ala Ile Leu Arg Leu Gly Asp Gln Val Ile
20 25 30

Arg Ser Lys Arg Asn Ser Gln Thr Thr Val Ile Gly Ala Pro Gly Gln
35 40 45

Pro Ile Trp Asn Gln Asp Phe Gln Phe Leu Val Ser Asn Pro Arg Glu
50 55 60

Gln Val Leu Gln Ile Glu Val Asn Asp Arg Leu Gly Phe Ala Asp Met
65 70 75 80

Ala Ile Gly Thr Gly Glu
85

<210> 611
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 611

Leu Ser Val Thr Leu Val Asp Ala Gln Lys Leu Arg Tyr Met Phe Phe
1 5 10 15

Gly Lys Thr Asp Pro Tyr Ala Ile Leu Arg Leu Gly Asp Gln Val Ile
20 25 30

Arg Ser Lys Arg Asn Ser Gln Thr Thr Val Ile Gly Ala Pro Gly Gln
35 40 45

Pro Ile Trp Asn Gln Asp Phe Gln Phe Leu Val Ser Asn Pro Arg Glu
50 55 60

Gln Val Leu Gln Ile Glu Val Asn Asp Arg Leu Gly Phe Ala Asp Met
65 70 75 80

Ala Ile Gly Thr Gly Glu
85

<210> 612
<211> 86

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 612

Leu Ser Val Thr Leu Val Asn Ala Gln Lys Leu Pro Tyr Met Phe Ser
1 5 10 15

Gly Arg Thr Asp Pro Tyr Val Ile Leu Arg Ile Gly Asp Gln Val Ile
20 25 30

Arg Ser Lys Lys Asn Ser Gln Thr Thr Val Ile Gly Ala Pro Gly Gln
35 40 45

Pro Ile Trp Asn Gln Asp Phe Gln Phe Leu Val Ser Asn Pro Arg Glu
50 55 60

Gln Val Leu Gln Ile Glu Val Asn Asp Cys Leu Gly Phe Ala Asp Met
65 70 75 80

Ala Ile Gly Ile Gly Glu
85

<210> 613
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 613

Leu Ser Val Thr Leu Val Asp Ala Arg Lys Leu Pro Tyr Phe Phe Gly
1 5 10 15

Lys Thr Asp Pro Tyr Val Ile Leu Ser Leu Gly Asp Gln Thr Ile Arg
20 25 30

Ser Lys Lys Asn Ser Gln Thr Thr Val Ile
35 40

<210> 614
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 614

Leu Ser Val Thr Leu Val Asp Ala Arg Lys Leu Ser Phe Val Leu Phe
1 5 10 15

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Gly Lys Thr Asp Pro Tyr Val Val Met Ile Leu Gly Asp Gln Glu Ile
20 25 30

Lys Ser Lys Lys Asn Ser Gln Thr Thr Val Ile Gly Gln Pro Gly Glu
35 40 45

Pro Ile Trp Asn Gln Asp Phe His Met Leu Val Ala Asn Pro Arg Lys
50 55 60

Gln Lys Leu Cys Ile Gln Val Lys Asp Ser Val Gly Leu Thr Asp Val
65 70 75 80

Thr Ile Gly Thr Gly Glu
85

<210> 615
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 615

Phe Arg Cys Val Asn Leu Asp Asn Lys Asp Leu Phe Ser Lys Ser Asp
1 5 10 15

Pro Phe Leu Arg Ile Ser Arg Val Val Glu Thr Ser Ala Ala Val Pro
20 25 30

Ile Cys Arg Thr Glu Val Val Asp Asn Asn Leu Asn Pro Met Trp Arg
35 40 45

Pro Val Cys Leu Thr Met Gln Gln Phe Gly Ser Lys Asp Thr Pro Leu
50 55 60

Val Ile Glu Cys Leu Asp Phe Asn Thr Ser Gly Asn His Glu Leu Ile
65 70 75 80

Gly Lys Thr Glu

<210> 616
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 616

Phe Arg Cys Val Asn Leu Asp Asn Lys Asp Leu Phe Ser Lys Ser Asp
1 5 10 15

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Pro Phe Leu Arg Ile Ser Arg Val Val Glu Thr Ser Ala Ala Val Pro
20 25 30

Ile Cys Arg Thr Glu Val Val Asp Asn Asn Leu Asn Pro Met Trp Arg
35 40 45

Pro Val Cys Leu Thr Met Gln Gln Phe Gly Ser Lys Asp Thr Pro Leu
50 55 60

Val Ile Glu Cys Leu Asp Phe Asn Thr Ser Gly Asn His Glu Leu Ile
65 70 75 80

Gly Lys Thr Glu

<210> 617
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 617

Phe Arg Cys Val Asn Leu Asp Asn Lys Asp Leu Phe Ser Lys Ser Asp
1 5 10 15

Pro Phe Leu Arg Ile Ser Arg Val Val Glu Thr Ser Ala Ala Val Pro
20 25 30

Ile Cys Arg Thr Glu Val Val Asp Asn Asn Leu Asn Pro Met Trp Arg
35 40 45

Pro Val Cys Leu Thr Met Gln Gln Phe Gly Ser Lys Asp Thr Pro Leu
50 55 60

Val Ile Glu Cys Leu Asp Phe Asn Thr Ser Gly Asn His Glu Leu Met
65 70 75 80

Lys Asp Arg Glu

<210> 618
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 618

Val Phe Arg Gly Leu Asn Leu Glu Ser Lys Asp Thr Phe Ser Lys Ser
1 5 10 15

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Asp Pro Phe Leu Val Ile Ser Lys Ile Val Glu His Gly Thr Pro Ile
20 25 30

Pro Val Ser Lys Thr Glu Val Leu Lys Asn Asp Pro Asn Pro Leu Trp
35 40 45

Lys Pro Val Ser Leu Ser Val Gln Gln Val Gly Ser Lys Asp Ser Pro
50 55 60

Leu Val Ile Glu Cys Leu Asp Phe Asn Gly Asn Gly Asn His Asp Leu
65 70 75 80

Ile Gly Lys Val Gln
85

<210> 619
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 619

Val Phe Arg Gly Leu Asn Leu Glu Ser Lys Asp Thr Phe Ser Lys Ser
1 5 10 15

Asp Pro Phe Leu Val Ile Ser Lys Ile Val Glu His Gly Thr Pro Ile
20 25 30

Pro Val Ser Lys Thr Glu Val Leu Lys Asn Asp Pro Asn Pro Leu Trp
35 40 45

Lys Pro Val Ser Leu Ser Val Gln Gln Val Gly Ser Lys Asp Ser Pro
50 55 60

Leu Val Ile Glu Cys Leu Asp Phe Asn Gly Asn Gly Asn His Asp Leu
65 70 75 80

Ile Gly Lys Val Gln
85

<210> 620
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 620

Val Phe Arg Gly Leu Asn Leu Glu Ser Lys Asp Thr Phe Ser Lys Ser
1 5 10 15

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Asp Pro Phe Leu Val Ile Ser Lys Ile Val Glu His Gly Thr Pro Ile
20 25 30

Pro Val Ser Lys Thr Glu Val Leu Lys Asn Asp Pro Asn Pro Leu Trp
35 40 45

Lys Pro Val Ser Leu Ser Val Gln Gln Val Gly Ser Lys Asp Ser Pro
50 55 60

Leu Val Ile Glu Cys Leu Asp Phe Asn Gly Asn Gly Asn His Asp Leu
65 70 75 80

Ile Gly Lys Val Gln
85

<210> 621
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 621

Val Phe Arg Cys Ser Asn Leu Glu Ser Lys Asp Leu Phe Ser Lys Ser
1 5 10 15

Asp Pro Phe Leu Val Val Ser Lys Ile Val Glu His Gly Thr Pro Ile
20 25 30

Pro Val Ser Lys Thr Glu Val Arg Lys Asn Asp Leu Asn Pro Ile Trp
35 40 45

Lys Pro Val Phe Leu Ser Val Gln Gln Val Gly Ser Lys Asp Ser Pro
50 55 60

Val Ile Ile Glu Cys Ser Asp Phe Asn Ser Asn Gly Lys His Ser Leu
65 70 75 80

Ile Gly Lys Val Gln
85

<210> 622
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 622

Val Phe Arg Cys Ser Asn Leu Glu Ser Lys Asp Leu Phe Ser Lys Ser
1 5 10 15

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Asp Pro Phe Leu Val Val Ser Lys Ile Val Glu His Gly Thr Pro Ile
20 25 30

Pro Val Ser Lys Thr Glu Val Arg Lys Asn Asp Leu Asn Pro Ile Trp
35 40 45

Lys Pro Val Phe Leu Ser Val Gln Gln Val Gly Ser Lys Asp Ser Pro
50 55 60

Val Ile Ile Glu Cys Ser Asp Phe Asn Ser Asn Gly Lys His Ser Leu
65 70 75 80

Ile Gly Lys Val Gln
85

<210> 623
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 623

Ile Met Glu Met Val Phe Arg Cys Ser Asp Leu Glu Ile Lys Asp Leu
1 5 10 15

Leu Ser Lys Ser Asp Pro Phe Leu Leu Ile Ser Arg Ile Ser Glu Ser
20 25 30

Gly Val Pro Val Pro Ile Cys Lys Thr Glu Val Arg Lys Asn Asp Leu
35 40 45

Asn Pro Lys Trp Lys Pro Val Ile Leu Asn Leu Gln Gln Ile Gly Ser
50 55 60

Lys Glu Asn Pro Leu Ile Ile Glu Cys Phe Asn Phe Ser Ser Asn Gly
65 70 75 80

Lys His Asp Leu Ile Gly Lys Ile Val
85

<210> 624
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 624

Phe Ser Ala Ser Asn Leu Arg Asp Arg Asp Val Ile Ser Lys Ser Asp
1 5 10 15

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Ala Met Val Val Val Tyr Thr Lys Gly Arg Asp Gly Thr Leu Ala Glu
20 25 30

Leu Phe Arg Ser Glu Val Val Leu Asn Ser Leu Asn Pro Lys Trp Ile
35 40 45

Lys Asn Phe Thr Ile Gly Tyr Gln Phe Glu Ile Val Gln Thr Leu Leu
50 55 60

Phe Arg Val Tyr Asp Ile Asp Thr Gln Phe Gln Asn Ser Lys Glu Glu
65 70 75 80

Leu Leu Lys Leu Asp Glu Gln Gln Phe Leu Gly Glu Ala Thr
85 90

<210> 625
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 625

Phe Ser Ala Ser Asn Leu Arg Asp Arg Asp Val Ile Ser Lys Ser Asp
1 5 10 15

Ala Met Val Val Val Tyr Thr Lys Gly Arg Asp Gly Thr Leu Ala Glu
20 25 30

Leu Phe Arg Ser Glu Val Val Leu Asn Ser Leu Asn Pro Lys Trp Ile
35 40 45

Lys Asn Phe Thr Ile Gly Tyr Gln Phe Glu Ile Val Gln Thr Leu Leu
50 55 60

Phe Arg Val Tyr Asp Ile Asp Thr Gln Phe Gln Asn Ser Lys Glu Glu
65 70 75 80

Leu Leu Lys Leu Asp Glu Gln Gln Phe Leu Gly Glu Ala Thr
85 90

<210> 626
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 626

Phe Ser Ala Ser Asn Leu Arg Asp Arg Asp Val Ile Ser Lys Ser Asp
1 5 10 15

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Ala Met Val Val Val Tyr Thr Lys Gly Arg Asp Gly Thr Leu Ala Glu
20 25 30

Leu Phe Arg Ser Glu Val Val Leu Asn Ser Leu Asn Pro Lys Trp Ile
35 40 45

Lys Asn Phe Thr Ile Gly Tyr Gln Phe Glu Ile Val Gln Thr Leu Leu
50 55 60

Phe Arg Val Tyr Asp Ile Asp Thr Gln Phe Gln Asn Ser Lys Glu Glu
65 70 75 80

Leu Leu Lys Leu Asp Glu Gln Gln Phe Leu Gly Glu Ala Thr
85 90

<210> 627
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 627

Phe Ser Ala Ser Asn Leu Arg Asp Arg Asp Val Leu Ser Lys Ser Asp
1 5 10 15

Pro Met Val Val Val Tyr Gln Lys Glu Lys Asp Ala Thr Leu Ser Glu
20 25 30

Val Phe Arg Ser Glu Val Val Leu Asn Ser Leu Ala Pro Lys Trp Ile
35 40 45

Lys Lys Phe Ile Val Ala Tyr His Phe Glu Thr Val Gln Thr Leu Val
50 55 60

Phe Arg Val Tyr Asp Val Asp Thr Lys Phe Gln Asn Ser Arg Glu Glu
65 70 75 80

Met Leu Lys Leu Asp Glu Gln Gln Phe Leu Gly Glu Ala Thr
85 90

<210> 628
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 628

Phe Ser Ala Ser Asn Leu Arg Asp Arg Asp Val Leu Ser Lys Ser Asp
1 5 10 15

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Pro Met Val Val Val Tyr Gln Lys Glu Lys Asp Ala Thr Leu Ser Glu
20 25 30

Val Phe Arg Ser Glu Val Val Leu Asn Ser Leu Ala Pro Lys Trp Ile
35 40 45

Lys Lys Phe Ile Val Ala Tyr His Phe Glu Thr Val Gln Thr Leu Val
50 55 60

Phe Arg Val Tyr Asp Val Asp Thr Lys Phe Gln Asn Ser Arg Glu Glu
65 70 75 80

Met Leu Lys Leu Asp Glu Gln Gln Phe Leu Gly Glu Ala Thr
85 90

<210> 629
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 629

Leu Ser Ala Ser Asn Leu Gly Asp Gln Glu Phe Phe Thr Lys Ser Asn
1 5 10 15

Pro Met Val Ile Val Tyr Ser Lys Ser Lys Glu Gly Ala Leu Glu Glu
20 25 30

Leu Gly Arg Thr Glu Val Ile Leu Asn Ser Leu Asn Pro Ser Trp Asn
35 40 45

Ala Arg Ile Asn Val His Tyr Gln Phe Glu Val Leu Gln Pro Ile Val
50 55 60

Phe Gln Val Tyr Asp Ile Asp Pro Gln Phe His Asp Val Asn Glu Lys
65 70 75 80

Met Leu Lys Leu Glu Glu Gln Gln Phe Leu Gly Glu Ala Val
85 90

<210> 630
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 630

Leu Ser Ala Ser Asn Leu Leu Asp Cys Asp Ile Thr Ser Lys Ser Asp
1 5 10 15

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Pro Met Ala Val Met Tyr Leu Arg Lys Lys Asp Gly Arg Leu Glu Glu
20 25 30

Ile Gly Arg Thr Glu Val Ile Leu Asn Asn Leu Asn Pro Lys Trp Ile
35 40 45

Glu Lys Ile Thr Val Ser Phe Gln Phe Glu Ala Val Gln Thr Leu Val
50 55 60

Phe His Val Tyr Asp Val Asp Thr Arg Tyr His Asn Val Pro Val Lys
65 70 75 80

Thr Leu Lys Leu Lys Asp Gln Asp Phe Leu Gly Glu Gly Thr
85 90

<210> 631
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 631

Leu Ser Ala Ser Asn Leu Leu Asp Cys Asp Ile Thr Ser Lys Ser Asp
1 5 10 15

Pro Met Ala Val Met Tyr Leu Arg Lys Lys Asp Gly Arg Leu Glu Glu
20 25 30

Ile Gly Arg Thr Glu Val Ile Leu Asn Asn Leu Asn Pro Lys Trp Ile
35 40 45

Glu Lys Ile Thr Val Ser Phe Gln Phe Glu Ala Val Gln Thr Leu Val
50 55 60

Phe His Val Tyr Asp Val Asp Thr Arg Tyr His Asn Val Pro Val Lys
65 70 75 80

Thr Leu Lys Leu Lys Asp Gln Asp Phe Leu Gly Glu Gly Thr
85 90

<210> 632
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 632

Val Asn Gln Leu Thr Leu Ser Ala Ser Asn Leu Leu Asp Cys Asp Ile
1 5 10 15

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Thr Ser Lys Ser Asp Pro Met Ala Val Met Tyr Leu Arg Lys Lys Asp
20 25 30

Gly Arg Leu Glu Glu Ile Gly Arg Thr Glu Val Ile Leu Asn Asn Leu
35 40 45

Asn Pro Lys Trp Ile Glu Lys Ile Thr Val Ser Phe Gln Phe Glu Ala
50 55 60

Val Gln Thr Leu Val Phe His Val Tyr Asp Val Asp Thr Arg Tyr His
65 70 75 80

Asn Val Pro Val Lys Val Ile Phe
85

<210> 633
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 633

Phe Ser Ala Ser Lys Leu Arg Asn Met Asp Ala Phe Ser Lys Ser Asp
1 5 10 15

Pro Met Leu Val Ile Tyr Ile Arg Lys Asp Ala Arg Leu Glu Glu Ile
20 25 30

Gly Arg Thr Glu Val Ile Leu Asn Ser Leu Glu Pro Ser Trp Ile Thr
35 40 45

Lys Ala Thr Ile Ser Tyr Gln Phe Glu Ile Ile Gln Pro Leu Val Phe
50 55 60

Lys Ile Tyr Asp Ile Asp Thr Arg Tyr His Asn Thr Pro Val Lys Thr
65 70 75 80

Leu Asn Leu Ala Gln Gln Asp Phe Leu Gly Glu Ala Cys
85 90

<210> 634
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 634

Met Thr Val Ala Leu Ile Glu Gly Thr Gly Ile Thr Asn Ser Asn Ser
1 5 10 15

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Lys Glu Leu Phe Asp Met Tyr Ala Val Phe Thr Cys Asn Ala Lys Arg
20 25 30

Lys Thr Ser Ser Val Lys Phe Gln Thr Ser Glu Pro Lys Trp Asn Glu
35 40 45

Ile Tyr Glu Phe Asp Ala Met Asp Asp Pro Pro Ser Arg Met Asp Val
50 55 60

Ala Ile His Asp Ala Asn Gly Pro Phe Asp Gln Ser Pro Ile Gly His
65 70 75 80

Ala Glu

<210> 635
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 635

Leu Thr Val Ala Leu Ile Glu Gly Ser Gly Val Val Gly Ser Gly Thr
1 5 10 15

Pro Gly Leu Pro Asp Pro Tyr Val Val Phe Thr Cys Asn Gly Lys Arg
20 25 30

Lys Thr Ser Ser Val Lys Phe Gln Thr Ser Glu Pro Lys Trp Asn Glu
35 40 45

Ile Phe Glu Phe Asn Ala Met Asp Asp Pro Pro Ser Arg Leu Glu Val
50 55 60

Val Val His Asp Ser Glu Gly Pro His Asn Lys Ile Pro Ile Gly Gln
65 70 75 80

Thr Glu

<210> 636
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 636

Leu Thr Val Ala Leu Ile Glu Gly Thr Lys Leu Ala Pro Val Asp Ala
1 5 10 15

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Thr Gly Phe Ser Asp Pro Tyr Val Val Phe Thr Cys Asn Gly Lys Ser
20 25 30

Lys Thr Ser Ser Ile Lys Phe Gln Thr Leu Glu Pro Gln Trp Asn Asp
35 40 45

Ile Phe Glu Phe Asp Ala Met Asp Asp Pro Pro Ser Val Met Asn Val
50 55 60

His Val Tyr Asp Phe Asp Gly Pro Phe Asp Glu Val Thr Ser Leu Gly
65 70 75 80

His Ala Glu

<210> 637
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 637

Leu Thr Val Ala Leu Ile Asp Gly Thr Asn Leu Ala Ala Thr Lys Ser
1 5 10 15

Ser Gly Tyr Ser Asp Pro Tyr Val Val Phe Thr Cys Asn Gly Lys Thr
20 25 30

Lys Thr Ser Ser Ile Lys Phe His Thr Leu Glu Pro Arg Trp Asn Glu
35 40 45

Ile Phe Glu Phe Asp Ala Met Glu Asp Pro Pro Ser Val Met Lys Ile
50 55 60

Asn Val Tyr Asp Phe Asp Gly Pro Phe Asp Glu Val Glu Ser Leu Gly
65 70 75 80

His Ala Glu

<210> 638
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 638

Leu Thr Val Ala Leu Ile Glu Gly Val Asp Leu Ala Ala Val Asp Pro
1 5 10 15

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Ser Gly His Cys Asp Pro Tyr Ile Val Phe Thr Ser Asn Gly Lys Thr
20 25 30

Arg Thr Ser Ser Ile Lys Phe Gln Lys Ser Asn Pro Gln Trp Asn Glu
35 40 45

Ile Phe Glu Phe Asp Ala Met Ala Asp Pro Pro Ser Val Leu Asn Val
50 55 60

Glu Val Phe Asp Phe Asp Gly Pro Phe Asp Glu Ala Val Ser Leu Gly
65 70 75 80

His Ala Glu

<210> 639
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 639

Leu Thr Ile Ala Leu Ile Lys Gly Thr Asn Leu Ala Ser Val Glu Ala
1 5 10 15

Thr Glu Leu Phe Asp Pro Tyr Val Val Phe Thr Cys Asn Gly Lys Thr
20 25 30

Arg Thr Ser Ser Val Lys Leu Gln Ala Gln Asp Pro Gln Trp Asn Glu
35 40 45

Val Ile Glu Phe Asp Ala Met Glu Glu Pro Pro Ser Val Leu Asp Val
50 55 60

Glu Val Phe Asp Phe Asp Gly Pro Phe Asp Gln Gly Ala Ser Leu Gly
65 70 75 80

His Ala Glu

<210> 640
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 640

Leu Thr Val Ala Leu Leu Glu Ala Thr Ser Leu Pro Pro Val Ser Ser
1 5 10 15

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Gly Ser Val Asp Pro Tyr Val Val Phe Ser Cys Asn Gly Ile Thr Arg
20 25 30

Thr Ser Ser Val Gln Leu Gln Thr His Asp Pro Gln Trp Asn Glu Ile
35 40 45

Met Glu Phe Asp Ala Met Glu Glu Pro Pro Ala Thr Leu Asp Val Glu
50 55 60

Val Phe Asn Phe Asp Gly Pro Phe Asp Leu Ala Val Ser Leu Gly His
65 70 75 80

Ala Glu

<210> 641
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 641

Arg Arg Thr Lys Glu Pro Thr Trp Asn Glu Glu Phe Thr Phe Asn Ile
1 5 10 15

Ser Leu Ser Arg Glu Asn Leu Leu Gln Val Ala Ala Trp Asp Ala Asn
20 25 30

Leu Val Thr Pro His Lys Arg Met Gly Asn Ala Gly
35 40

<210> 642
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 642

Gly Thr Ser Asp Pro Tyr Val Val Met Asp Leu Asp Gly Gln Val Ala
1 5 10 15

Lys Ser Lys Thr Lys Trp Gly Thr Lys Glu Pro Lys Trp Asn Glu Asp
20 25 30

Phe Val Phe Asn Ile Lys Leu Pro Pro Ala Lys Lys Ile Glu Ile Ala
35 40 45

Ala Trp Asp Ala Asn Leu Val Thr Pro His Lys Arg Met Gly Asn Ser
50 55 60

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Glu
65

<210> 643
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 643

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asp Leu Asp Phe His
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Phe Val Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Arg Asp Thr Val Ser Tyr Arg Thr Glu Thr
35 40 45

Ala Val Asp Gln Trp Phe Pro Ile Trp Gly Asn Asp Glu Phe Leu Phe
50 55 60

Gln Leu Ser Val Pro Glu Leu Ala Leu Leu Trp Phe Lys Val Gln Asp
65 70 75 80

Tyr Asp Asn Asp Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 644
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 644

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asp Leu Asp Phe His
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Phe Val Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Arg Asp Thr Val Ser Tyr Arg Thr Glu Thr
35 40 45

Ala Val Asp Gln Trp Phe Pro Ile Trp Gly Asn Asp Glu Phe Leu Phe
50 55 60

Gln Leu Ser Val Pro Glu Leu Ala Leu Leu Trp Phe Lys Val Gln Asp
65 70 75 80

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Tyr Asp Asn Asp Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 645
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 645

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asp Leu Asp Phe His
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Phe Val Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Arg Asp Thr Val Ser Tyr Arg Thr Glu Thr
35 40 45

Ala Val Asp Gln Trp Phe Pro Ile Trp Gly Asn Asp Glu Phe Leu Phe
50 55 60

Gln Leu Ser Val Pro Glu Leu Ala Leu Leu Trp Phe Lys Val Gln Asp
65 70 75 80

Tyr Asp Asn Asp Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 646
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 646

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asp Leu Asp Phe His
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Phe Val Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Arg Asp Thr Val Ser Tyr Arg Thr Glu Thr
35 40 45

Ala Val Asp Gln Trp Phe Pro Ile Trp Gly Asn Asp Glu Phe Leu Phe
50 55 60

Gln Leu Ser Val Pro Glu Leu Ala Leu Leu Trp Phe Lys Val Gln Asp
65 70 75 80

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Tyr Asp Asn Asp Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 647
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 647

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asn Met Asp Phe Pro
1 5 10 15

Leu Asp His Phe Asp Arg Tyr Ser Pro Pro Asp Phe Tyr Ala Lys Val
20 25 30

Gly Ile Ala Gly Val Pro Leu Asp Thr Ala Ser Tyr Arg Thr Glu Ile
35 40 45

Asp Lys Asp Glu Trp Phe Pro Ile Trp Asp Lys Glu Phe Glu Phe Pro
50 55 60

Leu Arg Val Pro Glu Leu Ser Leu Leu Cys Ile Thr Val Lys Asp Tyr
65 70 75 80

Asp Ser Asn Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 648
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 648

Leu Lys Val Lys Ile Tyr Thr Gly Glu Gly Trp Asn Met Asp Phe Pro
1 5 10 15

Leu Asp His Phe Asp Arg Tyr Ser Pro Pro Asp Phe Tyr Ala Lys Val
20 25 30

Gly Ile Ala Gly Val Pro Leu Asp Thr Ala Ser Tyr Arg Thr Glu Ile
35 40 45

Asp Lys Asp Glu Trp Phe Pro Ile Trp Asp Lys Glu Phe Glu Phe Pro
50 55 60

Leu Arg Val Pro Glu Leu Ser Leu Leu Cys Ile Thr Val Lys Asp Tyr
65 70 75 80

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Asp Ser Asn Thr Gln Asn Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 649
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 649

Leu Lys Val Lys Val Cys Met Gly Asp Gly Trp Leu Leu Asp Phe Lys
1 5 10 15

Lys Thr His Phe Asp Ser Tyr Ser Pro Pro Asp Phe Phe Val Arg Val
20 25 30

Gly Ile Ala Gly Ala Pro Val Asp Glu Val Met Glu Lys Thr Lys Ile
35 40 45

Glu Tyr Asp Thr Trp Thr Pro Ile Trp Asn Lys Glu Phe Thr Phe Pro
50 55 60

Leu Ala Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu His
65 70 75 80

Asp Val Asn Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 650
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 650

Leu Lys Val Lys Val Cys Met Gly Asp Gly Trp Leu Leu Asp Phe Lys
1 5 10 15

Lys Thr His Phe Asp Ser Tyr Ser Pro Pro Asp Phe Phe Val Arg Val
20 25 30

Gly Ile Ala Gly Ala Pro Val Asp Glu Val Met Glu Lys Thr Lys Ile
35 40 45

Glu Tyr Asp Thr Trp Thr Pro Ile Trp Asn Lys Glu Phe Thr Phe Pro
50 55 60

Leu Ala Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu His
65 70 75 80

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Asp Val Asn Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 651
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 651

Leu Lys Val Lys Val Cys Met Gly Asp Gly Trp Leu Leu Asp Phe Lys
1 5 10 15

Lys Thr His Phe Asp Ser Tyr Ser Pro Pro Asp Phe Phe Val Arg Val
20 25 30

Gly Ile Ala Gly Ala Pro Val Asp Glu Val Met Glu Lys Thr Lys Ile
35 40 45

Glu Tyr Asp Thr Trp Thr Pro Ile Trp Asn Lys Glu Phe Thr Phe Pro
50 55 60

Leu Ala Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu His
65 70 75 80

Asp Val Asn Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 652
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 652

Leu Lys Val Thr Val Tyr Met Gly Asp Gly Trp Arg Phe Asp Phe Arg
1 5 10 15

Lys Thr His Phe Asp Lys Cys Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Glu Ala Asp Thr Arg Met Glu Gln Thr Lys Val
35 40 45

Lys Met Asp Thr Trp Ile Pro Ala Trp Asp His Glu Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Ser
65 70 75 80

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Asp Asn His Gln Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 653
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 653

Leu Arg Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Phe Asp Phe Arg
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Gly Asp Thr Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Asn Trp Ile Pro Ala Trp Asp Glu Val Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Leu Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 654
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 654

Leu Arg Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Phe Asp Phe Arg
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Gly Asp Thr Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Asn Trp Ile Pro Ala Trp Asp Glu Val Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Leu Glu Val His Glu Tyr
65 70 75 80

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Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 655
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 655

Leu Arg Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Phe Asp Phe Arg
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Gly Asp Thr Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Asn Trp Ile Pro Ala Trp Asp Glu Val Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Leu Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 656
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 656

Leu Arg Val Thr Ile Tyr Met Gly Glu Gly Trp Tyr Phe Asp Phe Arg
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Thr Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Asn Trp Val Pro Ser Trp Asp Glu Val Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Leu Glu Val His Glu Tyr
65 70 75 80

```
Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
                85                  90
```

<210> 657
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 657

```
Leu Arg Val Thr Ile Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Pro
1               5                   10                  15

His Thr His Phe Asp Arg Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
            20                  25                  30

Gly Ile Ala Gly Val Pro Ala Asp Thr Val Met Lys Lys Thr Lys Thr
        35                  40                  45

Leu Glu Asp Asn Trp Ile Pro Ala Trp Asp Glu Val Phe Glu Phe Pro
    50                  55                  60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65                  70                  75                  80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Ile Cys
                85                  90
```

<210> 658
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 658

```
Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1               5                   10                  15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
            20                  25                  30

Gly Ile Ala Gly Val Pro Asn Asp Thr Ile Met Lys Arg Thr Lys Ala
        35                  40                  45

Ile Glu Asp Asn Trp Leu Pro Thr Trp Asn Glu Ala Phe Glu Phe Pro
    50                  55                  60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65                  70                  75                  80
```


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Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 659
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 659

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Asn Asp Thr Ile Met Lys Arg Thr Lys Ala
35 40 45

Ile Glu Asp Asn Trp Leu Pro Thr Trp Asn Glu Val Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Ala Cys
85 90

<210> 660
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 660

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ser Asp Thr Val Met Lys Lys Thr Lys Ala
35 40 45

Asn Lys Asp Asn Trp Leu Pro Thr Trp Asn Glu Thr Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 661
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 661

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Phe Ser Pro Pro Asp Phe Tyr Ala Arg Ile
20 25 30

Gly Ile Ala Gly Val Pro Phe Asp Thr Val Met Lys Lys Thr Lys Ser
35 40 45

Ile Glu Asp Ser Trp Leu Pro Ser Trp Asn Glu Val Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 662
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 662

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Phe Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Phe Asp Thr Val Met Lys Lys Thr Lys Ser
35 40 45

Ile Glu Asp Ser Trp Leu Pro Ser Trp Asn Glu Val Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

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Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 663
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 663

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Phe Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Phe Asp Thr Ile Met Lys Lys Thr Lys Thr
35 40 45

Val Glu Asp Ser Trp Leu Pro Ser Trp Asn Glu Val Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 664
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 664

Leu Lys Val Thr Val Tyr Met Gly Glu Gly Trp Tyr Tyr Asp Phe Asp
1 5 10 15

His Thr His Phe Asp Gln Phe Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Phe Asp Thr Ile Met Lys Lys Thr Lys Thr
35 40 45

Val Glu Asp Ser Trp Leu Pro Ser Trp Asn Glu Val Phe Glu Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 665
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 665

Leu Lys Val Thr Ile Tyr Met Gly Glu Gly Trp Phe Leu Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Lys Phe Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Asn Asp Thr Val Met Lys Lys Thr Glu Lys
35 40 45

Val Glu Asp Asn Trp Ser Pro Ser Trp Asn Gln Val Phe Lys Phe Pro
50 55 60

Leu Ala Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 666
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 666

Leu Lys Val Thr Ile Tyr Met Gly Glu Gly Trp Phe His Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Tyr Asp Thr Val Met Lys Lys Thr Lys Ser
35 40 45

Val Glu Asp Asn Trp Ser Pro Ser Trp Asn Glu Glu Phe Lys Phe Pro
50 55 60

Leu Ser Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

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Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 667
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 667

Leu Lys Val Thr Val Phe Met Gly Glu Gly Trp Tyr Ile Asp Phe Lys
1 5 10 15

His Thr His Phe Asp Ala Tyr Thr Pro Pro Asp Phe Tyr Ala Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Asn Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Met Asp Thr Pro Thr Trp Asp Glu Lys Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 668
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 668

Leu Lys Val Thr Val Phe Met Gly Glu Gly Trp Tyr Tyr Asp Phe Asn
1 5 10 15

His Thr His Phe Asp Ala Tyr Ala Pro Pro Asp Phe Tyr Ala Lys Ile
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Asn Val Met Lys Lys Thr Arg Thr
35 40 45

Leu Glu Asn Asn Trp Ile Pro Thr Trp Asp Glu Lys Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Val Tyr
65 70 75 80

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Asp Met Ser Glu Lys Asp Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 669
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 669

Leu Lys Val Thr Val Phe Met Gly Glu Gly Trp Tyr Tyr Asp Phe Glu
1 5 10 15

His Thr His Phe Asp Ala Tyr Ser Pro Pro Asp Phe Tyr Ala Arg Ile
20 25 30

Gly Ile Ala Gly Val Asp Ala Asp Ile Val Met Lys Lys Thr Lys Thr
35 40 45

Leu Glu Asp Asn Trp Ile Pro Thr Trp Asp Glu Gln Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 670
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 670

Leu Lys Val Lys Val Tyr Met Gly Lys Gly Trp His Leu Asp Phe Lys
1 5 10 15

Arg Thr His Phe Asp Ala Tyr Ser Pro Pro Asp Phe Tyr Val Lys Ile
20 25 30

Gly Ile Ala Gly Val Ala Ala Asp Ser Arg Val Lys Lys Thr Lys Ala
35 40 45

Ile Glu Asp Asn Trp Ile Pro Ile Trp Asn Asp Glu Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Ile Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 671
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 671

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Ser
1 5 10 15

Lys Thr His Phe Asp Thr Phe Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Arg Ala Asp Cys Val Met Lys Lys Thr Arg Thr
35 40 45

Ile Glu Asp Gln Trp Val Pro Met Trp Asp Glu Glu Phe Thr Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Val Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys His Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 672
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 672

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Ser
1 5 10 15

Lys Thr His Phe Asp Thr Phe Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Arg Ala Asp Cys Val Met Lys Lys Thr Arg Thr
35 40 45

Ile Glu Asp Gln Trp Val Pro Met Trp Asp Glu Glu Phe Thr Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Val Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

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Asp Met Ser Glu Lys His Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 673
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 673

Leu Lys Val Lys Val Tyr Met Gly Asp Arg Trp Arg Met Asp Phe Ser
1 5 10 15

Lys Thr His Phe Asp Ala Phe Ser Pro Pro Asp Phe Tyr Thr Lys Val
20 25 30

Gly Ile Ala Gly Val Lys Ala Asp Ser Val Met Lys Lys Thr Arg Val
35 40 45

Ile Glu Asp Gln Trp Val Pro Met Trp Asp Glu Glu Phe Thr Phe Leu
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Val Glu Val Gln Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys His Asp Phe Gly Gly Gln Thr Val
85 90

<210> 674
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 674

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Thr
1 5 10 15

Gln Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Ser Val Met Lys Arg Thr Arg Ala
35 40 45

Ile Glu Asp Asn Trp Val Pro Val Trp Glu Glu Asp Phe Thr Phe Lys
50 55 60

Leu Thr Val Pro Glu Ile Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Val
85 90

<210> 675
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 675

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Thr
1 5 10 15

Gln Thr His Phe Asp Gln Tyr Ser Pro Pro Asp Phe Tyr Ala Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Ser Val Met Lys Arg Thr Arg Ala
35 40 45

Ile Glu Asp Asn Trp Val Pro Val Trp Glu Glu Asp Phe Thr Phe Lys
50 55 60

Leu Thr Val Pro Glu Ile Ala Leu Leu Arg Val Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Val
85 90

<210> 676
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 676

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Lys
1 5 10 15

Ser Thr His Phe Asp Thr Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Cys Thr Met Lys Lys Thr Arg Thr
35 40 45

Ile Glu Asp Asp Trp Thr Pro Val Trp Asp Glu Glu Leu Val Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

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Asp Met Ser Asp Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 677
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa can be any naturally occurring amino acid

<400> 677

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Lys
1 5 10 15

Gln Thr Tyr Phe Asp Ala Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Ile
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Xaa Val Met Lys Arg Thr Lys Ala
35 40 45

Ile Glu Asp Asp Trp Thr Pro Val Trp Asn Glu Glu Phe Val Phe Pro
50 55 60

Leu Thr Val Pro Glu Ile Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 678
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 678

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp His Leu Asp Phe Lys
1 5 10 15

Gln Thr His Phe Asp Leu Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Glu Ile Met Lys Lys Thr Lys Thr
35 40 45

Lys Glu Asp Lys Trp Thr Pro Val Trp Asp Glu Ala Phe Thr Phe Pro
50 55 60

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Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 679
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 679

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp His Leu Asp Phe Lys
1 5 10 15

Gln Thr His Phe Asp Leu Tyr Ser Pro Pro Asp Phe Tyr Thr Arg Val
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Glu Ile Met Lys Lys Thr Lys Thr
35 40 45

Lys Glu Asp Lys Trp Thr Pro Val Trp Asp Glu Glu Phe Thr Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Ala Gly Gln Thr Cys
85 90

<210> 680
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 680

Leu Gln Val Arg Val Tyr Met Gly Asp Gly Trp Arg Leu Asp Phe Ser
1 5 10 15

His Thr His Phe Asp Ala Tyr Ser Pro Pro Asp Phe Tyr Thr Lys Val
20 25 30

Ile Gly Val Pro Ala Asp Ser Arg Lys Lys Lys Thr Arg Ile Leu Glu
35 40 45

Asp Asp Trp Cys Pro Val Trp Asp Glu Glu Phe Asn Phe Pro Leu Thr
50 55 60

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Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Arg Glu Tyr Asp Met
65 70 75 80

Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 681
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 681

Leu Lys Val Lys Val Tyr Met Gly Asp Gly Trp Arg Met Asp Phe Ser
1 5 10 15

His Thr His Phe Asp Ala Tyr Ser Pro Pro Asp Phe Tyr Thr Lys Met
20 25 30

Phe Ile Val Gly Val Pro Ala Asp Asn Ala Lys Lys Lys Thr Lys Ile
35 40 45

Ile Glu Asp Asn Trp Tyr Pro Ile Trp Asp Glu Glu Phe Ser Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Arg Glu Tyr
65 70 75 80

Asp Met Ser Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 682
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 682

Leu Lys Val Lys Val Tyr Met Gly Glu Gly Trp His Lys Asp Phe Lys
1 5 10 15

Gln Thr His Phe Asp Thr Tyr Ser Pro Pro Asp Phe Tyr Val Glu Val
20 25 30

Gly Ile Ala Gly Val Pro Leu Asp Ser Val Met Arg Lys Thr Lys Ala
35 40 45

Val Glu Asp Asn Trp Val Pro Val Trp Glu Glu Glu Phe Ala Phe Pro
50 55 60

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Leu Thr Val Pro Glu Ile Ala Val Leu Arg Val Glu Val His Glu Gln
65 70 75 80

Asp Val Ser Glu Asp Asp Phe Gly Gly Gln Thr Ala
85 90

<210> 683
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 683

Leu Lys Val Thr Val Tyr Met Gly Asp Gly Trp Asp Lys Asp Phe Asp
1 5 10 15

Gln Thr His Phe Asp Thr Tyr Ser Pro Pro Asp Phe Tyr Ala Lys Leu
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Glu Val Lys Lys Arg Thr Lys Thr
35 40 45

Met Asp Asp Asn Trp Ile Pro Ser Trp Asp Glu Gln Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Lys Val Leu Asp Tyr
65 70 75 80

Asn Leu Ser Asp Lys Asp Glu Phe Ala Gly Gln Thr Cys
85 90

<210> 684
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 684

Leu Lys Val Thr Val Tyr Met Gly Asp Gly Trp Asp Lys Asp Phe Asp
1 5 10 15

Gln Thr Asp Phe Asp Thr Tyr Ser Pro Pro Asp Phe Tyr Ala Lys Leu
20 25 30

Gly Ile Ala Gly Val Pro Ala Asp Glu Val Lys Lys Arg Thr Glu Thr
35 40 45

Ile Asp Asp Asn Trp Ile Pro Ser Trp Asn Glu Gln Phe Glu Phe Pro
50 55 60

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Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Lys Val Leu Asp Tyr
65 70 75 80

Asn Leu Ser Asp Lys Asp Glu Phe Ala Gly Gln Thr Cys
85 90

<210> 685
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 685

Leu Lys Val Lys Val Tyr Leu Gly Lys Gly Trp Ser Leu Asp Phe Ser
1 5 10 15

Pro Ser Asp Phe Asp Ser Tyr Ser Pro Pro Asp Phe Tyr Val Lys Val
20 25 30

Cys Ile Val Gly Val Pro Ala Asp Met Ile Lys Lys Lys Thr Ser Val
35 40 45

Ile Ser Asn Asn Trp Phe Pro Val Trp Asn Glu Glu Phe Asp Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Gly Ile Glu Val Arg Glu Asp
65 70 75 80

Asp Lys His Gln Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 686
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 686

Leu Lys Val Lys Val Tyr Leu Gly Lys Gly Trp Ser Leu Asp Phe Ser
1 5 10 15

Pro Ser Asp Phe Asp Ser Tyr Ser Pro Pro Asp Phe Tyr Val Lys Val
20 25 30

Cys Ile Val Gly Val Pro Ala Asp Met Ile Lys Lys Lys Thr Ser Val
35 40 45

Ile Ser Asn Asn Trp Phe Pro Val Trp Asn Glu Glu Phe Asp Phe Pro
50 55 60

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Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Arg Glu Glu
65 70 75 80

Asp Lys His Gln Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 687
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 687

Leu Lys Val Lys Val Tyr Met Gly Asn Gly Trp Ser Ser Asp Phe Ser
1 5 10 15

Lys Thr His Phe Asp Ser Phe Ser Pro Pro Asp Phe Tyr Thr Lys Val
20 25 30

Cys Ile Val Gly Val Pro Ala Asp Lys Ala Asn Lys Lys Thr Lys Val
35 40 45

Ile Gln Asp Asn Trp Phe Pro Val Trp Asp Glu Glu Phe Glu Phe Pro
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Arg Glu Tyr
65 70 75 80

Asp Lys His Glu Lys Asp Asp Phe Gly Gly Gln Thr Cys
85 90

<210> 688
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 688

Leu Lys Val Lys Val Tyr Lys Gly Val Gly Trp Arg Ser Asp Phe Ser
1 5 10 15

Pro Thr His Phe Asp Arg Phe Ser Pro Pro Asp Phe Tyr Thr Lys Val
20 25 30

Cys Ile Ala Gly Val Gly Ala Asp Ser Val Lys Met Lys Thr Ser Val
35 40 45

Lys Met Asp Asn Trp Tyr Pro Val Trp Asp Glu Glu Phe Glu Phe Gln
50 55 60

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Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Lys Asp Lys
65   70   75   80

Asp Lys Gly Ser Asp Asp Phe Ala Gly Gln Thr Cys
                85   90

<210> 689
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 689

Leu Lys Val Lys Val Tyr Lys Gly Val Gly Trp Ser Ser Asp Phe Ser
1   5   10   15

Pro Thr His Phe Asp Arg Phe Ser Pro Pro Asp Phe Tyr Thr Lys Val
            20   25   30

Ser Ile Ala Gly Val Arg Ala Asp Cys Ala Lys Lys Lys Thr Ser Val
        35   40   45

Lys Met Asp Asn Trp Asn Pro Ile Trp Asp Glu Glu Phe Glu Phe Arg
    50   55   60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val Lys Asp Lys
65   70   75   80

Asp Gln Thr Lys Asp Asp Phe Ala Gly Gln Thr Cys
                85   90

<210> 690
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 690

Leu Lys Val Lys Val Tyr Met Gly Lys Gly Trp Asp Ser Gly Phe Gln
1   5   10   15

Arg Thr Cys Phe Asn Thr Trp Ser Ser Pro Asn Phe Tyr Thr Arg Val
            20   25   30

Gly Ile Thr Gly Val Arg Gly Asp Lys Val Met Lys Lys Thr Lys Lys
        35   40   45

Glu Gln Lys Thr Trp Glu Pro Phe Trp Asn Glu Glu Phe Glu Phe Gln
    50   55   60

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Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Asp Tyr
65 70 75 80

Asn Met Pro Glu Lys Asp Asp Phe Ser Gly Gln Thr Cys
85 90

<210> 691
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 691

Leu Lys Val Lys Val Tyr Met Gly Lys Gly Trp Asp Ser Gly Phe Gln
1 5 10 15

Arg Thr Cys Phe Asn Thr Trp Ser Ser Pro Asn Phe Tyr Thr Arg Val
20 25 30

Gly Ile Thr Gly Val Arg Gly Asp Lys Val Met Lys Lys Thr Lys Lys
35 40 45

Glu Gln Lys Thr Trp Glu Pro Phe Trp Asn Glu Glu Phe Glu Phe Gln
50 55 60

Leu Thr Val Pro Glu Leu Ala Leu Leu Arg Ile Glu Val His Asp Tyr
65 70 75 80

Asn Met Pro Glu Lys Asp Asp Phe Ser Gly Gln Thr Cys
85 90

<210> 692
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 692

Asp Leu Phe Ser Pro Pro Asp Phe Phe Thr Arg Leu Leu Val Thr Gly
1 5 10 15

Val Pro Ala Asp Val Ala Lys Trp Lys Thr Ser Val Ile Asp Asp Val
20 25 30

Trp Glu Pro His Trp Asn Glu Asp His Glu Phe Tyr Leu Lys Cys Pro
35 40 45

Glu Leu Ala Leu Leu Arg Ile Glu Val Arg Asp His Asp Glu Gly Ser
50 55 60

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Gln Asp Glu Phe Glu Gly Gln Ala Cys
65 70

<210> 693
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 693

Leu Lys Val Lys Ile Tyr Met Gly Asp Gly Trp Ile Val Asp Phe Lys
1 5 10 15

Lys Arg Ile Gly Arg Leu Ser Lys Pro Asp Leu Tyr Val Arg Ile Ser
20 25 30

Ile Ala Gly Val Pro His Asp Glu Lys Ile Met Asn Thr Thr Val Lys
35 40 45

Asn Asn Glu Trp Lys Pro Thr Trp Gly Glu Glu Phe Thr Phe Pro Leu
50 55 60

Thr Tyr Pro Asp Leu Ala Leu Ile Ser Phe Glu Val Tyr Asp Tyr Glu
65 70 75 80

Val Ser Thr Pro Asp Tyr Phe Cys Gly Gln Thr Cys
85 90

<210> 694
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 694

Leu Lys Val Lys Ile Tyr Met Gly Asp Gly Trp Ile Val Asp Phe Lys
1 5 10 15

Lys Arg Ile Gly Arg Leu Ser Lys Pro Asp Leu Tyr Val Arg Ile Ser
20 25 30

Ile Ala Gly Val Pro His Asp Glu Lys Ile Met Asn Thr Thr Val Lys
35 40 45

Asn Asn Glu Trp Lys Pro Thr Trp Gly Glu Glu Phe Thr Phe Pro Leu
50 55 60

Thr Tyr Pro Asp Leu Ala Leu Ile Ser Phe Glu Val Tyr Asp Tyr Glu
65 70 75 80

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Val Ser Thr Pro Asp Tyr Phe Cys Gly Gln Thr Cys
85 90

<210> 695
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 695

Leu Lys Val Lys Ile Tyr Met Gly Asp Gly Trp Ile Val Asp Phe Lys
1 5 10 15

Lys Arg Ile Gly Arg Leu Ser Lys Pro Asp Leu Tyr Val Arg Ile Ser
20 25 30

Ile Ala Gly Val Pro His Asp Glu Asn Ile Met Lys Thr Thr Val Lys
35 40 45

Asn Asn Glu Trp Thr Pro Thr Trp Gly Glu Glu Phe Thr Phe Pro Leu
50 55 60

Thr Tyr Pro Asp Leu Ala Leu Ile Ser Phe Glu Val Tyr Asp Tyr Glu
65 70 75 80

Val Ser Thr Ala Asp Ala Phe Cys Gly Gln Thr Cys
85 90

<210> 696
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 696

Leu Lys Val Lys Ile Tyr Met Gly Asp Gly Trp Ile Val Asp Phe Lys
1 5 10 15

Lys Arg Ile Gly Arg Leu Ser Lys Pro Asp Leu Tyr Val Arg Ile Ser
20 25 30

Ile Ala Gly Val Pro His Asp Glu Asn Ile Met Lys Thr Thr Val Lys
35 40 45

Asn Asn Glu Trp Thr Pro Thr Trp Gly Glu Glu Phe Thr Phe Pro Leu
50 55 60

Thr Tyr Pro Asp Leu Ala Leu Ile Ser Phe Glu Val Tyr Asp Tyr Glu
65 70 75 80

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Val Ser Thr Ala Asp Ala Phe Cys Gly Gln Thr Cys
85 90

<210> 697
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 697

Leu Lys Val Thr Val Leu Leu Gly Thr Asp Trp His Lys Asn Tyr Asp
1 5 10 15

Val Phe Lys Lys Pro Gly Tyr Phe Val Lys Val Ala Ile His Gly Met
20 25 30

His Asp Asp Glu Gln Lys Phe Lys Thr His Val Cys Lys Arg Ser Arg
35 40 45

Glu Pro His Trp Glu Val Glu Glu Phe Val Phe Gln Ile Arg Val Pro
50 55 60

Lys Leu Ala Ile Leu Arg Leu Glu Val Arg Glu Tyr Asp Arg Ile Val
65 70 75 80

Arg Asp Asp Met Val Gly Gln Ser Cys
85

<210> 698
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 698

Lys Gln Ser Val Gly Asn Pro Ser Val Phe Cys Lys Ile Thr Leu Gly
1 5 10 15

Asn Asn Pro Pro Arg Gln Thr Lys Val Ile Ser Thr Gly Pro Asn Pro
20 25 30

Glu Trp Asp Glu Ser Phe Ser Trp Ser Phe Glu Ser Pro Pro Lys Gly
35 40 45

Gln Lys Leu His Ile Ser Cys Lys Asn Lys Ser Lys Met Gly Lys Ser
50 55 60

Ser Phe Gly Lys Val Thr
65 70

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<210> 699
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 699

Leu Val Val Thr Ile Lys Arg Gly Asn Asn Met Lys Gln Ser Val Gly
1 5 10 15

Asn Pro Ser Val Phe Cys Lys Ile Thr Leu Gly Asn Asn Pro Pro Arg
20 25 30

Gln Thr Lys Val Ile Ser Thr Gly Pro Asn Pro Glu Trp Asp Glu Ser
35 40 45

Phe Ser Trp Ser Phe Glu Ser Pro Pro Lys Gly Gln Lys Leu His Ile
50 55 60

Ser Cys Lys Asn Lys Ser Lys Met Gly Lys Ser Ser Phe Gly Lys Val
65 70 75 80

Thr

<210> 700
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 700

Leu Val Val Ile Ile Lys Arg Gly Asn Asn Met Lys Gln Ser Val Gly
1 5 10 15

Asn Pro Ser Val Tyr Cys Lys Ile Thr Leu Gly Asn Asn Pro Pro Arg
20 25 30

Leu Thr Lys Val Val Ser Thr Gly Pro Asn Pro Glu Trp Asp Glu Ser
35 40 45

Phe Ser Trp Ser Phe Glu Ser Pro Pro Lys Gly Gln Lys Leu His Ile
50 55 60

Ser Cys Lys Asn Lys Ser Lys Val Gly Lys Ser Lys Phe Gly Lys Val
65 70 75 80

Thr

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<210> 701
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 701

Leu Val Val Ile Val Lys Arg Gly Asn Asn Met Arg Gln Ser Val Gly
1 5 10 15

Ile Pro Ser Val Tyr Cys Lys Ile Thr Leu Gly Asn Ser Pro Pro Lys
20 25 30

Leu Thr Lys Val Val Ser Thr Gly Pro Asn Pro Glu Trp Glu Glu Ser
35 40 45

Phe Thr Trp Ser Phe Glu Ser Pro Pro Lys Gly Gln Lys Leu His Ile
50 55 60

Ser Cys Lys Asn Lys Ser Lys Val Gly Lys Ser Lys Phe Gly Lys Val
65 70 75 80

Thr

<210> 702
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 702

Leu Thr Val Thr Ile Lys Arg Gly Asn Asn Leu Arg Gln Ser Val Gly
1 5 10 15

Asn Pro Ser Ala Phe Cys Lys Leu Thr Leu Gly Asn Asn Pro Pro Arg
20 25 30

Leu Thr Lys Ile Val Ser Thr Gly Ala Thr Pro Glu Trp Asp Glu Ala
35 40 45

Phe Ala Trp Ala Phe Asp Ser Pro Pro Lys Gly Gln Lys Leu His Ile
50 55 60

Ser Cys Lys Asn Asn Ser Lys Phe Gly Lys Lys Ser Phe Gly Lys Val
65 70 75 80

Thr

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<210> 703
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 703

Leu Thr Val Asn Val Met Arg Ala Asn Asn Leu Lys Gln Ser Met Ala
1   5   10   15

Thr Thr Asn Ala Phe Cys Gln Leu Thr Ile Gly Asn Cys Pro Pro Arg
            20   25   30

Gln Thr Lys Val Val Ser Asn Ser Thr Thr Pro Glu Trp Lys Glu Gly
        35   40   45

Phe Thr Trp Ala Phe Asp Val Pro Pro Lys Gly Gln Lys Leu His Ile
    50   55   60

Ile Cys Lys Ser Lys Ser Thr Phe Gly Lys Thr Thr Leu Gly Arg Val
65   70   75   80

Thr

<210> 704
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 704

Leu Thr Val Asn Val Met Arg Ala Asn Asn Leu Lys Gln Ser Met Ala
1   5   10   15

Thr Thr Asn Ala Phe Cys Gln Leu Thr Ile Gly Asn Cys Pro Pro Arg
            20   25   30

Gln Thr Lys Val Val Ser Asn Ser Thr Thr Pro Glu Trp Lys Glu Gly
        35   40   45

Phe Thr Trp Ala Phe Asp Val Pro Pro Lys Gly Gln Lys Leu His Ile
    50   55   60

Ile Cys Lys Ser Lys Ser Thr Phe Gly Lys Thr Thr Leu Gly Arg Val
65   70   75   80

Thr

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<210> 705
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 705

Leu Thr Val Thr Ile Leu Arg Gly Asn Asn Leu Lys Gln Thr Met Gly
1 5 10 15

Ser Thr Asn Ala Phe Cys Cys Leu Gln Ile Gly Asn Gly Pro Pro Arg
20 25 30

Gln Thr Lys Val Val Asn Asn Ser Ile Cys Pro Val Trp Asn Glu Gly
35 40 45

Phe Thr Trp Leu Phe Asp Ile Pro Pro Lys Gly Gln Lys Leu Tyr Ile
50 55 60

Leu Cys Lys Ser Lys Asn Thr Phe Gly Lys Ser Thr Leu Gly Arg Val
65 70 75 80

Thr

<210> 706
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 706

Leu Thr Val Ala Ile Lys Arg Gly Asp Asn Leu Lys Arg Ser Asn Ala
1 5 10 15

Phe Cys Arg Leu Ile Ile Asp Asn Cys Pro Thr Lys Lys Thr Lys Val
20 25 30

Val Lys Arg Ser Ser Ser Pro Val Trp Lys Glu Ser Phe Thr Trp Asp
35 40 45

Phe Ala Ala Pro Pro Arg Gly Gln Phe Leu Glu Ile Val Cys Lys Ser
50 55 60

Asn Asn Ile Phe Arg Asn Lys Asn Leu Gly Lys Val Arg
65 70 75

<210> 707
<211> 88

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 707

Leu Glu Val Tyr Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Ser Asp Pro
20 25 30

Asp Lys Ser Val Ser Thr Lys Ile Ile Asn Gly Gly Gly Arg Asn Pro
35 40 45

Val Phe Asp Asp Asn Val Lys Leu Asp Val Arg Val Leu Asp Thr Ser
50 55 60

Leu Lys Cys Glu Ile Tyr Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Thr Leu
85

<210> 708
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 708

Leu Glu Val Tyr Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Ser Asp Pro
20 25 30

Asp Lys Ser Val Ser Thr Lys Ile Ile Asn Gly Gly Gly Arg Asn Pro
35 40 45

Val Phe Asp Asp Asn Val Lys Leu Asp Val Arg Val Leu Asp Thr Ser
50 55 60

Leu Lys Cys Glu Ile Tyr Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Thr Leu
85

<210> 709
<211> 88

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 709

Leu Glu Val Tyr Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1   5   10   15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Ser Asp Pro
            20   25   30

Asp Lys Ser Val Ser Thr Lys Ile Ile Asn Gly Gly Gly Arg Asn Pro
        35   40   45

Val Phe Asp Asp Asn Val Lys Leu Asp Val Arg Val Leu Asp Thr Ser
    50   55   60

Leu Lys Cys Glu Ile Tyr Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65   70   75   80

Asp Gln Leu Leu Gly Phe Thr Leu
                85

<210> 710
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 710

Leu Glu Val Phe Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1   5   10   15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Asn Asp Pro
            20   25   30

Glu Asn Ser Leu Ser Thr Lys Ile Ile Asn Gly Gly Gly Gln Asn Pro
        35   40   45

Val Phe Asp Asp Thr Leu Gln Phe Asp Val Lys Asn Leu Asp Cys Ser
    50   55   60

Leu Lys Cys Glu Ile Phe Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65   70   75   80

Asp Gln Leu Leu Gly Phe Ser Leu
                85

<210> 711
<211> 88

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 711

Leu Glu Val Phe Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Asn Asp Pro
20 25 30

Glu Asn Ser Leu Ser Thr Lys Ile Ile Asn Gly Gly Gly Gln Asn Pro
35 40 45

Val Phe Asp Asp Thr Leu Gln Phe Asp Val Lys Asn Leu Asp Cys Ser
50 55 60

Leu Lys Cys Glu Ile Phe Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Ser Leu
85

<210> 712
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 712

Leu Glu Val Phe Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Asn Asp Pro
20 25 30

Glu Asn Ser Leu Ser Thr Lys Ile Ile Asn Gly Gly Gly Gln Asn Pro
35 40 45

Val Phe Asp Asp Thr Leu Gln Phe Asp Val Lys Asn Leu Asp Cys Ser
50 55 60

Leu Lys Cys Glu Ile Phe Met Met Ser Arg Val Lys Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Ser Leu
85

<210> 713
<211> 88

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 713

Leu Asp Val Phe Val His Gln Ala Arg Asp Ile His Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Leu Cys Leu Thr Ser Asp Pro
20 25 30

Asp Val Ser Cys Ser Thr Lys Val Ile Asn Gly Gly Gly Arg Asn Pro
35 40 45

Val Phe Asp Asp Gly Leu Arg Leu Asp Val Arg Thr Val Asp Ala Ser
50 55 60

Leu Lys Cys Glu Ile Trp Met Leu Ser Arg Val Arg Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Ala Leu
85

<210> 714
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 714

Val Asp Val Tyr Ile His Gln Ala Arg Asp Ile His Lys Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Lys Ile Ser Leu Thr Ser Asp Pro
20 25 30

Glu Asn Ser Val Asn Thr Lys Ile Ile Asn Gly Gly Gly Arg Asn Pro
35 40 45

Val Phe Asn Asp Asn Leu Arg Leu Ser Val Arg Thr Val Asp Ser Ser
50 55 60

Leu Lys Cys Glu Ile Trp Met Leu Ser Arg Val Lys Asn Tyr Leu Glu
65 70 75 80

Asp Gln Leu Leu Gly Phe Ala Leu
85

<210> 715
<211> 90

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 715

Val Asp Val His Val Gln Ser Ala Arg Asp Ile Gln Asn Ile Cys Ile
1 5 10 15

Tyr His Lys Gln Asp Val Tyr Ala Arg Leu Ser Leu Pro Gly Glu Gly
20 25 30

Ala Pro Ala Ala Ser Thr Gln Val Ile Asn Gly Gly Gly Arg Asn Pro
35 40 45

Val Phe Asp Gln Ser Leu Arg Leu Gly Val Arg Ala Gly Asp Val Asp
50 55 60

Gly Ala Leu Arg Cys Glu Val Trp Met Leu Ser Arg Val Lys Asn Tyr
65 70 75 80

Leu Gln Asp Gln Leu Leu Gly Phe Ala Leu
85 90

<210> 716
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 716

Leu Gln Val Tyr Val His Asn Ala Arg Asn Ile Asn Asn Ile Cys Ile
1 5 10 15

Tyr Asp Asn Gln Asp Val Tyr Ala Lys Phe Ser Leu Thr Tyr Asn Pro
20 25 30

Asp Asp Thr Ile Ser Thr Arg Ile Ile His Arg Ala Gly Lys Asn Pro
35 40 45

Glu Phe Asn Gln Lys Leu Met Ile Asp Val Thr Gln Ile Asp Ala His
50 55 60

Ala Ala Val Leu Lys Cys Glu Ile Trp Met Met Ser Arg Ala Arg His
65 70 75 80

Tyr Met Glu Asp Gln Leu Leu Gly Phe Ala Leu
85 90

<210> 717
<211> 94

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 717

Leu Asp Ile Tyr Val His Gly Ala Arg Gly Ile His Asn Ile Cys Ile
1 5 10 15

Tyr Ala Ala Gln Asp Val Tyr Ala Arg Leu Ala Leu Thr Ser Ser Pro
20 25 30

Asp Asp Ala Pro Ala Leu Asp Thr Arg Val Ala Ala Gly Gly Gly Ala
35 40 45

Asn Pro Arg Phe Asp Glu Arg Leu Pro Pro Leu Arg Val Arg Arg Ala
50 55 60

Arg Leu Gly Thr Asp Val Leu Lys Cys Glu Ile Trp Met Arg Ser Cys
65 70 75 80

Ala Arg Arg Leu Leu Asp Asp Gln Leu Leu Gly Phe Ala Leu
85 90

<210> 718
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 718

Leu Glu Ile Glu Val Ile Ser Ala Glu Gly Leu Lys Val Asp Arg Lys
1 5 10 15

Pro Leu Lys Lys Lys Thr Tyr Ser Val Val Arg Ile Asp Glu Lys Ser
20 25 30

Trp Ala Ser Lys Val Asp Glu Leu Gly Gly Ser Tyr Pro Ile Trp Lys
35 40 45

Asp Arg Phe Asp Met Glu Met Pro Ile Asn Ala Ser Val Arg Phe Ile
50 55 60

Ser Ile Glu Val Tyr Tyr Arg Thr Ser Gly Ser Gly Arg Asp Lys Asn
65 70 75 80

Val Gly Tyr Ala Lys
85

<210> 719
<211> 85

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 719

Leu Glu Ile Glu Val Ile Ser Ala Glu Gly Leu Lys Val Asp Arg Lys
1 5 10 15

Pro Leu Lys Lys Lys Thr Tyr Ser Val Val Arg Ile Asp Glu Lys Ser
20 25 30

Trp Ala Ser Lys Val Asp Glu Leu Gly Gly Ser Tyr Pro Ile Trp Lys
35 40 45

Asp Arg Phe Asp Met Glu Met Pro Ile Asn Ala Ser Val Arg Phe Ile
50 55 60

Ser Ile Glu Val Tyr Tyr Arg Thr Ser Gly Ser Gly Arg Asp Lys Asn
65 70 75 80

Val Gly Tyr Ala Lys
85

<210> 720
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa can be any naturally occurring amino acid

<400> 720

Leu Glu Ile Glu Val Ile Ser Ala Glu Gly Leu Lys Val Asp Arg Lys
1 5 10 15

Pro Leu Lys Lys Lys Thr Tyr Ser Val Xaa Arg Ile Asp Glu Lys Ser
20 25 30

Trp Ala Ser Lys Val Asp Glu Leu Gly Gly Ser Tyr Pro Ile Trp Lys
35 40 45

Asp Arg Phe Asp Met Glu Met Pro Ile Asn Ala Ser Val Arg Phe Ile
50 55 60

Ser Ile Glu Val Tyr Tyr Arg Thr Ser Gly Ser Gly Arg Asp Lys Asn
65 70 75 80

Val Gly Tyr Ala Lys
85

<210> 721
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 721

Leu Glu Ile Asp Leu Arg Ser Ala Glu Gly Leu Lys Leu Asn Arg Arg
1 5 10 15

Pro Ile Lys Lys Lys Thr Phe Ala Val Val Lys Ile Asp Glu Lys Cys
20 25 30

Arg Lys Ser Asn Leu Asp Glu Ser Arg Arg Ser Asn Pro Thr Trp Asn
35 40 45

Tyr Lys Ser Glu Met Pro Ile Asn Gly Asn Glu Gln Phe Ile Phe Ile
50 55 60

Glu Val Phe Tyr Arg Thr Gly Ser Gly His Asp Lys Lys Ile Gly Glu
65 70 75 80

Ala Lys

<210> 722
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 722

Leu Glu Ile Asp Leu Arg Ser Ala Glu Gly Leu Lys Leu Asn Arg Arg
1 5 10 15

Pro Ile Lys Lys Lys Thr Phe Ala Val Val Lys Ile Asp Glu Lys Cys
20 25 30

Arg Lys Ser Asn Leu Asp Glu Ser Arg Arg Ser Asn Pro Thr Trp Asn
35 40 45

Tyr Lys Ser Glu Met Pro Ile Asn Gly Asn Glu Gln Phe Ile Phe Ile
50 55 60

Glu Val Phe Tyr Arg Thr Gly Ser Gly His Asp Lys Lys Ile Gly Glu
65 70 75 80

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Ala Lys

<210> 723
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 723

Leu Glu Ile Asp Leu Arg Ser Ala Glu Gly Leu Lys Leu Asn Arg Arg
1   5   10   15

Pro Ile Lys Lys Lys Thr Phe Ala Val Val Lys Ile Asp Glu Lys Cys
            20   25   30

Arg Lys Ser Asn Leu Asp Glu Ser Arg Arg Ser Asn Pro Thr Trp Asn
        35   40   45

Tyr Lys Ser Glu Met Pro Ile Asn Gly Asn Glu Gln Phe Ile Phe Ile
    50   55   60

Glu Val Phe Tyr Arg Thr Gly Ser Gly His Asp Lys Lys Ile Gly Glu
65   70   75   80

Ala Lys

<210> 724
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 724

Leu Glu Val Thr Leu Ile Ser Ala Gln Gly Leu Lys Pro Pro Ser Gly
1   5   10   15

Leu Arg Arg Arg Leu Leu Gln Ala Tyr Ala Val Ala Trp Val Asp Ala
            20   25   30

Ala Arg Arg Leu Gln Thr Arg Pro Asp Arg Ala Gly Gly Val Asp Pro
        35   40   45

Glu Trp His Glu Arg Leu Leu Phe Arg Val His Glu Ala Ala Leu Ala
    50   55   60

Asp Asp Ser Arg Ala Ala Val Thr Val Glu Ile Tyr Ala Ala Pro Ala
65   70   75   80

Gly Gly Trp His Ile Gly Gly Asp Ser Leu Val Gly Ser Ala Arg
85 90 95

<210> 725
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 725

Leu Glu Val Thr Val Ile Ser Ala Gln Asp Leu His Arg Arg Leu Gly
1 5 10 15

Arg Arg Val Arg Ala Ala Tyr Ala Val Ala Trp Ala Asp Ala Ala His
20 25 30

Lys Leu Arg Thr Gly Val Asp Leu Ala Gly Gly Ala Asp Pro Thr Trp
35 40 45

Asn Asp Arg Phe Leu Phe Arg Val Glu Glu Ala Phe Leu Arg Ser Asp
50 55 60

Thr Ala Ala Val Thr Val Glu Val Arg Ala Pro Arg Arg Phe Gly Gly
65 70 75 80

Asp Ala Val Leu Gly Val Thr Arg
85

<210> 726
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 726

Leu Glu Leu Asn Ile Ile Ser Ala Gln Asp Leu Ala Pro Val Ser Arg
1 5 10 15

Lys Met Lys Thr Tyr Ala Val Ala Trp Val His Ser Glu Arg Lys Leu
20 25 30

Thr Thr Arg Val Asp Tyr Thr Gly Gly Gly Asn Pro Thr Trp Asn Asp
35 40 45

Lys Phe Val Phe Arg Val Ser Glu Asp Phe Leu Tyr Ala Asp Thr Ser
50 55 60

Ala Val Val Val Glu Ile Tyr Ala Leu His Trp Phe Arg Asp Val His
65 70 75 80

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Val Gly Thr Val Arg
85

<210> 727
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 727

Leu Glu Leu Asn Ile Ile Ser Ala Gln Asp Leu Ala Pro Val Ala Arg
1 5 10 15

Lys Thr Lys Thr Tyr Ala Val Ala Trp Val His Ser Glu Arg Lys Leu
20 25 30

Thr Thr Arg Val Asp Tyr Asn Gly Gly Thr Asn Pro Thr Trp Asn Asp
35 40 45

Lys Phe Val Phe Arg Val Asn Glu Glu Phe Leu Tyr Ala Asp Thr Ser
50 55 60

Ala Val Val Ile Glu Ile Tyr Ala Leu His Trp Phe Arg Asp Val His
65 70 75 80

Val Gly Thr Val Arg
85

<210> 728
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 728

Leu Glu Leu Asn Ile Ile Ser Ala Gln Glu Leu Ala Pro Val Ala Arg
1 5 10 15

Cys Met Lys Thr Tyr Ala Ile Ala Trp Ile Asp Pro Glu Arg Lys Leu
20 25 30

Thr Thr Arg Val Asp Asn Thr Gly Gly Thr Ser Pro Thr Trp Asn Asp
35 40 45

Lys Phe Val Phe Arg Leu Asp Glu Glu Ala Leu Tyr Asp Ala Thr Ser
50 55 60

Ile Val Val Ile Glu Ile Tyr Ala Leu His Trp Phe Lys Asp Ile His
65 70 75 80

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Val Gly Thr Val Gln
85

<210> 729
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 729

Leu Glu Leu Asn Val Ile Ser Ala Gln Asp Leu Ala Glu Val Gly Arg
1 5 10 15

Ser Met Arg Thr Tyr Ala Val Ala Trp Val Asp Pro Asp Arg Lys Leu
20 25 30

Ser Thr Arg Val Asp Ser Gln Ser Gly Thr Asn Pro Ala Trp Asn Asp
35 40 45

Lys Phe Val Phe Arg Val Asp Glu Asp Phe Leu Tyr Asp Glu Asn Ser
50 55 60

Thr Ile Thr Ile Asp Ile Tyr Ala Ile His Trp Phe Lys Asp Ile His
65 70 75 80

Val Gly Thr Ala His
85

<210> 730
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 730

Leu Glu Ile Asn Leu Ile Ser Ala Gln Asp Leu Ala Pro Val Ser Arg
1 5 10 15

Asn Met Lys Thr Tyr Ser Val Ala Trp Ile Asn Thr Asp Pro Met Arg
20 25 30

Lys Leu Thr Thr Arg Val Asp Gln Ser Asn Arg Ala Asn Pro Ile Trp
35 40 45

Asn Glu Lys Phe Val Phe Arg Val Asn Asp Lys Ile Leu Tyr Val Asp
50 55 60

Ala Ser Ala Ile Val Ile Glu Ile Tyr Ala Ala Ala Trp Ala Lys Asp
65 70 75 80

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Ala Leu Val Gly Thr Val Asn
85

<210> 731
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 731

Leu Glu Ile Asn Leu Ile Ser Ala Gln Asp Leu Ala Pro Val Ser Arg
1 5 10 15

Asn Met Lys Thr Tyr Ser Val Ala Trp Ile Asn Thr Asp Pro Met Arg
20 25 30

Lys Leu Thr Thr Arg Val Asp Gln Ser Asn Arg Ala Asn Pro Ile Trp
35 40 45

Asn Glu Lys Phe Val Phe Arg Val Asn Asp Lys Ile Leu Asp Val Asp
50 55 60

Ala Ser Ala Ile Val Ile Glu Ile Tyr Ala Ala Ala Trp Ala Lys Asp
65 70 75 80

Ala Leu Val Gly Thr Val Asn
85

<210> 732
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 732

Leu Glu Ile Asn Leu Ile Ser Ala Gln Gly Leu Lys Glu Pro Thr Gly
1 5 10 15

Lys Leu Arg Arg Leu Gln Thr Tyr Ala Ser Val Trp Val Asp Ser Ser
20 25 30

Ser Lys Leu Arg Thr Arg Ile Asp Arg Ile Gly Ser Glu Asn Pro Ile
35 40 45

Trp Asn Asp Lys Phe Val Phe Gln Val Ser Pro Glu Phe Leu Ser Ser
50 55 60

Glu Thr Ser Gly Val Ser Ile Glu Ile Tyr Ala Val Gly Tyr Leu Arg
65 70 75 80

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Asp His Leu Ile Gly Thr Val Arg
85

<210> 733
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 733

Leu Glu Val Thr Val Val Ser Gly Lys His Leu Lys Asn Val Asn Trp
1 5 10 15

Arg Arg Gly Asp Leu Arg Ala Tyr Val Val Ala Tyr Leu Asp Pro Ser
20 25 30

Arg Arg Ala Ala Thr Arg Pro Asp Asp Val Gly Gly Cys Lys Pro Ala
35 40 45

Trp Asn Glu Arg Val Val Leu Pro Leu Pro Pro His Leu Ser Pro His
50 55 60

Asp Pro Ser Leu Leu Leu Ser Leu Asp Val Phe His Ser Lys Pro Ser
65 70 75 80

Asp Ser Pro Lys Pro Leu Val Gly Ser Ala Arg
85 90

<210> 734
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 734

Leu Val Val Thr Val Val Ser Ala Lys His Leu Lys Asn Val Asn Trp
1 5 10 15

Arg Asn Gly Asp Leu Lys Pro Tyr Val Val Leu Tyr Leu Asp Gln Asp
20 25 30

His Pro Leu Ser Thr Arg Ser Asp Asp Ser Ser Ser Ile Lys Pro Val
35 40 45

Trp Asn Glu Arg Ile Thr Leu Pro Leu Thr Arg Ser Val His Glu Ser
50 55 60

Val Leu Asn Ile Glu Val Phe His Ser Asn Ser Ser Asp Leu Ala Lys
65 70 75 80

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Thr Leu Val Gly Ser Val Arg
                85

<210> 735
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 735

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Val Glu Val Thr Val Ser Ser Ala Arg Asp Leu Lys Asn Val Asn Trp
1               5                   10                  15

Arg Asn Gly Asp Leu Lys Pro Tyr Ala Val Leu Trp Val Asp Asp Gly
            20                  25                  30

Ala Lys Cys Ser Thr Arg Val Asp Leu Asp Asn Ala Asp Asn Pro Asn
        35                  40                  45

Trp Asp Asp Lys Leu Thr Leu Pro Leu Pro Pro Ser Ser Arg Leu Asp
    50                  55                  60

Asp Ala Leu Leu Tyr Leu Asp Val Val His Ala Asn Ala Ala Glu Gly
65                  70                  75                  80

Val Lys Pro Leu Val Gly Ser Ala Arg
                85
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<210> 736
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 736

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Val Glu Val Thr Val Ala Ser Ala Arg Asp Leu Lys Asn Val Asn Trp
1               5                   10                  15

Arg Asn Gly Asp Leu Lys Pro Tyr Ala Val Val Trp Ile Asp Asp Gly
            20                  25                  30

Ala Lys Cys Ser Thr Arg Val Asp Leu Asp Asn Ala Asp Asn Pro Thr
        35                  40                  45

Trp Asp Asp Lys Leu Thr Val Pro Leu Pro Pro Ser Thr Arg Leu Asp
    50                  55                  60

Asp Ala Val Leu Tyr Leu Asp Val Val His Ala Asn Ala Ala Glu Gly
65                  70                  75                  80
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Val Lys Pro Leu Val Gly Ser Ala Arg
85

<210> 737
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 737

Val Glu Val Thr Val Gly Ala Ala Arg Asp Leu Lys Asn Val Asn Trp
1 5 10 15

Arg Asn Gly Asp Leu Lys Pro Tyr Ala Val Leu Trp Ile Asp Ala Gly
20 25 30

Ala Arg Cys Ser Thr Arg Val Asp Leu Asp Asn Gly Glu Asn Pro Thr
35 40 45

Trp Asp Asp Lys Val Val Val Pro Leu Pro Pro Ala Ser Arg Leu Gln
50 55 60

Asp Ala Val Leu Tyr Leu Asp Ile Val His Ala Asn Ala Pro Glu Gly
65 70 75 80

Val Lys Pro Leu Val Gly Ser Ala Arg
85

<210> 738
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 738

Val Glu Val Thr Ile Ser Ser Ala Lys Asp Ile Lys Asn Val Asn Trp
1 5 10 15

Arg Asn Gly Pro Asn Lys Pro Tyr Ala Val Val Trp Ile Asp Pro Lys
20 25 30

Phe Lys Ser Ser Thr Arg Val Asp Glu Asp Gly Asn Thr Cys Thr Thr
35 40 45

Trp Asn Glu Thr Phe Val Ile Ala Leu Pro Pro Ala Asn Asp Asp Asp
50 55 60

Asp Lys Val Tyr Ile Asn Ile Val His Ala Gly Arg Glu Glu Asn Thr
65 70 75 80

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Lys Pro Leu Ile Gly Ser Ala His
85

<210> 739
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 739

Val Glu Val Thr Ile Ser Ser Ala Lys Asp Ile Lys Asn Val Asn Trp
1 5 10 15

Arg Asn Gly Pro Asn Lys Pro Tyr Ala Val Val Trp Ile Asp Pro Lys
20 25 30

Phe Lys Ser Ser Thr Arg Val Asp Glu Asp Gly Asn Thr Cys Thr Thr
35 40 45

Trp Asn Glu Thr Phe Val Ile Ala Leu Pro Pro Ala Asn Asp Asp Asp
50 55 60

Asp Lys Val Tyr Ile Asn Ile Val His Ala Gly Arg Glu Glu Asn Thr
65 70 75 80

Lys Pro Leu Ile Gly Ser Ala His
85

<210> 740
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 740

Leu Glu Leu Thr Leu Leu Ser Ala Ser Asp Leu Arg Gly Val Asn Leu
1 5 10 15

Val Ser Lys Met Glu Val Tyr Ala Val Val Tyr Leu Ala Gly Asp Pro
20 25 30

Arg Ala Arg Gln Arg Val Ala Thr Asp Arg Ala Gly Gly Arg Asn Pro
35 40 45

Ser Trp Lys Gly Lys Asp Ala Thr Val Arg Leu Ala Val Pro Ala Ser
50 55 60

Gly Ala Gly Ser Gly Ala Val Arg Val Leu Leu Arg Ala Glu Arg Ala
65 70 75 80

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Gly Leu Gly Gly Asp Arg Asp Val Gly Glu Val Phe
85 90

<210> 741
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 741

Leu Glu Leu Thr Leu Ile Ser Ala Lys Asp Leu Lys Asp Val Asn Leu
1 5 10 15

Leu Ser Lys Met Glu Val Tyr Ala Val Val Ser Leu Ser Gly Asp Arg
20 25 30

Arg Ser Arg Gln Arg Ile Ala Thr Asp Arg Ala Gly Gly Arg Asn Pro
35 40 45

Ala Trp Asn Ala Ala Pro Leu Arg Phe Thr Val Pro Ala Ser Gly Ala
50 55 60

Gly Ser Leu His Val Leu Leu Arg Ala Glu Arg Ala Leu Gly Asp Arg
65 70 75 80

Asp Val Gly Glu Val His
85

<210> 742
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 742

Leu Glu Val Thr Leu Ile Ser Ala Arg Asn Leu Lys Lys Val Asn Leu
1 5 10 15

Ile Thr Pro Met Glu Val Tyr Ala Val Val Ser Val Ser Gly Asn Pro
20 25 30

Leu Ala Arg Gln Cys Thr Leu Pro Asp Arg His Gly Gly Arg Asn Pro
35 40 45

Thr Trp Asn Ala Thr Leu His Leu Ala Val Pro Ala Ala Ala Pro Gly
50 55 60

Ala Phe Leu His Val Leu Leu Arg Thr Glu Arg Ala Leu Gly Asp Arg
65 70 75 80

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Asp Val Gly Glu Val Phe
85

<210> 743
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 743

Leu Glu Val Thr Leu His Ser Ala Arg Asp Leu Lys Asn Val Asn Phe
1 5 10 15

Ile Ser Arg Met Glu Val Tyr Ala Val Ala Thr Ile Ser Gly Asp Pro
20 25 30

Leu Thr Arg Gln Cys Thr Pro Pro Asp Pro Tyr Gly Gly Arg His Pro
35 40 45

Ala Trp Asn Ala Thr Leu Arg Phe Thr Val Pro Pro Thr Ala Ala Ser
50 55 60

Ala Ala Gly Cys Leu His Val Leu Leu Arg Ala Glu Arg Ser Leu Gly
65 70 75 80

Asp Arg Asp Ile Gly Glu Val Ile
85

<210> 744
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 744

Leu Glu Leu Thr Leu Val Ser Ala Ser Asp Leu Lys Lys Val Thr Leu
1 5 10 15

Phe Ser Arg Met His Val Tyr Ala Val Ala Ser Ile Ser Gly Ser Asn
20 25 30

Val Pro Met Pro Met His Gly Thr His Ala Asp Arg Asn Gly Gly Ser
35 40 45

Asn Pro Ala Trp Asn Thr Val Leu His Phe Pro Val Pro Ala Arg Phe
50 55 60

Asp Thr Arg Gly Leu Ala Leu His Val Gln Leu Arg Ala Arg Arg Ser
65 70 75 80

Phe Gly Gly His Arg Asp Val Gly Asp Val Phe
85 90

<210> 745
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 745

Leu Glu Leu Thr Leu Val Ser Ala Ser Asp Leu Lys Lys Val Thr Leu
1 5 10 15

Phe Ser Arg Met His Val Tyr Ala Val Ala Ser Ile Ser Gly Ser Asn
20 25 30

Val Pro Met Pro Met His Gly Thr His Ala Asp Arg Asn Gly Gly Ser
35 40 45

Asn Pro Ala Trp Asn Thr Val Leu His Phe Pro Val Pro Ala Arg Phe
50 55 60

Asp Thr Arg Gly Leu Ala Leu His Val Gln Leu Arg Ala Arg Arg Ser
65 70 75 80

Phe Gly Gly His Arg Asp Val Gly Asp Val Phe
85 90

<210> 746
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 746

Leu Glu Val Thr Leu Val Ser Ala Lys Asn Leu Lys Lys Val Thr Met
1 5 10 15

Phe Ser Lys Met Arg Val Tyr Ala Val Ala Ser Ile Ser Gly Gly Asp
20 25 30

Pro Arg Val Pro Thr His Arg Thr His Ala Asp Arg Glu Gly Gly Arg
35 40 45

Ser Pro Met Trp His Ala Pro Leu Arg Phe Pro Ile Pro Asp Ala Gly
50 55 60

Ala Asp Met Arg Ala Ile Ala Leu His Val Leu Leu Arg Ala Glu Arg
65 70 75 80

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Val Phe Gly Asp Ser Asp Val Gly Glu Val Phe
85 90

<210> 747
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 747

Leu Glu Leu Asn Val Tyr Ser Ala Lys Asp Leu Glu Asn Val Asn Leu
1 5 10 15

Ile Thr Lys Met Asp Val Tyr Ala Val Val Trp Ile Thr Gly Asp Asp
20 25 30

Ser Arg Lys Asn His Lys Glu Lys Thr Pro Ile Asp Arg Thr Gly Glu
35 40 45

Ser Glu Pro Thr Trp Asn His Thr Val Lys Phe Ser Val Asp Gln Arg
50 55 60

Leu Ala His Glu Gly Arg Leu Thr Leu Val Val Lys Leu Val Cys Asp
65 70 75 80

Arg Ile Phe Gly Asp Lys Asp Leu Gly Glu Val Gln
85 90

<210> 748
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 748

Leu Glu Leu Lys Ile Val Ser Ala Ser Asp Val Asn His Ile Asp Ala
1 5 10 15

Thr Asp Lys Met Asp Val Tyr Ala Val Val Ser Ile Asn Gly Asp Thr
20 25 30

Thr Gln Gln Lys Gln Ala Ala Lys Thr Pro Ile Asp Tyr Asp Gly Gly
35 40 45

Ser Asn Pro Thr Trp Asn His Thr Val Lys Phe Ser Val Asn Glu Arg
50 55 60

Glu Ala Asn Glu Gly Leu Leu Thr Ile Thr Val Lys Leu Phe Ser Tyr
65 70 75 80

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Trp Leu Glu Gly Asp Asn Asp Leu Tyr Leu Gly Glu Val Asn
85 90

<210> 749
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 749

Leu Glu Leu Asn Ile Asn Ser Ala Arg Asn Leu Leu Asn Val Asn Leu
1 5 10 15

Ile Thr Lys Met Asn Val Phe Thr Ala Ile Thr Ile Asn Gly Glu Asn
20 25 30

Thr Arg Lys Lys Gln Lys Ala Lys Thr Thr Val Asp Arg Tyr Gly Gly
35 40 45

Ser Asn Pro Thr Trp Asn Gln Thr Ile Lys Phe Ser Val Asp Glu Arg
50 55 60

Ser Ala Arg Gly Gly His Ser Ser Leu Val Met Arg Val Ile Ser Arg
65 70 75 80

Arg Val Leu Gly Asn Lys Glu Ile Gly Arg Val Asn
85 90

<210> 750
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 750

Leu Glu Leu Asn Ile Ile Ser Ala Lys Asp Ile Lys Asn Val Asn Leu
1 5 10 15

Phe Ser Lys Met Asp Val Tyr Ala Ala Val Ser Leu Ser Gly Asp Pro
20 25 30

Leu His Pro Gln Gly Ala Thr Thr His Val His Lys Asp Ala Gly Ser
35 40 45

Asn Pro Thr Trp Asn Tyr Pro Val Lys Phe Ser Val Asn Glu Ser Leu
50 55 60

Ala Lys Glu Asn Arg Leu Ser Leu Glu Ile Lys Leu Ile Ser Asp Arg
65 70 75 80

Thr Leu Gly Asp Thr Val Ile Gly Thr Val His
85 90

<210> 751
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 751

Leu Glu Leu Val Ile Lys Phe Ala Lys Asn Ile Glu Asp Val Asn Ala
1 5 10 15

Phe Ser Ser Met Asp Val Tyr Ala Ser Val Ala Ile Leu Lys Asp Arg
20 25 30

Lys Val Lys Asn Arg Ile Asn Thr Pro Val Ala Phe Ala Ala Tyr Thr
35 40 45

Asn Pro Lys Trp Asn Gln Met Met Lys Phe Ser Ile Asp Glu Lys Ser
50 55 60

Ala Gln Glu Gly Arg Leu Met Leu Leu Val Glu Leu Met Ser His Arg
65 70 75 80

Pro Phe Leu Gly Asp Lys Glu Ile Gly Phe Val Arg
85 90

<210> 752
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 752

Leu Asp Leu Thr Ile Ile Ser Ala Glu Asp Leu Lys Asp Val Gln Leu
1 5 10 15

Ile Gly Lys Gln Asp Leu Tyr Ala Val Val Ser Ile Asn Gly Asp Ala
20 25 30

Arg Thr Lys Gln Lys Thr Lys Val Asp Lys Asp Cys Gly Thr Lys Pro
35 40 45

Lys Trp Lys His Gln Met Lys Leu Thr Val Asp Asp Ala Ala Ala Arg
50 55 60

Asp Asn Arg Leu Thr Leu Val Phe Glu Ile Val Ala Asp Arg Pro Ile
65 70 75 80

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Ala Gly Asp Lys Pro Val Gly Glu Val Ser
85 90

<210> 753
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 753

Leu Asp Leu Thr Ile Ile Ser Ala Glu Asp Leu Lys Asp Val Gln Leu
1 5 10 15

Ile Gly Lys Gln Asp Leu Tyr Ala Val Val Ser Ile Asn Gly Asp Ala
20 25 30

Arg Thr Lys Gln Lys Thr Lys Val Asp Lys Asp Cys Gly Thr Lys Pro
35 40 45

Lys Trp Lys His Gln Met Lys Leu Thr Val Asp Asp Ala Ala Ala Arg
50 55 60

Asp Asn Arg Leu Thr Leu Val Phe Glu Ile Val Ala Asp Arg Pro Ile
65 70 75 80

Ala Gly Asp Lys Pro Val Gly Glu Val Ser
85 90

<210> 754
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 754

Leu Glu Leu Thr Val Tyr Glu Ala Asp Asp Leu His Asn Ala Ile His
1 5 10 15

Gly Arg Ile Ile Lys Ala Ala Glu Ser Leu Lys Glu Ser Leu Gly Val
20 25 30

His Arg Leu Ala His Arg Ile Tyr Val Asp Val Asp Val Gly Ala Ala
35 40 45

Arg Val Ala Arg Thr Arg Glu Val Glu Phe His Pro Thr Asn Pro Val
50 55 60

Trp Asn Gln Ser Phe Arg Leu His Cys Ala Tyr Pro Ala Ala Pro Val
65 70 75 80

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Ala Phe Thr Val Lys Ser Gln His Leu Val Gly Ala Gly Val Leu Gly
85 90 95

Ala Ala Arg

<210> 755
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 755

Leu Glu Leu Thr Val Tyr Glu Ala Asp Asp Leu His Asn Ala Ile His
1 5 10 15

Gly Arg Ile Ile Lys Ala Ala Glu Ser Leu Lys Glu Ser Leu Gly Val
20 25 30

His Arg Leu Ala His Arg Ile Tyr Val Asp Val Asp Val Gly Ala Ala
35 40 45

Arg Val Ala Arg Thr Arg Glu Val Glu Phe His Pro Thr Asn Pro Val
50 55 60

Trp Asn Gln Ser Phe Arg Leu His Cys Ala Tyr Pro Ala Ala Pro Val
65 70 75 80

Ala Phe Thr Val Lys Ser Gln His Leu Val Gly Ala Gly Val Leu Gly
85 90 95

Ala Ala Arg

<210> 756
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 756

Ser Pro Lys Trp Asn Glu Thr Phe His Ile Tyr Ser Ala His Ser Ile
1 5 10 15

Ser Asn Ile Ile Phe Thr Val Lys Gln Asp Asn Pro Ile Gly Ala Thr
20 25 30

Leu Ile Gly Arg Ala Tyr
35

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<210> 757
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 757

Tyr Ala Thr Val Asp Leu Asp Lys Ala Arg Val Gly Arg Thr Arg Met
1 5 10 15

Ile Gly Asn Gln Pro Ser Asn Pro Lys Trp Asn Glu Thr Phe Glu Ile
20 25 30

Tyr Cys Ala His Tyr Ile Ser Asn Ile Val Phe Thr Val Lys Asp Asp
35 40 45

Asn Pro Ile Gly Ala Thr Leu Ile Gly Arg Ala Tyr
50 55 60

<210> 758
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 758

Leu His Val Thr Ile Phe Glu Val Asp His Leu Lys Ala Gly Ser Val
1 5 10 15

Val Val Phe Ser Glu Ser Leu Arg Arg Thr Leu Arg Lys Pro Leu Val
20 25 30

Leu Ala Lys Gly Thr Pro Lys Ile Tyr Ala Ser Ile Asp Leu Asp Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Met Ile Glu Asn Glu Pro Asn Asn Pro
50 55 60

Lys Trp Asn Glu Ser Phe His Ile Tyr Cys Gly His Pro Ser Thr Asn
65 70 75 80

Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Ala Tyr
100

<210> 759
<211> 100
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 759

Leu His Ala Thr Ile Phe Glu Val Asp Lys Leu Lys Asn Ile Gly Gly
1   5   10   15

Gly Asn Ile Leu Ser Lys Ile Arg Gln Asn Phe Glu Glu Thr Val Gly
            20   25   30

Phe Gly Lys Gly Thr Thr Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys
        35   40   45

Ala Arg Val Gly Arg Thr Arg Ile Ile Glu Lys Glu His Val Asn Pro
    50   55   60

Gln Trp Asn Glu Ser Phe His Ile Tyr Cys Ala His Leu Ala Ser Asp
65   70   75   80

Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
                85   90   95

Gly Arg Ala Tyr
            100

<210> 760
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 760

Leu His Ala Thr Ile Phe Glu Val Asp Lys Leu Lys Asn Ile Gly Gly
1   5   10   15

Gly Asn Ile Leu Ser Lys Ile Arg Gln Asn Phe Glu Glu Thr Val Gly
            20   25   30

Phe Gly Lys Gly Thr Thr Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys
        35   40   45

Ala Arg Val Gly Arg Thr Arg Ile Ile Glu Lys Glu His Val Asn Pro
    50   55   60

Gln Trp Asn Glu Ser Phe His Ile Tyr Cys Ala His Leu Ala Ser Asp
65   70   75   80

Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
                85   90   95

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Gly Arg Ala Tyr
100

<210> 761
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 761

Leu His Ala Thr Ile Tyr Glu Val Asp Glu Leu His Gly Gly Gly Gly
1 5 10 15

Gly Asn Phe Phe Ser Lys Leu Lys Gln Asn Ile Glu Glu Thr Val Gly
20 25 30

Ile Gly Lys Gly Val Thr Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Ile Ile Glu Asn Glu Thr Thr Asn Pro
50 55 60

Lys Trp Asn Glu Ser Phe His Ile Tyr Cys Gly His Leu Ala Ser Asn
65 70 75 80

Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Ala Tyr
100

<210> 762
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 762

Leu His Ala Thr Ile Tyr Glu Ile Asp Arg Leu His Thr Gly Gly Ser
1 5 10 15

Ser Asn Val Phe Ser Met Leu Arg Gln Asn Phe Glu Glu Ala Val Gly
20 25 30

Ile Gly Lys Gly Gln Thr Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Ile Leu Glu Ser Glu Pro Ser Asn Pro
50 55 60

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Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Lys Ala Ser Asn
65 70 75 80

Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Thr Tyr
100

<210> 763
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 763

Leu His Val Thr Ile Tyr Glu Val Asp Gln Leu His Ser Gly Gly Gly
1 5 10 15

Gly Asn Phe Phe Thr Lys Leu Lys Ala Asn Ile Glu Glu Thr Val Gly
20 25 30

Phe Gly Lys Gly Thr Pro Lys Ile Tyr Ala Ser Ile Asp Leu Glu Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Met Ile Glu His Glu Pro Asn Asn Pro
50 55 60

Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser Asn
65 70 75 80

Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Ala Tyr
100

<210> 764
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 764

Leu His Val Thr Val Tyr Glu Val Asp Arg Leu His Ala Gly Gly Gly
1 5 10 15

Gly Asn Ile Phe Ser Lys Leu Arg Ala Asn Ile Glu Glu Lys Val Gly
20 25 30

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Phe Gly Lys Gly Thr Pro Lys Ile Tyr Ala Ser Ile Asp Leu Glu Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Met Ile Glu His Glu Pro Thr Asn Pro
50 55 60

Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Leu Ala Ser Asn
65 70 75 80

Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Ala Tyr
100

<210> 765
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 765

Leu His Val Thr Val Tyr Glu Val Asp Lys Leu Arg Glu Gly Gly Gly
1 5 10 15

Pro Asn Val Phe Gly Lys Leu Met Ala Asn Ile Gln Glu Thr Val Gly
20 25 30

Phe Gly Glu Gly Thr Pro Lys Ile Tyr Ala Thr Ile Asp Leu Glu Lys
35 40 45

Ser Arg Val Gly Arg Thr Arg Met Ile Glu Asn Glu Pro Gln Asn Pro
50 55 60

Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His His Ala Ser Asn
65 70 75 80

Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Leu
85 90 95

Gly Arg Ala Tyr
100

<210> 766
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 766

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Leu His Val Thr Ile Tyr Glu Val Asp Lys Leu His Ser Gly Gly Gly
1   5   10   15

Pro His Phe Phe Arg Lys Leu Val Glu Asn Ile Glu Glu Thr Val Gly
            20   25   30

Phe Gly Lys Gly Val Ser Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys
        35   40   45

Ala Arg Val Gly Arg Thr Arg Ile Leu Glu Asn Glu Gln Ser Asn Pro
    50   55   60

Arg Trp Tyr Glu Ser Phe His Val Tyr Cys Ala His Gln Ala Ser Asn
65   70   75   80

Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
                85   90   95

Gly Arg Ala Tyr
            100

<210> 767
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 767

Leu His Val Thr Ile Tyr Glu Val Asp Lys Leu Lys Thr Ser Gly Gly
1   5   10   15

Asn Val Phe Thr Lys Leu Val Gln Asn Ile Glu Glu Thr Val Gly Phe
            20   25   30

Gly Lys Gly Val Thr Lys Leu Tyr Ala Thr Ile Asp Leu Glu Lys Ala
        35   40   45

Arg Val Gly Arg Thr Arg Ile Ile Glu Lys Asp His Ser Asn Pro Arg
    50   55   60

Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser Asn Ile
65   70   75   80

Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile Gly
                85   90   95

Arg Ala Tyr

<210> 768
<211> 101

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 768

```
Leu His Ala Thr Ile Tyr Glu Val Asp Asp Leu His Thr Gly Gly Leu
1               5                   10                  15

Arg Ser Gly Phe Phe Gly Lys Ile Leu Ala Asn Val Glu Glu Thr Ile
            20                  25                  30

Gly Val Gly Lys Gly Glu Thr Gln Leu Tyr Ala Thr Ile Asp Leu Gln
        35                  40                  45

Arg Ala Arg Val Gly Arg Thr Arg Lys Ile Lys Asp Glu Ala Lys Asn
    50                  55                  60

Pro Lys Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Leu Ala Ser
65                  70                  75                  80

Asp Ile Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu
                85                  90                  95

Ile Gly Arg Ala Tyr
            100
```

<210> 769
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 769

```
Tyr Ala Thr Ile Asp Leu Gln Lys Ala Arg Val Gly Arg Thr Arg Lys
1               5                   10                  15

Ile Lys Asn Glu Pro Lys Asn Pro Lys Trp Tyr Glu Ser Phe His Ile
            20                  25                  30

Tyr Cys Ala His Leu Ala Ser Asp Ile Ile Phe Thr Val Lys Asp Asp
        35                  40                  45

Asn Pro Ile Gly Ala Thr Leu Ile Gly Arg Ala Tyr
    50                  55                  60
```

<210> 770
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 770

Tyr Ala Thr Ile Asp Leu Gln Lys Ala Arg Val Gly Arg Thr Arg Lys
1 5 10 15

Ile Thr Asp Glu Pro Lys Asn Pro Lys Trp Tyr Glu Ser Phe His Ile
20 25 30

Tyr Cys Ala His Met Ala Ser Asp Ile Ile Phe Thr Val Lys Asp Asp
35 40 45

Asn Pro Ile Gly Ala Thr Leu Ile Gly Arg Ala Tyr
50 55 60

<210> 771
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 771

Leu His Ala Thr Ile Tyr Glu Val Asp His Leu His Ala Glu Gly Gly
1 5 10 15

Arg Ser Gly Phe Leu Gly Ser Ile Leu Ala Asn Val Glu Glu Thr Ile
20 25 30

Gly Val Gly Lys Gly Glu Thr Gln Leu Tyr Ala Thr Ile Asp Leu Glu
35 40 45

Lys Ala Arg Val Gly Arg Thr Arg Lys Ile Thr Lys Glu Pro Lys Asn
50 55 60

Pro Lys Trp Phe Glu Ser Phe His Ile Tyr Cys Gly His Met Ala Lys
65 70 75 80

His Val Ile Phe Thr Val Lys Asp Ala Asn Pro Ile Gly Ala Thr Leu
85 90 95

Ile Gly Arg Gly Tyr
100

<210> 772
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 772

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Leu His Val Thr Ile Phe Glu Val Asp Asn Leu Gln Gly Glu Glu Glu
1   5   10   15

Gly Gly His Phe Phe Ser Lys Ile Lys Gln His Phe Glu Glu Thr Val
            20   25   30

Gly Ile Gly Lys Gly Thr Pro Lys Leu Tyr Ala Thr Ile Asp Leu Glu
        35   40   45

Lys Ala Arg Val Gly Arg Thr Arg Ile Ile Glu Asn Glu Pro Lys Asn
    50   55   60

Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser
65   70   75   80

Asn Val Ile Phe Thr Ile Lys Asp Asp Asn Pro Phe Gly Ala Ser Leu
                85   90   95

Ile Gly Arg Ala Tyr
            100

<210> 773
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 773

Leu His Val Thr Ile Phe Glu Val Asp Asn Leu Gln Gly Glu Glu Glu
1   5   10   15

Gly Gly His Phe Phe Ser Lys Ile Lys Gln His Phe Glu Glu Thr Val
            20   25   30

Gly Ile Gly Lys Gly Thr Pro Lys Leu Tyr Ala Thr Ile Asp Leu Glu
        35   40   45

Lys Ala Arg Val Gly Arg Thr Arg Ile Ile Glu Asn Glu Pro Lys Asn
    50   55   60

Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser
65   70   75   80

Asn Val Ile Phe Thr Ile Lys Asp Asp Asn Pro Phe Gly Ala Ser Leu
                85   90   95

Ile Gly Arg Ala Tyr
            100

<210> 774
<211> 100

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 774

Leu His Val Thr Ile Tyr Glu Val Asp Asn Leu Gln Lys Glu Gly Gly
1 5 10 15

Gly His Phe Phe Ser Lys Ile Lys Glu His Val Glu Glu Thr Ile Gly
20 25 30

Phe Gly Lys Gly Thr Pro Ala Ile Tyr Ala Thr Val Asp Leu Glu Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Lys Ile Lys Asn Glu Pro Asn Asn Pro
50 55 60

Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser Asn
65 70 75 80

Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile Gly Ala Thr Leu Ile
85 90 95

Gly Arg Ala Tyr
100

<210> 775
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 775

Leu His Ala Thr Ile Tyr Glu Val Asp Lys Leu His Gly Ser Ser Gly
1 5 10 15

Asn Phe Leu Arg Lys Ile Thr Gly Lys Leu Glu Glu Thr Val Gly Leu
20 25 30

Gly Lys Gly Val Ser Lys Leu Tyr Ala Thr Val Asp Leu Glu Arg Ala
35 40 45

Arg Val Gly Arg Thr Arg Val Ile Glu Lys Glu Pro Ser Asn Pro Asn
50 55 60

Trp Ser Glu Ser Phe His Ile Tyr Cys Ala His Val Ala Ala Asn Val
65 70 75 80

Ile Phe Thr Val Lys Glu Ser Asn Pro Ile Gly Ala Ser Leu Ile Gly
85 90 95

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Arg Ala Tyr

<210> 776
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 776

```
Leu His Ala Thr Ile Phe Glu Ala Ala Ser Leu Ser Asn Pro His Arg
1               5                   10                  15

Ala Ser Gly Ser Ala Pro Lys Phe Ile Arg Lys Phe Val Glu Gly Ile
            20                  25                  30

Glu Asp Thr Val Gly Val Gly Lys Gly Ala Thr Lys Val Tyr Ser Thr
        35                  40                  45

Ile Asp Leu Glu Lys Ala Arg Val Gly Arg Thr Arg Met Ile Thr Asn
    50                  55                  60

Glu Pro Ile Asn Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala
65                  70                  75                  80

His Met Ala Ser Asn Val Ile Phe Thr Val Lys Ile Asp Asn Pro Ile
                85                  90                  95

Gly Ala Thr Asn Ile Gly Arg Ala Tyr
            100                 105
```

<210> 777
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 777

```
Leu His Ala Thr Ile Phe Glu Ala Glu Ser Leu Ser Asn Pro His Arg
1               5                   10                  15

Ala Thr Gly Gly Ala Pro Lys Phe Ile Arg Lys Leu Val Glu Gly Ile
            20                  25                  30

Glu Asp Thr Val Gly Val Gly Lys Gly Ala Thr Lys Ile Tyr Ala Thr
        35                  40                  45

Val Asp Leu Glu Lys Ala Arg Val Gly Arg Thr Arg Met Ile Ser Asn
    50                  55                  60
```

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Glu Pro Val Asn Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala
65 70 75 80

His Met Ala Ala Asp Val Ile Phe Thr Val Lys Ile Asp Asn Ser Ile
85 90 95

Gly Ala Ser Leu Ile Gly Arg Ala Tyr
100 105

<210> 778
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 778

Leu His Val Thr Ile Phe Glu Ala Asn Ser Ile Ser His Pro Asp Arg
1 5 10 15

Lys Thr Gly Gly Ala Pro Lys Phe Phe Arg Lys Leu Val Glu Asn Ile
20 25 30

Glu Glu Thr Val Gly Phe Gly Lys Gly Ala Ser Met Leu Tyr Ala Ser
35 40 45

Val Asp Leu Asp Lys Ala Arg Val Gly Arg Thr Arg Ile Ile Lys Asp
50 55 60

Glu Pro Val Asn Pro Lys Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala
65 70 75 80

His Met Ala Ala Asn Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile
85 90 95

Gly Ala Thr Leu Ile Gly Arg Ala Tyr
100 105

<210> 779
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 779

Leu His Val Thr Ile Phe Glu Ala Asn Ser Ile Ser His Pro Asp Arg
1 5 10 15

Lys Thr Gly Gly Ala Pro Lys Phe Phe Arg Lys Leu Val Glu Asn Ile
20 25 30

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Glu Glu Thr Val Gly Phe Gly Lys Gly Ala Ser Met Leu Tyr Ala Ser
35 40 45

Val Asp Leu Asp Lys Ala Arg Val Gly Arg Thr Arg Ile Ile Lys Asp
50 55 60

Glu Pro Val Asn Pro Lys Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala
65 70 75 80

His Met Ala Ala Asn Val Ile Phe Thr Val Lys Asp Asp Asn Pro Ile
85 90 95

Gly Ala Thr Leu Ile Gly Arg Ala Tyr
100 105

<210> 780
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 780

Tyr Ala Thr Ile Asp Leu Gly Lys Ala Arg Val Gly Arg Thr Arg Leu
1 5 10 15

Leu Asp Glu His Lys Asn Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr
20 25 30

Cys Ala His Met Ala Ser Asp Val Val Phe Thr Val Lys Ala Asp Asn
35 40 45

Pro Ile Gly Ala Glu Leu Ile Gly Arg Ala Tyr
50 55

<210> 781
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 781

Leu His Val Thr Ile Phe Glu Val Asp Lys Leu Arg Thr Asn Phe Gly
1 5 10 15

Arg Glu Ile Phe Asn Lys Val Val Gln Gly Ile Glu Gly Ala Ile Gly
20 25 30

Phe Asn Lys Thr Ala Ser Thr Leu Tyr Ala Thr Ile Asp Leu Gly Lys
35 40 45

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Ala Arg Val Gly Arg Thr Arg Leu Leu Asp Glu His Lys Asn Pro Arg
50 55 60

Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser Asp Val
65 70 75 80

Val Phe Thr Val Lys Ala Asp Asn Pro Ile Gly Ala Glu Leu Ile Gly
85 90 95

Arg Ala Tyr

<210> 782
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 782

Leu His Val Thr Ile Phe Glu Val Asp Arg Leu His Thr Asn Phe Gly
1 5 10 15

Arg Asp Phe Phe Asn Lys Val Val Gln Gly Ile Glu Gly Ala Ile Gly
20 25 30

Phe Asn Lys Ala Ala Ser Arg Leu Tyr Ala Thr Ile Asp Leu Gly Lys
35 40 45

Ala Arg Val Gly Arg Thr Arg Leu Leu Asp Asp His Lys Asn Pro Arg
50 55 60

Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ala Asn Val
65 70 75 80

Ile Ile Thr Val Lys Phe Asp Asn Pro Ile Gly Ala Glu Val Ile Gly
85 90 95

Arg Ala Tyr

<210> 783
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 783

Tyr Ala Thr Val Asp Ile Asp Lys Ala Arg Val Ala Arg Thr Arg Thr
1 5 10 15

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Val Glu Pro Thr Gly Thr Pro Arg Trp Lys Glu Ser Phe His Ile Tyr
20 25 30

Cys Ala His Tyr Ala Gly Asp Val Ile Phe Thr Val Lys Ala Glu Asn
35 40 45

Pro Val Gly Ala Thr Leu Ile Gly Arg Ala Tyr
50 55

<210> 784
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 784

Met His Val Thr Ile Phe Glu Ala Glu Ser Leu Ser Asn Pro Ser Arg
1 5 10 15

Pro Ser Ser Gln Ala Pro Gln Phe Leu Arg Lys Leu Val Glu Gly Ile
20 25 30

Glu Asp Thr Val Gly Val Gly Lys Gly Thr Ser Lys Val Tyr Ala Thr
35 40 45

Ile Gly Leu Asp Lys Ala Arg Val Gly Arg Thr Arg Thr Leu Ala Asp
50 55 60

Asp Thr Ala Ala Pro Arg Trp Tyr Glu Ser Phe His Val Tyr Cys Ala
65 70 75 80

His Leu Ala Thr His Val Ala Phe Thr Leu Lys Ala Lys Asn Pro Ile
85 90 95

Gly Ala Ser Leu Leu Gly Val Gly Tyr
100 105

<210> 785
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 785

Leu Glu Ala Thr Ile Leu Glu Ala Asp His Leu Ser Asn Pro Thr Arg
1 5 10 15

Ala Thr Gly Ala Ala Pro Gly Ile Phe Arg Lys Phe Val Glu Gly Phe
20 25 30

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Glu Asp Ser Leu Gly Leu Gly Lys Gly Ala Thr Arg Leu Tyr Ala Thr
35 40 45

Ile Asp Leu Gly Arg Ala Arg Val Gly Arg Thr Arg Val Val Asp Asp
50 55 60

Glu Pro Val Asn Pro Arg Trp Tyr Glu Val Phe His Ile Tyr Cys Ala
65 70 75 80

His Phe Ala Ala Asp Val Val Phe Ser Val Lys
85 90

<210> 786
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 786

Leu Glu Ala Thr Ile Leu Glu Ala Asp His Leu Ser Asn Pro Thr Arg
1 5 10 15

Ala Thr Gly Ala Ala Pro Gly Ile Phe Arg Lys Phe Val Glu Gly Phe
20 25 30

Glu Asp Ser Leu Gly Leu Gly Lys Gly Ala Thr Arg Leu Tyr Ala Thr
35 40 45

Ile Asp Leu Gly Arg Ala Arg Val Gly Arg Thr Arg Val Val Asp Asp
50 55 60

Glu Pro Val Asn Pro Arg Trp Tyr Glu Val Phe His Ile Tyr Cys Ala
65 70 75 80

His Phe Ala Ala Asp Val Val Phe Ser Val Lys Ala Ala Gln Pro Ile
85 90 95

Gly Ala Thr Leu Ile Gly Arg Ala Tyr
100 105

<210> 787
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 787

Leu Asp Ala Thr Ile Phe Glu Ala Thr Asn Leu Thr Asn Pro Thr Arg
1 5 10 15

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Leu Thr Gly Asn Ala Pro Glu Gly Phe Arg Lys Trp Trp Glu Gly Leu
20 25 30

Glu Asn Gly Leu Glu Lys Thr Thr Gly Leu Gly Pro Gly Gly Thr Arg
35 40 45

Leu Tyr Ala Thr Val Asp Leu Gly Arg Ala Arg Leu Gly Arg Thr Arg
50 55 60

Val Ile Asp Asp Glu Pro Val Ser Pro Arg Trp Asp Glu Arg Phe His
65 70 75 80

Phe Tyr Cys Ala His Phe Ala Glu Asn Val Val Phe Ser Val Lys Val
85 90 95

Ala Leu Ser Val Asp Ala Lys Leu Ile Gly Arg Ala Tyr
100 105

<210> 788
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 788

Leu Asp Ala Thr Ile Phe Glu Ala Thr Asn Leu Thr Asn Pro Thr Arg
1 5 10 15

Leu Thr Gly Asn Ala Pro Glu Gly Phe Arg Lys Trp Trp Glu Gly Leu
20 25 30

Glu Asn Gly Leu Glu Lys Thr Thr Gly Leu Gly Pro Gly Gly Thr Arg
35 40 45

Leu Tyr Ala Thr Val Asp Leu Gly Arg Ala Arg Leu Gly Arg Thr Arg
50 55 60

Val Ile Asp Asp Glu Pro Val Ser Pro Arg Trp Asp Glu Arg Phe His
65 70 75 80

Phe Tyr Cys Ala His Phe Ala Glu Asn Val Val Phe Ser Val Lys Val
85 90 95

Ala Leu Ser Val Asp Ala Lys Leu Ile Gly Arg Ala Tyr
100 105

<210> 789
<211> 105
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated peptide

<400> 789

Leu Asp Ala Thr Ile Phe Glu Ala Thr Asn Leu Thr Asn Pro Thr Arg
1 5 10 15

Leu Thr Gly Ser Ala Pro Glu Gly Ile Arg Lys Trp Trp Glu Gly Val
20 25 30

Glu Lys Thr Thr Gly Val Gly Gln Gly Gly Thr Arg Leu Tyr Ala Thr
35 40 45

Val Asp Leu Gly Lys Ala Arg Leu Gly Arg Thr Arg Val Ile Asp Asp
50 55 60

Glu Pro Val Asn Pro Arg Trp Asp Glu Arg Phe His Leu Tyr Cys Ala
65 70 75 80

His Phe Ala Asp Asn Val Val Phe Ser Val Lys Val Ser Leu Pro Ile
85 90 95

Asp Ala Ala Leu Ile Gly Arg Ala Tyr
100 105

<210> 790
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 790

Leu Asp Ala Thr Ile Phe Glu Ala Thr Asn Leu Thr Asn Pro Thr Arg
1 5 10 15

Leu Thr Gly Ser Ala Pro Glu Gly Ile Arg Lys Trp Trp Glu Gly Val
20 25 30

Glu Lys Thr Thr Gly Val Gly Gln Gly Gly Thr Arg Leu Tyr Ala Thr
35 40 45

Val Asp Leu Gly Lys Ala Arg Leu Gly Arg Thr Arg Val Ile Asp Asp
50 55 60

Glu Pro Val Asn Pro Arg Trp Asp Glu Arg Phe His Leu Tyr Cys Ala
65 70 75 80

His Phe Ala Asp Asn Val Val Phe Ser Val Lys Val Ser Leu Pro Ile
85 90 95

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Asp Ala Ala Leu Ile Gly Arg Ala Tyr
100 105

<210> 791
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 791

Leu Asp Leu Thr Ile Val Glu Ala Arg Arg Leu Pro Asn Met Asp Phe
1 5 10 15

Met Val Asn His Leu Arg Ser Cys Leu Thr Cys Glu Pro Cys Lys Ser
20 25 30

Pro Ala Gln Thr Ala Ala Lys Glu Gly Asp Ser Lys Ile Arg Gly His
35 40 45

Arg Lys Ile Ile Thr Ser Asp Pro Tyr Val Thr Val Cys Leu Pro Gln
50 55 60

Ala Thr Val Ala Arg Thr Arg Val Leu Lys Asn Ser Gln Asn Pro Lys
65 70 75 80

Trp Asn Glu His Phe Ile Ile Pro Leu Ala His Pro Val Thr Glu Leu
85 90 95

Asp Ile Asn Val Lys Asp Asn Asp Leu Phe Gly Ala Asp Ala Ile Gly
100 105 110

Thr Ala Lys
115

<210> 792
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 792

Leu Asp Leu Thr Ile Val Glu Ala Arg Arg Leu Pro Asn Met Asp Phe
1 5 10 15

Met Val Asn His Leu Arg Ser Cys Leu Thr Cys Glu Pro Cys Lys Ser
20 25 30

Pro Ala Gln Thr Ala Ala Lys Glu Gly Asp Ser Lys Ile Arg Gly His
35 40 45

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Arg Lys Ile Ile Thr Ser Asp Pro Tyr Val Thr Val Cys Leu Pro Gln
50 55 60

Ala Thr Val Ala Arg Thr Arg Val Leu Lys Asn Ser Gln Asn Pro Lys
65 70 75 80

Trp Asn Glu His Phe Ile Ile Pro Leu Ala His Pro Val Thr Glu Leu
85 90 95

Asp Ile Asn Val Lys Asp Asn Asp Leu Phe Gly Ala Asp Ala Ile Gly
100 105 110

Thr Ala Lys
115

<210> 793
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 793

Leu Asp Leu Thr Ile Ile Glu Ala Arg Lys Leu Pro Asn Met Asp Ile
1 5 10 15

Val Ser Asn His Leu Arg Lys Cys Leu Thr Cys Glu Thr Cys Lys Ala
20 25 30

Pro Ser Gln Ala Ala Ala Ala Gln Glu Pro Gly Glu Val Gly Lys Val
35 40 45

His His His His Lys Ile Met Thr Ser Asp Pro Tyr Val Thr Ile Thr
50 55 60

Val Pro Gln Ser Thr Leu Ala Arg Thr Pro Val Leu Lys Ser Ala Asp
65 70 75 80

Asn Pro Glu Trp Asn Glu Arg Phe Ile Ile Pro Met Ala His Pro Leu
85 90 95

Thr Glu Leu Glu Ile Asn Val Lys Asp Asp Asp Leu Leu Gly Ala Glu
100 105 110

Val Ile Gly Thr Thr Lys
115

<210> 794
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

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<223> Synthetically generated peptide

<400> 794

Leu Asp Leu Lys Ile Val Lys Ala Arg Arg Leu Pro Asn Met Asp Met
1 5 10 15

Phe Ser Glu His Leu Arg Arg Leu Phe Thr Ala Cys Asn Ala Cys Ala
20 25 30

Arg Pro Thr Asp Thr Asp Asp Val Asp Pro Arg Asp Lys Gly Glu Phe
35 40 45

Gly Asp Lys Asn Ile Arg Ser His Arg Lys Val Ile Thr Ser Asp Pro
50 55 60

Tyr Val Thr Val Val Val Pro Gln Ala Thr Leu Ala Arg Thr Arg Val
65 70 75 80

Leu Lys Asn Ser Gln Glu Pro Leu Trp Asp Glu Lys Phe Asn Ile Ser
85 90 95

Ile Ala His Pro Phe Ala Tyr Leu Glu Phe Gln Val Lys Asp Asp Asp
100 105 110

Val Phe Gly Ala Gln Ile Ile Gly Thr Ala Lys
115 120

<210> 795
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 795

Leu Asp Leu Lys Ile Val Lys Ala Arg Arg Leu Pro Asn Met Asp Met
1 5 10 15

Phe Ser Glu His Leu Arg Arg Leu Phe Thr Ala Cys Asn Ala Cys Ala
20 25 30

Arg Pro Thr Asp Thr Asp Asp Val Asp Pro Arg Asp Lys Gly Glu Phe
35 40 45

Gly Asp Lys Asn Ile Arg Ser His Arg Lys Val Ile Thr Ser Asp Pro
50 55 60

Tyr Val Thr Val Val Val Pro Gln Ala Thr Leu Ala Arg Thr Arg Val
65 70 75 80

Leu Lys Asn Ser Gln Glu Pro Leu Trp Asp Glu Lys Phe Asn Ile Ser
85 90 95

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Ile Ala His Pro Phe Ala Tyr Leu Glu Phe Gln Val Lys Asp Asp Asp
100 105 110

Val Phe Gly Ala Gln Ile Ile Gly Thr Ala Lys
115 120

<210> 796
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 796

Leu Asp Leu Lys Ile Val Lys Ala Arg Arg Leu Pro Asn Met Asp Met
1 5 10 15

Phe Ser Glu His Leu Arg Arg Leu Phe Thr Ala Cys Asn Ala Cys Ala
20 25 30

Arg Pro Thr Asp Thr Asp Asp Val Asp Pro Arg Asp Lys Gly Glu Phe
35 40 45

Gly Asp Lys Asn Ile Arg Ser His Arg Lys Val Ile Thr Ser Asp Pro
50 55 60

Tyr Val Thr Val Val Val Pro Gln Ala Thr Leu Ala Arg Thr Arg Val
65 70 75 80

Leu Lys Asn Ser Gln Glu Pro Leu Trp Asp Glu Lys Phe Asn Ile Ser
85 90 95

Ile Ala His Pro Phe Ala Tyr Leu Glu Phe Gln Val Lys Asp Asp Asp
100 105 110

Val Phe Gly Ala Gln Ile Ile Gly Thr Ala Lys
115 120

<210> 797
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 797

Leu Asp Leu Trp Val Val Glu Ala Arg Leu Leu Pro Asn Met Asp Met
1 5 10 15

Phe Ser Glu His Val Arg Arg Cys Phe Ala Ala Cys Lys Pro Pro Thr
20 25 30

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Ser Cys Ala Thr Ala Arg Gln Pro Arg His Ala Arg Gly His His Arg
35 40 45

Arg Lys Ile Ile Thr Ser Asp Pro Tyr Val Thr Leu Ser Val Ala Gly
50 55 60

Ala Val Val Ala Arg Thr Arg Val Ile Pro Asn Asp Gln Asp Pro Val
65 70 75 80

Trp Asp Glu Arg Phe Ala Val Pro Leu Ala His Tyr Ala Ala Ala Leu
85 90 95

Glu Phe His Val Lys Asp Asn Asp Thr Phe Gly Ala Gln Leu Ile Gly
100 105 110

Thr Val Thr
115

<210> 798
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 798

Leu Asp Ile Trp Ile Thr Glu Ala Lys Cys Leu Pro Asn Met Asp Ile
1 5 10 15

Met Ser Glu Arg Met Arg Arg Phe Phe Thr Gly Tyr Gly Ala Cys Gly
20 25 30

Ser Ser Cys Ala Gly Asp Asn Ala Arg Arg Gly Gly Val Gly Val Arg
35 40 45

Pro Lys Lys Ile Ile Thr Ser Asp Pro Tyr Val Ser Val Cys Leu Ala
50 55 60

Gly Ala Thr Val Ala Gln Thr Arg Val Ile Pro Asn Ser Glu Asn Pro
65 70 75 80

Arg Trp Glu Glu Arg Phe Arg Val Glu Val Ala His Ala Val Ser Arg
85 90 95

Leu Glu Phe His Val Lys Asp Asn Asp Val Phe Gly Ala Gln Leu Ile
100 105 110

Gly Val Ala Ser
115

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<210> 799
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 799

Leu Asp Ile Trp Ile Thr Glu Ala Lys Cys Leu Pro Asn Met Asp Ile
1   5   10   15

Met Ser Glu Arg Met Arg Arg Phe Phe Thr Gly Tyr Gly Ala Cys Gly
            20   25   30

Ser Ser Cys Gly Gly Thr Gly Asp Asn Ala Arg Arg Ala Gly Gly Gly
        35   40   45

Val Arg Pro Lys Lys Ile Ile Thr Ser Asp Pro Tyr Val Ser Val Cys
    50   55   60

Leu Ala Gly Ala Thr Val Ala Gln Thr Arg Val Ile Pro Asn Ser Glu
65   70   75   80

Asn Pro Arg Trp Glu Glu Arg Phe Arg Val Glu Val Ala His Ala Val
                85   90   95

Ser Arg Leu Glu Phe His Val Lys Asp Asn Asp Val Phe Gly Ala Gln
            100   105   110

Leu Ile Gly Val Ala Ser
        115

<210> 800
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 800

Leu Asp Ile Gln Ile Val Glu Ala Lys Cys Leu Pro Asn Met Asp Leu
1   5   10   15

Met Thr Glu Arg Met Arg Lys Cys Phe Thr Gly Tyr Gly Ala Cys Ser
            20   25   30

Thr Glu Cys Gly Lys Ser Asp Pro His Thr Asp Val Arg Lys Ile Ile
        35   40   45

Thr Ser Asp Pro Tyr Val Ser Val Cys Leu Ser Gly Ala Thr Val Ala
    50   55   60

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Gln Thr Arg Val Ile Ala Asn Ser Glu Asn Pro Lys Trp Asp Glu His
65 70 75 80

Phe Tyr Val Gln Val Ala His Ser Val Ser Arg Val Glu Phe His Val
85 90 95

Lys Asp Asn Asp Val Phe Gly Ala Glu Leu Ile Gly Val Ala Ser
100 105 110

<210> 801
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 801

Leu Asp Leu Phe Ile Ile Glu Ala Lys Ser Leu Pro Asn Leu Asp Leu
1 5 10 15

Ser Thr Glu Ala Ile Arg Lys Cys Leu Thr Met Gly Asn Ser Cys Thr
20 25 30

Pro Pro Phe Val Lys Gly Leu Lys Thr His Ser Gly Lys Asp Lys Ile
35 40 45

Ile Thr Ser Asp Pro Tyr Val Ser Ile Cys Leu Ala Gly Ala Thr Ile
50 55 60

Ala Gln Thr Arg Val Ile Pro Asn Cys Glu Asn Pro Leu Trp Asp Glu
65 70 75 80

His Phe Leu Val Pro Val Ala His Pro Ala His Lys Ile Glu Phe Leu
85 90 95

Val Lys Asp Asn Asp Ile Leu Gly Ala Glu Leu Ile Gly Val Val Glu
100 105 110

<210> 802
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 802

Leu Met Val Glu Leu Leu His Gly Arg Arg Ile Arg Lys Val Asp Gly
1 5 10 15

Glu Lys Ser Ser Lys Phe Thr Ser Asp Pro Tyr Val Thr Val Ser Ile
20 25 30

Ser Gly Ala Val Ile Gly Arg Thr Phe Val Ile Ser Asn Ser Glu Asn
35 40 45

Pro Val Trp Met Gln His Phe Asp Val Pro Val Ala His Ser Ala Ala
50 55 60

Glu Val His Phe Val Val Lys Asp Asn Asp Pro Ile Gly Ser Lys Ile
65 70 75 80

Ile Gly Val Val Gly
85

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<210> 803
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 803

Leu Asp Ile Trp Val Lys Glu Ala Lys His Leu Pro Asn Met Ile Cys
1 5 10 15

Tyr Arg Asn Lys Leu Val Gly Gly Ile Ser Phe Ser Glu Leu Gly Arg
20 25 30

Arg Ile Arg Lys Val Asp Gly Glu Lys Ser Ser Lys Phe Thr Ser Asp
35 40 45

Pro Tyr Val Thr Val Ser Ile Ser Gly Ala Val Ile Gly Arg Thr Phe
50 55 60

Val Ile Ser Asn Ser Glu Asn Pro Val Trp Met Gln His Phe Asp Val
65 70 75 80

Pro Val Ala His Ser Ala Ala Glu Val His Phe Val Val Lys Asp Asn
85 90 95

Asp Pro Ile Gly Ser Lys Ile Ile Gly Val Val Gly
100 105

<210> 804
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 804

Leu Asp Ile Trp Val Lys Glu Ala Lys His Leu Pro Asn Met Asp Gly
1 5 10 15

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Phe His Asn Arg Leu Gly Gly Met Leu Ser Gly Leu Gly Arg Lys Lys
20 25 30

Val Glu Gly Glu Lys Ser Ser Lys Ile Thr Ser Asp Pro Tyr Val Thr
35 40 45

Val Ser Ile Ser Gly Ala Val Ile Gly Arg Thr Phe Val Ile Ser Asn
50 55 60

Ser Glu Asn Pro Val Trp Met Gln His Phe Asp Val Pro Val Ala His
65 70 75 80

Ser Ala Ala Glu Val His Phe Val Val Lys Asp Ser Asp Ile Ile Gly
85 90 95

Ser Gln Ile Met Gly Ala Val Gly
100

<210> 805
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 805

Leu Asp Ile Trp Val Lys Glu Ala Lys His Leu Pro Asn Met Asp Gly
1 5 10 15

Phe His Asn Thr Leu Val Gly Gly Met Phe Phe Gly Leu Gly Arg Arg
20 25 30

Asn His Lys Val Asp Gly Glu Asn Ser Ser Lys Ile Thr Ser Asp Pro
35 40 45

Tyr Val Thr Val Ser Ile Ser Gly Ala Val Ile Gly Arg Thr Phe Val
50 55 60

Ile Ser Asn Ser Glu Asn Pro Val Trp Met Gln His Phe Asp Val Pro
65 70 75 80

Val Ala His Ser Ala Ala Lys Val His Phe Val Val Lys Asp Ser Asp
85 90 95

Ile Ile Gly Ser Gln Ile Ile Gly Ala Val Glu
100 105

<210> 806
<211> 104
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 806

Leu Asp Ile Trp Val Arg Glu Ala Lys Asn Leu Pro Asn Met Asp Leu
1 5 10 15

Phe His Lys Lys Leu Asp Asn Leu Leu Gly Gly Leu Ala Lys Leu Gly
20 25 30

Ser Lys Lys Glu Gly Ser Pro Lys Ile Thr Ser Asp Pro Tyr Val Thr
35 40 45

Val Ser Val Ser Asn Ala Val Val Ala Arg Thr Tyr Val Ile Asn Asn
50 55 60

Ser Glu Asn Pro Ile Trp Met Gln His Phe Tyr Val Pro Val Ala His
65 70 75 80

Tyr Ala Ser Glu Val His Phe Val Val Lys Asp Asn Asp Val Val Gly
85 90 95

Ser Gln Ile Ile Gly Ala Val Gly
100

<210> 807
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 807

Leu Asp Ile Trp Val Ser Cys Ala Asn Asn Leu Pro Asn Leu Asp Leu
1 5 10 15

Phe His Lys Thr Leu Gly Val Val Phe Gly Gly Met Thr Asn Met Ile
20 25 30

Glu Gly Gln Leu Ser Lys Lys Ile Thr Ser Asp Pro Tyr Val Ser Ile
35 40 45

Ser Val Ala Gly Ala Val Ile Gly Arg Thr Tyr Val Ile Ser Asn Ser
50 55 60

Glu Asn Pro Val Trp Gln Gln His Phe Tyr Val Pro Val Ala His His
65 70 75 80

Ala Ala Glu Val His Phe Val Val Lys Asp Ser Asp Ala Val Gly Ser
85 90 95

Gln Leu Ile Gly Ile Val Thr
100

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<210> 808
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 808

Leu Asp Ile Trp Ile Tyr His Ala Lys Asn Leu Pro Asn Met Asp Met
1 5 10 15

Phe His Lys Thr Leu Gly Asp Met Phe Gly Arg Leu Pro Gly Lys Ile
20 25 30

Glu Gly Gln Leu Thr Ser Lys Ile Thr Ser Asp Pro Tyr Val Ser Val
35 40 45

Ser Val Ala Gly Ala Val Ile Gly Arg Thr Tyr Val Met Ser Asn Ser
50 55 60

Glu Asn Pro Val Trp Met Gln His Phe Tyr Val Pro Val Ala His His
65 70 75 80

Ala Ala Glu Val His Phe Val Val Lys Asp Ser Asp Val Val Gly Ser
85 90 95

Gln Leu Ile Gly Leu Val Thr
100

<210> 809
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 809

Leu Glu Ile Trp Val Tyr Glu Ala Lys Asn Leu Pro Asn Met Asp Met
1 5 10 15

Phe His Lys Thr Ile Gly Asp Met Phe Gly Gln Met Ser Asn Lys Ile
20 25 30

Thr Ser Asp Pro Tyr Val Ser Ile Asn Ile Ala Asp Ala Thr Ile Gly
35 40 45

Arg Thr Tyr Val Ile Asn Asn Asn Glu Asn Pro Val Trp Met Gln His
50 55 60

Phe Asn Val Pro Val Ala His Tyr Ala Ala Glu Val Gln Phe Leu Val
65 70 75 80

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Lys Asp Asp Asp Ile Val Gly Ser Gln Leu Met Gly Thr Val Ala
85 90 95

<210> 810
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<220>
<221> misc_feature
<222> (86)..(86)
<223> Xaa can be any naturally occurring amino acid

<400> 810

Leu Asp Ile Trp Val Leu Glu Ala Asn Asn Leu Pro Asn Met Asp Met
1 5 10 15

Phe His Arg Thr Leu Gly Asp Met Phe Ala Asn Phe Ser Ser Asn Ile
20 25 30

Ser Lys Lys Val Gly Gly Arg Ser Asp Glu Lys Ile Thr Ser Asp Pro
35 40 45

Tyr Val Thr Ile Ala Val Ala Gly Ala Val Ile Gly Arg Thr Phe Val
50 55 60

Ile Ser Asn Asn Glu Asn Pro Val Trp Met Gln His Phe Asn Val Pro
65 70 75 80

Val Ala His His Ala Xaa Glu Val Gln Phe Val Val Lys Asp Ser Asp
85 90 95

Ile Leu Gly Ser Asp Ile Ile Gly Val Val Ala
100 105

<210> 811
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 811

Leu Asp Ile Trp Val Leu Glu Ala Asn Asn Leu Pro Asn Met Asp Met
1 5 10 15

Phe His Arg Thr Leu Gly Asp Met Phe Ala Asn Phe Ser Ser Asn Ile
20 25 30

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Ser Lys Lys Val Gly Gly Arg Ser Asp Glu Lys Ile Thr Ser Asp Pro
35 40 45

Tyr Val Thr Ile Ala Val Ala Gly Ala Val Ile Gly Arg Thr Phe Val
50 55 60

Ile Ser Asn Asn Glu Asn Pro Val Trp Met Gln His Phe Asn Val Pro
65 70 75 80

Val Ala His His Ala Ala Glu Val Gln Phe Val Val Lys Asp Ser Asp
85 90 95

Ile Leu Gly Ser Asp Ile Ile Gly Val Val Ala
100 105

<210> 812
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 812

Leu Asp Ile Trp Val Leu Glu Ala Lys Asn Leu Pro Asn Met Asp Met
1 5 10 15

Phe His Lys Thr Leu Gly Asp Met Phe Gly Asn Phe Ser Ser Asn Ile
20 25 30

Ser Lys Lys Ile Gly Gly Arg Ser Glu Gly Lys Asn Thr Ser Asp Pro
35 40 45

Tyr Val Thr Ile Ala Val Ser Gly Ala Val Ile Gly Arg Thr Phe Val
50 55 60

Ile Asn Asn Asp Glu Asn Pro Val Trp Arg Gln His Phe Tyr Val Pro
65 70 75 80

Val Ala His His Ala Ala Glu Val Gln Phe Val Val Lys Asp Ile Asp
85 90 95

Ile Leu Gly Ser Glu Ile Ile Gly Val Val Thr
100 105

<210> 813
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 813

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Leu Asp Val Trp Val Tyr Asp Ala Arg Asn Leu Pro Asn Lys Asp Leu
1 5 10 15

Phe Ser Lys Arg Val Gly Asp Leu Leu Gly Pro Arg Leu Ile Gly Ala
20 25 30

Val Gly Ser Lys Met Ser Ser Ala Asn Met Thr Ser Asp Pro Tyr Val
35 40 45

Thr Ile Gln Val Ser Tyr Ala Thr Val Ala Arg Thr Tyr Val Val Pro
50 55 60

Asn Asn Glu Asn Pro Val Trp Thr Gln Asn Phe Leu Val Pro Val Gly
65 70 75 80

His Asp Ala Ala Glu Val Glu Phe Val Val Lys Asp Asn Asp Val Phe
85 90 95

Gly Ala Gln Leu Ile Gly Thr Val Ser
100 105

<210> 814
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 814

Leu Asp Val Trp Val Tyr Asp Ala Arg Asn Leu Pro Asn Lys Asp Leu
1 5 10 15

Phe Ser Lys Arg Val Gly Asp Leu Leu Gly Pro Arg Leu Ile Gly Ala
20 25 30

Val Gly Ser Lys Met Ser Ser Ala Asn Met Thr Ser Asp Pro Tyr Val
35 40 45

Thr Ile Gln Val Ser Tyr Ala Thr Val Ala Arg Thr Tyr Val Val Pro
50 55 60

Asn Asn Glu Asn Pro Val Trp Thr Gln Asn Phe Leu Val Pro Val Gly
65 70 75 80

His Asp Ala Ala Glu Val Glu Phe Val Val Lys Asp Asn Asp Val Phe
85 90 95

Gly Ala Gln Leu Ile Gly Thr Val Ser
100 105

<210> 815
<211> 101

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 815

Leu Asp Ile Trp Ile His Glu Ala Arg Asn Leu Pro Asn Met Asp Ile
1 5 10 15

Val Ser Lys Thr Val Val Asp Ile Leu Gly Thr Lys Lys Lys Lys Lys
20 25 30

Ala Ala Asn Gly Ala Met Thr Ser Asp Pro Tyr Val Thr Val Gln Leu
35 40 45

Ala Ser Ala Thr Val Ala Arg Thr Tyr Val Val Asn Asp Asp Glu Asn
50 55 60

Pro Val Trp Ala Gln His Phe Leu Ile Pro Val Ala His Glu Ala Pro
65 70 75 80

Ala Val His Phe Leu Val Lys Asp Ser Asp Val Phe Gly Ala Glu Leu
85 90 95

Ile Gly Glu Val Val
100

<210> 816
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 816

Leu Asp Ile Trp Ile His Glu Ala Arg Asn Leu Pro Asn Met Asp Ile
1 5 10 15

Val Ser Lys Thr Val Val Asp Ile Leu Gly Thr Lys Lys Lys Lys Lys
20 25 30

Ala Ala Asn Gly Ala Met Thr Ser Asp Pro Tyr Val Thr Val Gln Leu
35 40 45

Ala Ser Ala Thr Val Ala Arg Thr Tyr Val Val Asn Asp Asp Glu Asn
50 55 60

Pro Val Trp Ala Gln His Phe Leu Ile Pro Val Ala His Glu Ala Pro
65 70 75 80

Ala Val His Phe Leu Val Lys Asp Ser Asp Val Phe Gly Ala Glu Leu
85 90 95

Ile Gly Glu Val Val
100

<210> 817
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 817

Leu Asp Leu Thr Ile His Glu Ala Arg Gly Leu Pro Asn Met Asp Phe
1 5 10 15

Leu Ser Thr Leu Leu Arg Arg Leu Cys Leu Cys Leu Arg Pro Pro Ala
20 25 30

Arg Arg Pro Ser Pro Gly Gln Ser Arg Gly Ser Val Pro Ala Asp Glu
35 40 45

Asp Gly Arg Arg Gln Pro His Gly His His Leu Leu Pro Thr Ser Asp
50 55 60

Pro Tyr Ala Ala Val Val Val Ala Gly Asn Thr Leu Ala Arg Thr His
65 70 75 80

Val Val Arg Asp Ser Glu Asp Pro Glu Trp Ser Thr His Val Leu Leu
85 90 95

His Leu Ala His His Ala Thr Gly Val Ala Phe His Val Lys Asp Ala
100 105 110

Asp Pro Phe Gly Ser Asp Leu Ile Gly Val Ala Ile
115 120

<210> 818
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 818

Tyr Val Asn Ile Gln Phe Gly Asp Gln Ile Phe Thr Ser Lys Ile Thr
1 5 10 15

Gln Gly Lys Gly Lys Lys Val Trp Trp Asn Glu Lys Phe Arg Phe Pro
20 25 30

Leu Ser Ser Asp Glu Cys Lys Glu Leu Ala Lys Val Thr Leu Lys Ile
35 40 45

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Met Glu Arg Asp Lys Phe Ser Glu Asp Ser Leu Val Gly Glu Thr Lys
50 55 60

<210> 819
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 819

Leu Asp Val Thr Leu Lys Ser Ala Ser Asp Leu Arg Glu Asp Met Ser
1 5 10 15

Val Lys Leu Asp Ala Tyr Cys Val Val Ser Cys Ala Ser Thr Ala His
20 25 30

Arg Ser Asn Thr Val Thr Asp Ala Gly Lys Thr Met Asn Trp Glu Gln
35 40 45

Thr Phe His Phe Asp Lys Val Ala Ser Thr Ser Val Leu Lys Leu Glu
50 55 60

<210> 820
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 820

Leu Glu Ile Asn Val Thr Ser Ala Lys Gly Leu Lys Lys Val Ser Lys
1 5 10 15

Met Asp Val Phe Val Ala Val Lys Leu Ser Gly Asp Pro Lys Cys Ser
20 25 30

Asp His Arg Glu Gln Arg Thr Gln Ala Ala Arg Asp Gly Gly Thr Ser
35 40 45

Pro Lys Trp Ser Asn Asp Val Met Lys Phe Ile Leu Asp Gln Asn Leu
50 55 60

Ala Glu Ala Asn Arg Leu Val Ile Thr Phe Lys Ile Lys Cys Glu Gln
65 70 75 80

Arg Gly Gly Val Asp Lys Asp Ile Gly Glu Val His
85 90

<210> 821
<211> 90

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 821

Val Glu Ile Asn Val Leu Ser Ala Gln Asp Leu Asn Ser Ile Asn Leu
1 5 10 15

Leu Phe Arg Pro Thr Val Tyr Val Ser Val Ser Val Thr Arg Gly Ser
20 25 30

Arg Asp Lys Gln Val Thr Pro Ala Ala Ala Trp Asp Lys Lys Phe Leu
35 40 45

Arg Trp Asn Tyr Arg Met Lys Phe Tyr Ile Glu Asp Asp Lys Val Arg
50 55 60

Arg Asn Glu Ser Val Phe Val Phe Gln Ile Lys Cys Lys Arg Phe Phe
65 70 75 80

Gly Ser Asp Gln Val Val Gly Lys Leu Phe
85 90

<210> 822
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 822

Leu Tyr Val Tyr Ile Leu Gln Ala Lys Asp Leu Pro Ala Lys Glu Thr
1 5 10 15

Phe Ala Lys Leu His Val Gly Arg His Lys Ser Lys Thr Arg Val Ala
20 25 30

Arg Asp Thr Ser Ser Pro Ile Trp Asn Glu Glu Phe Val Phe Arg Ile
35 40 45

Ser Asp Val Asp Glu Gly Asp Asp Val Val Val Ser Ile Leu His His
50 55 60

Glu Gln Gln Asp His Gln Ser Ile Val Ser Thr Gly Leu Ile Gly Lys
65 70 75 80

Val Arg

<210> 823
<211> 84

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 823

Leu Tyr Ile Arg Val Ala Lys Ala Lys Arg Ala Lys Asn Asp Gly Ser
1 5 10 15

Asn Pro Val Tyr Ala Lys Leu Val Ile Gly Thr Asn Gly Val Lys Thr
20 25 30

Arg Ser Gln Thr Gly Lys Asp Trp Asp Gln Val Phe Ala Phe Glu Lys
35 40 45

Glu Ser Leu Asn Ser Thr Ser Leu Glu Val Ser Val Trp Ser Glu Glu
50 55 60

Lys Ile Glu Lys Glu Asp Lys Thr Thr Thr Thr Thr Glu Ser Cys Leu
65 70 75 80

Gly Thr Val Ser

<210> 824
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 824

Met Thr Val Gln Ile Leu Glu Ala Lys Gly Leu His Ile Ile Asp Asp
1 5 10 15

Gly Asn Ser His Ser Phe Phe Cys Thr Leu Arg Leu Val Val Asp Ser
20 25 30

Gln Gly Ala Glu Pro Gln Lys Leu Phe Pro Gln Ser Ala Arg Thr Lys
35 40 45

Cys Val Lys Pro Ser Thr Thr Ile Val Asn Asp Leu Met Glu Cys Thr
50 55 60

Ser Lys Trp Asn Glu Leu Phe Ile Phe Glu Ile Pro Arg Lys Gly Val
65 70 75 80

Ala Arg Leu Glu Val Glu Val Thr Asn Leu Ala Ala Lys Ala Gly Lys
85 90 95

Gly Glu Val Val Gly Ser Leu Ser
100

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<210> 825
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 825

Ile Asp Leu Lys Ile Ile Ser Cys Lys Asp Ile Asn Ala Phe Asn Phe
1 5 10 15

Phe Gln Lys Leu Thr Leu Tyr Ala Gln Val Ser Ile Ser Thr Thr Asn
20 25 30

Pro Lys Thr Lys Leu Thr Lys Gln Gln Gln Arg Thr Pro Thr His Arg
35 40 45

Asp Thr Asp Asp Asp Gly Thr Asn Pro Glu Trp Asn His Gln Thr Arg
50 55 60

Phe Asn Leu Ser Phe Leu Ser Ser His Pro Asp Pro Ser Glu Phe Phe
65 70 75 80

Leu Ser Phe Glu Arg Arg His Asp Gly Leu Ile Leu Gly Asn Lys Phe
85 90 95

Leu Gly Glu Cys Arg
100

<210> 826
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 826

Val Thr Ile Arg Ser Ile Ser Cys Arg Gly Val Lys Ala Phe Val Pro
1 5 10 15

Phe Gln Lys Pro Pro Leu Tyr Ala Ala Val Ser Leu Ala Gly Arg Arg
20 25 30

Glu Lys Thr Ser Gly Asp Pro Asp Gly Gly Glu Asn Pro Asp Trp Asp
35 40 45

Ala Ala Val Phe Ala Phe Asp Leu Pro Ala Ala Ala Asp Gly Met Leu
50 55 60

Gln Phe Glu Val Lys Ala Gln Val Pro Leu Leu Gly Ser Lys Leu Val
65 70 75 80

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Gly Lys Val Ser

<210> 827
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 827

```
Phe Glu Leu Arg Ile Ile Gln Ala Arg Asn Ile Glu Ser Val Lys Ser
1               5                   10                  15

Thr Lys Asn Leu Phe Ala Arg Leu Tyr Leu Pro Thr Gly Asn Asn Lys
            20                  25                  30

Arg Ile Gln Leu Asn Ser Lys Ser Val Ser Thr Lys Ser Val Pro Phe
        35                  40                  45

Trp Asp Glu Ser Phe Asn Leu Asp Cys Ser Cys Pro Gln Glu Phe Leu
    50                  55                  60

Glu Asn Leu Asn Gln Gln Ser Leu Glu Val Glu Leu Arg Gln Arg Lys
65                  70                  75                  80

Ile Trp Gly Ser Gln Leu Ile Gly Lys Phe Glu
                85                  90
```

<210> 828
<211> 102
<212> PRT
<213> Oryza sativa

<400> 828

```
Met Ser Ser Asp Gly Gly Pro Val Leu Gly Gly Val Glu Pro Val Gly
1               5                   10                  15

Asn Glu Asn Asp Leu His Leu Val Asp Leu Ala Arg Phe Ala Val Thr
            20                  25                  30

Glu His Asn Lys Lys Ala Asn Ser Leu Leu Glu Phe Glu Lys Leu Val
        35                  40                  45

Ser Val Lys Gln Gln Val Val Ala Gly Thr Leu Tyr Tyr Phe Thr Ile
    50                  55                  60

Glu Val Lys Glu Gly Asp Ala Lys Lys Leu Tyr Glu Ala Lys Val Trp
65                  70                  75                  80

Glu Lys Pro Trp Met Asp Phe Lys Glu Leu Gln Glu Phe Lys Pro Val
```

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85 90 95

Asp Ala Ser Ala Asn Ala
100

<210> 829
<211> 134
<212> PRT
<213> Zea mays

<400> 829

Met Arg Lys His Arg Ile Val Ser Leu Val Ala Ala Leu Leu Ile Leu
1 5 10 15

Leu Ala Leu Ala Val Ser Ser Thr Arg Asn Ala Gln Glu Asp Ser Met
20 25 30

Ala Asp Asn Thr Gly Thr Leu Ala Gly Gly Ile Lys Asp Val Pro Gly
35 40 45

Asn Glu Asn Pro Leu His Leu Gln Glu Leu Ala Arg Phe Ala Val Asp
50 55 60

Glu His Asn Lys Lys Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu Val
65 70 75 80

Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr Ile
85 90 95

Glu Val Lys Asp Gly Glu Val Lys Lys Leu Tyr Glu Ala Lys Val Trp
100 105 110

Glu Lys Pro Trp Glu Asn Phe Lys Glu Leu Gln Glu Phe Lys Pro Val
115 120 125

Asp Glu Gly Ala Ser Ala
130

<210> 830
<211> 125
<212> PRT
<213> Triticum aestivum

<400> 830

Leu Leu Ala Ile Val Val Pro Phe Thr Gln Thr Arg Thr Gln Ser Ala
1 5 10 15

Arg Asp Lys Ala Ala Met Ala Glu Asp Ala Gly Pro Leu Val Gly Gly
20 25 30

Ile Lys Asp Ser Pro Met Gly Gln Glu Asn Asp Leu Asp Val Ile Ala
35 40 45

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Leu Ala Arg Phe Ala Val Ser Glu His Asn Asn Lys Ala Asn Ala Leu
50 55 60

Leu Glu Phe Glu Asn Val Val Lys Leu Lys Lys Gln Thr Val Ala Gly
65 70 75 80

Thr Met His Tyr Ile Thr Ile Arg Val Thr Glu Gly Gly Ala Lys Lys
85 90 95

Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln
100 105 110

Leu Gln Glu Phe Lys Pro Val Glu Asp Ala Ala Ile Ala
115 120 125

<210> 831
<211> 140
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 831

Met Trp Lys Tyr Arg Val Leu Gly Ser Val Ala Ala Leu Leu Leu Leu
1 5 10 15

Leu Ala Val Val Val Pro Phe Thr Gln Thr Trp Thr Gln Ser Ala Arg
20 25 30

Asp Lys Ala Ala Met Ala Glu Asp Ala Gly Pro Leu Met Gly Gly Ile
35 40 45

Glu Asp Ser Pro Met Gly Gln Glu Asn Asp Leu Asp Val Ile Ala Leu
50 55 60

Ala Arg Phe Ala Val Ser Glu His Asn Lys Lys Ala Asn Ala Leu Leu
65 70 75 80

Glu Phe Glu Asn Val Val Lys Leu Lys Lys Gln Thr Val Ala Gly Thr
85 90 95

Met Tyr Tyr Ile Thr Ile Arg Val Thr Glu Gly Gly Thr Lys Lys Leu
100 105 110

Tyr Glu Ala Lys Val Trp Glu Lys Leu Trp Glu Asn Phe Lys Gln Leu
115 120 125

Glu Glu Phe Lys Pro Val Gln Asp Ala Ala Ile Ala
130 135 140

<210> 832
<211> 135
<212> PRT
<213> Coix lacryma-jobi

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<400> 832

Met Arg Lys Gln Arg Ile Val Pro Leu Val Ala Ala Leu Leu Val Leu
1   5   10   15

Leu Ala Leu Ala Val Ser Ser Thr Arg Asn Ala Arg Glu Glu Glu Ser
            20   25   30

Met Ala Asp Asp Ala Gly Met Leu Ala Gly Gly Ile Lys Asp Val Pro
        35   40   45

Ala Asn Glu Asn Asp Leu His Leu Gln Glu Leu Ala Arg Phe Ala Val
    50   55   60

Asp Glu His Asn Lys Lys Ala Asn Ala Leu Leu Gly Tyr Glu Lys Leu
65   70   75   80

Val Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr
                85   90   95

Ile Glu Val Lys Asp Gly Glu Val Lys Lys Leu Tyr Glu Ala Lys Val
            100   105   110

Trp Glu Lys Pro Trp Glu Asn Phe Lys Glu Leu Leu Glu Phe Lys Pro
        115   120   125

Val Glu Glu Asp Ala Ser Ala
    130   135

<210> 833
<211> 135
<212> PRT
<213> Zea mays

<400> 833

Met Arg Lys His Arg Ile Val Ser Leu Val Ala Ala Leu Leu Val Leu
1   5   10   15

Leu Ala Leu Ala Ala Val Ser Ser Thr Arg Ser Thr Gln Lys Glu Ser
            20   25   30

Val Ala Asp Asn Ala Gly Met Leu Ala Gly Gly Ile Lys Asp Val Pro
        35   40   45

Ala Asn Glu Asn Asp Leu Gln Leu Gln Glu Leu Ala Arg Phe Ala Val
    50   55   60

Asn Glu His Asn Gln Lys Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu
65   70   75   80

Val Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr
                85   90   95

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Ile Glu Val Lys Asp Gly Glu Val Lys Lys Leu Tyr Glu Ala Lys Val
100 105 110

Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln Leu Gln Glu Phe Lys Pro
115 120 125

Val Glu Glu Gly Ala Ser Ala
130 135

<210> 834
<211> 130
<212> PRT
<213> Sorghum bicolor

<400> 834

Ala Arg Val Val Pro Leu Val Ala Ala Leu Leu Val Leu Leu Ala Leu
1 5 10 15

Ala Val Ser Ser Thr Arg Asn Arg Asn Ala Gln Glu Gly Glu Glu Ser
20 25 30

Met Ala Leu Asp Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp
35 40 45

Leu His Leu Gln Glu Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys
50 55 60

Lys Ala Asn Ala Leu Leu Gly Tyr Glu Lys Leu Val Lys Ala Lys Thr
65 70 75 80

Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr Val Glu Val Lys Asp
85 90 95

Gly Glu Val Lys Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp
100 105 110

Glu Asn Phe Lys Glu Leu Gln Glu Phe Lys Pro Val Glu Glu Gly Ala
115 120 125

Ser Ala
130

<210> 835
<211> 97
<212> PRT
<213> Arachis hypogaea

<400> 835

Ala Ala Val Gly Ala Pro Arg Glu Val Ala Gly Asn Glu Asn Ser Leu
1 5 10 15

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Glu Ile Asp Ser Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys
20 25 30

Gln Asn Gly Leu Leu Glu Phe Lys Arg Val Ile Ser Ala Lys Gln Gln
35 40 45

Val Val Ala Gly Thr Leu His His Ile Thr Leu Glu Ala Ala Ser Gly
50 55 60

Asp Ser Lys Asn Val Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Met
65 70 75 80

Asn Phe Lys Glu Val Gln Glu Phe Lys Leu Ala Gly Asp Gly Ser Asn
85 90 95

Ala

<210> 836
<211> 100
<212> PRT
<213> Castanea sativa

<400> 836

Ala Ala Leu Val Gly Gly Val Ser Asp Val Lys Gly His Glu Asn Ser
1 5 10 15

Leu Gln Ile Asp Leu Ala Arg Phe Ala Val Asp Asp His Asn Lys Lys
20 25 30

Ala Asn Thr Leu Leu Gln Phe Lys Lys Val Val Asn Ala Lys Gln Gln
35 40 45

Val Val Ser Gly Thr Ile Tyr Ile Leu Thr Leu Glu Val Glu Asp Gly
50 55 60

Gly Lys Lys Lys Val Tyr Glu Ala Lys Ile Trp Glu Lys Pro Trp Leu
65 70 75 80

Asn Phe Lys Glu Val Gln Glu Phe Lys Leu Ile Gly Asp Ala Pro Thr
85 90 95

His His Ser Ala
100

<210> 837
<211> 104
<212> PRT
<213> Saccharum officinarum

<400> 837

Ala Glu Ala His Asn Gly Arg Arg Val Gly Met Val Gly Asp Val Arg
1 5 10 15

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Asp Ala Pro Ala Gly His Glu Asn Leu Glu Ala Ile Glu Leu Ala Arg
20 25 30

Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn Ala Met Leu Glu Phe
35 40 45

Glu Arg Leu Val Lys Val Arg His Gln Val Val Ala Gly Thr Met His
50 55 60

His Phe Thr Val Gln Val Lys Glu Ala Gly Gly Gly Lys Lys Leu Tyr
65 70 75 80

Glu Ala Lys Val Trp Glu Lys Val Trp Glu Asn Phe Lys Gln Leu Gln
85 90 95

Ser Phe Gln Pro Val Gly Asp Ala
100

<210> 838
<211> 95
<212> PRT
<213> Vigna unguiculata

<400> 838

Ala Ala Gly Gly Asn Arg Asp Val Ala Gly Asn Gln Asn Ser Leu Glu
1 5 10 15

Ile Asp Ser Leu Ala Arg Phe Ala Val Glu Glu His Asn Lys Lys Gln
20 25 30

Asn Ala Leu Leu Glu Phe Gly Arg Val Val Ser Ala Gln Gln Gln Val
35 40 45

Val Ser Gly Thr Leu Tyr Thr Ile Thr Leu Glu Ala Lys Asp Gly Gly
50 55 60

Gln Lys Lys Val Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Leu Asn
65 70 75 80

Phe Lys Glu Leu Gln Glu Phe Lys His Val Gly Asp Ala Pro Ala
85 90 95

<210> 839
<211> 156
<212> PRT
<213> Oryza sativa

<400> 839

Met Ala Gly Ser Gly Val Leu Glu Val His Phe Val Asp Ala Lys Gly
1 5 10 15

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Leu Thr Gly Asn Asp Phe Leu Gly Lys Ile Asp Pro Tyr Val Val Val
20 25 30

Gln Tyr Arg Ser Gln Glu Arg Lys Ser Ser Val Ala Arg Asp Gln Gly
35 40 45

Lys Asn Pro Ser Trp Asn Glu Val Phe Lys Phe Gln Ile Asn Ser Thr
50 55 60

Ala Ala Thr Gly Gln His Lys Leu Phe Leu Arg Leu Met Asp His Asp
65 70 75 80

Thr Phe Ser Arg Asp Asp Phe Leu Gly Glu Ala Thr Ile Asn Val Thr
85 90 95

Asp Leu Ile Ser Leu Gly Met Glu His Gly Thr Trp Glu Met Ser Glu
100 105 110

Ser Lys His Arg Val Val Leu Ala Asp Lys Thr Tyr His Gly Glu Ile
115 120 125

Arg Val Ser Leu Thr Phe Thr Ala Ser Ala Lys Ala Gln Asp His Ala
130 135 140

Gln Gln Val Gly Gly Trp Ala His Ser Phe Arg Gln
145 150 155

<210> 840
<211> 144
<212> PRT
<213> Oryza sativa

<400> 840

Met Val Gln Gly Thr Leu Glu Val Leu Leu Val Gly Ala Lys Gly Leu
1 5 10 15

Glu Asn Thr Asp Tyr Leu Cys Asn Met Asp Pro Tyr Ala Val Leu Lys
20 25 30

Cys Arg Ser Gln Glu Gln Lys Ser Ser Val Ala Ser Gly Lys Gly Ser
35 40 45

Asp Pro Glu Trp Asn Glu Thr Phe Met Phe Ser Val Thr His Asn Ala
50 55 60

Thr Glu Leu Ile Ile Lys Leu Met Asp Ser Asp Ser Gly Thr Asp Asp
65 70 75 80

Asp Phe Val Gly Glu Ala Thr Ile Ser Leu Glu Ala Ile Tyr Thr Glu
85 90 95

Gly Ser Ile Pro Pro Thr Val Tyr Asn Val Val Lys Glu Glu Glu Tyr

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```
            100                     105                 110

Arg Gly Glu Ile Lys Val Gly Leu Thr Phe Thr Pro Glu Asp Asp Arg
        115                 120                 125

Asp Arg Gly Leu Ser Glu Glu Asp Ile Gly Gly Trp Lys Gln Ser Ser
    130                 135                 140
```

<210> 841
<211> 138
<212> PRT
<213> Cucurbita maxima

<400> 841

```
Met Gly Met Gly Met Met Glu Val His Leu Ile Ser Gly Lys Gly Leu
1               5                   10                  15

Gln Ala His Asp Pro Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile
            20                  25                  30

Asn Phe Lys Gly Gln Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly
        35                  40                  45

Pro Asp Pro Ile Trp Asn Glu Lys Phe Lys Phe Leu Val Glu Tyr Pro
    50                  55                  60

Gly Ser Gly Gly Asp Phe His Ile Leu Phe Lys Val Met Asp His Asp
65                  70                  75                  80

Ala Ile Asp Gly Asp Asp Tyr Ile Gly Asp Val Lys Ile Asp Val Gln
                85                  90                  95

Asn Leu Leu Ala Glu Gly Val Arg Lys Gly Trp Ser Glu Leu Pro Pro
            100                 105                 110

Arg Met Tyr Gln Val Leu Ala His Lys Ile Tyr Phe Lys Gly Glu Ile
        115                 120                 125

Glu Val Gly Val Phe Phe Gln Arg Gln Gly
    130                 135
```

<210> 842
<211> 150
<212> PRT
<213> Cucurbita maxima

<400> 842

```
Met Gly Met Gly Met Met Glu Val His Leu Ile Ser Gly Lys Gly Leu
1               5                   10                  15

Gln Ala His Asp Pro Leu Asn Lys Pro Ile Asp Pro Tyr Ala Glu Ile
            20                  25                  30
```

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Asn Phe Lys Gly Gln Glu Arg Met Ser Lys Val Ala Lys Asn Ala Gly
        35   40   45

Pro Asn Pro Leu Trp Asp Glu Lys Phe Lys Phe Leu Ala Glu Tyr Pro
    50   55   60

Gly Ser Gly Gly Asp Phe His Ile Leu Phe Lys Val Met Asp His Asp
65   70   75   80

Ala Ile Asp Gly Asp Asp Tyr Ile Gly Asp Val Lys Ile Asp Val Lys
                85   90   95

Asn Leu Leu Ala Glu Gly Val Arg Lys Gly Lys Ser Glu Met Pro Pro
            100   105   110

Arg Met Tyr His Val Leu Ala His Lys Ile His Phe Lys Gly Glu Ile
        115   120   125

Glu Val Gly Val Ser Phe Lys Leu Gln Gly Gly Gly Gly Cys Gly Gly
    130   135   140

Cys Tyr Pro Trp Glu Asn
145   150

<210> 843
<211> 146
<212> PRT
<213> Arabidopsis thaliana

<400> 843

Met Pro His Gly Thr Leu Glu Val Val Leu Val Ser Ala Lys Gly Leu
1   5   10   15

Glu Asp Ala Asp Phe Leu Asn Asn Met Asp Pro Tyr Val Gln Leu Thr
            20   25   30

Cys Arg Thr Gln Asp Gln Lys Ser Asn Val Ala Glu Gly Met Gly Thr
        35   40   45

Thr Pro Glu Trp Asn Glu Thr Phe Ile Phe Thr Val Ser Glu Gly Thr
    50   55   60

Thr Glu Leu Lys Ala Lys Ile Phe Asp Lys Asp Val Gly Thr Glu Asp
65   70   75   80

Asp Ala Val Gly Glu Ala Thr Ile Pro Leu Glu Pro Val Phe Val Glu
                85   90   95

Gly Ser Ile Pro Pro Thr Ala Tyr Asn Val Val Lys Asp Glu Glu Tyr
            100   105   110

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```
Lys Gly Glu Ile Trp Val Ala Leu Ser Phe Lys Pro Glu Asn Arg Ser
        115                 120                 125

Arg Gly Met Asp Glu Glu Ser Tyr Gly Gly Trp Lys Asn Ser Glu Ala
    130                 135                 140

Ser Tyr
145
```

<210> 844
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 844

```
Pro Gln Gln Val His Ile Thr Gln Gly Asp His Val Gly Lys Ala Val
1               5                   10                  15

Ile Val Ser Trp Val Thr His Phe Glu Pro Ala Ser Lys Val Val Val
            20                  25                  30

Tyr Trp Ser Glu Asn Ser Lys Tyr Lys Lys Ser Ala Glu Gly Thr Val
        35                  40                  45

Thr Thr Tyr Arg Phe Lys Asn Tyr Asn Gly Tyr Ile His His Cys Tyr
    50                  55                  60

Ile Lys Gly Leu Glu Tyr Asp Thr Lys Tyr Tyr Tyr Val Val Phe Ile
65                  70                  75                  80

Gly Asn Thr Arg Ala Ser Arg Glu Phe Trp Phe Arg
                85                  90
```

<210> 845
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 845

```
Pro Gln Gln Val His Ile Thr Gln Gly Asp His Val Gly Lys Ala Val
1               5                   10                  15

Ile Val Ser Trp Val Thr Met Phe Ser Pro His Ser Ala Lys Val Val
            20                  25                  30

Val Tyr Trp Ser Glu Asn Ser Lys Tyr Lys Lys Ser Ala Glu Gly Thr
        35                  40                  45
```

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Val Thr Thr Tyr Gln Ser Thr Phe Ala Asn Asn Ser Arg Tyr Ile His
    50   55   60

His Cys Tyr Ile Lys Gly Leu Glu Tyr Asp Thr Lys Tyr Tyr Tyr Val
65   70   75   80

Asp Val Lys Phe Gly Pro Ile Gly Leu Ile Asn Thr Arg Ala Ser Arg
                85   90   95

Glu Phe Trp Phe Arg
            100

<210> 846
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 846

Pro Gln Gln Val His Ile Thr Gln Gly Asp His Val Gly Lys Ala Val
1   5   10   15

Ile Val Ser Trp Val Thr Met Ala Arg Lys Leu Ser Pro Val Val Val
            20   25   30

Tyr Trp Ser Glu Asn Ser Lys Tyr Lys Lys Ser Ala Glu Gly Thr Val
        35   40   45

Thr Thr Tyr Arg Asp Tyr Asn Lys Thr Ser Gly Tyr Ile His His Cys
    50   55   60

Tyr Ile Lys Gly Leu Glu Tyr Asp Thr Lys Tyr Tyr Tyr Val Val Gly
65   70   75   80

Ile Gly Asn Thr Ser Arg Glu Phe Trp Phe Arg
                85   90