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(54) **Title:** D-DOMAIN CONTAINING POLYPEPTIDES AND USES THEREOF

(57) **Abstract:** D domain (DD) containing polypeptides (DDpp) that specifically bind targets of interest (*e.g.*, BCMA, CD123, CS1, HER2, AFP, and AFP p26) are provided, as are nucleic acids encoding the DDpp, vectors containing the nucleic acids and host cells containing the nucleic acids and vectors. DDpp such as DDpp fusion proteins, are also provided as are methods of making and using the DDpp. Such uses include, but are not limited to diagnostic and therapeutic applications.

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D-DOMAIN CONTAINING POLYPEPTIDES AND USES THEREOF

BACKGROUND

[0001] Antibody-based reagents have accelerated the pace of biological research and development. Antibody compositions represent one of the most important and successful classes of therapeutic and diagnostic agents utilized in the pharmaceutical industry. However, cost, time and efficacy have motivated the development of alternative affinity reagents.

[0002] A variety of non-antibody binding formats have emerged for applications historically served by antibodies. While many successes have been reported for unstructured, linear peptides, more robust results have been achieved by imposing a structural constraint on the peptide sequence – typically through the introduction of a disulfide bond. This constraint affords higher affinity and greater specificity through the more favorable thermodynamics of fixed-shape complementarity and surface presentations of residues (*e.g.,* hydrophobic amino acids) that might otherwise be buried and therefore not target-facing (Ladner, Trends in Biotech. 13(10): 426-430 (1995)). Conversely, formats that contain disulfide bonds are typically prone to improper pairing of cysteines, either intra-domain or inter-domain, that can lead to lower expression, product yield and product quality.

[0003] Structure found in protein subdomains has provided another source of structural constraint. Structures such as fibronectin type III repeats (adnectins), z-proteins (affibodies), knottins, lipocalins (anticalins) and ankyrin repeats (DARPins) have been developed with antibody-like affinities against a variety of different targets (Hey *et al.*, Trends in Biotech. 23(10): 514-422 (2005)). These domains typically contain two features that are analogous to the frameworks and complementarity determining regions (CDRs) found in antibody variable domains: a structural scaffold that imparts high thermodynamic stability and residues or loops that form the basis of the display library's variability.

SUMMARY

[0004] There remains a substantial unmet need for new target-binding compositions, and particularly for such agents containing alternative binding scaffolds (*e.g.,* non-antibody scaffolds). Agents of particular interest may be characterized by, for example, substantially reduced production costs and/or comparable or superior reagent, diagnostic and/or therapeutic properties as compared to antibodies. The present disclosure provides novel target-binding D domain (DD) polypeptides that are based on a non-antibody structural scaffold. In some embodiments, the D domain polypeptides (DDpps) are characterized by high target binding affinity and by a non-antibody structural scaffold. In some

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embodiments, the DDpps are target-specific binding polypeptides that can advantageously be used to target therapeutics (*e.g.,* immune cells) to particular cells (*e.g.,* diseased cells), thereby reducing or eliminating off-target effects. In some embodiments, the provided DDpps are used as therapeutics to bind cells or soluble factors involved in disease.

[0004a] In a first aspect, the present invention provides a protein comprising a D Domain (DD) target binding domain wherein the DD specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168.

[0004b] In a second aspect, the present invention provides a chimeric antigen receptor (CAR) which comprises a target binding domain comprising the protein according to the first aspect.

[0004c] In a third aspect, the present invention provides an isolated nucleic acid encoding the protein according to the first or the CAR according to the second aspect.

[0004d] In a fourth aspect, the present invention provides a vector comprising the nucleic acid of the third aspect, wherein optionally the nucleic acid is operably linked with a nucleotide sequence which regulates the expression of the protein encoded by the nucleic acid, wherein optionally the vector is a lentiviral vector.

[0004e] In a fifth aspect, the present invention provides a host cell comprising the nucleic acid according to the third aspect or the vector according to the fourth aspect, wherein optionally the cell is a T cell or a natural killer (NK) cell.

[0004f] In a sixth aspect, the present invention provides a pharmaceutical composition comprising the protein according to the first aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, or the cell according to the fifth aspect.

[0004g] In a seventh aspect, the present invention provides a kit comprising the protein according to the first aspect or the CAR according to the second aspect.

[0004h] In an eighth aspect, the present invention provides use of the protein according to the first aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, the cell according to the fifth aspect, or the pharmaceutical composition according to the sixth aspect in the manufacture of a medicament for the treatment of cancer.

[0004i] In a ninth aspect, the present invention provides a method of treating cancer in a subject comprising administering a therapeutically effective amount of the protein according to the first

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aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, the cell according to the fifth aspect, or the pharmaceutical composition according to the sixth aspect.

[0004j]In a tenth aspect, the present invention provides use of the protein according to the first aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, the cell according to the fifth aspect, or the pharmaceutical composition according to the sixth aspect in the manufacture of a medicament for the treatment of a B cell associated disorder (e.g., monoclonal gammopathy of undetermined significance (MGUS)).

[0004k] In an eleventh aspect, the present invention provides a method of treating a subject having a B cell associated disorder (e.g., monoclonal gammopathy of undetermined significance (MGUS)), comprising administering to the subject a therapeutically effective amount of the protein according to the first or second aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, the cell according to the fifth aspect, or the pharmaceutical composition according to the sixth aspect.

[0004l]In a twelfth aspect, the present invention provides use of the protein according to the first aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fourth aspect, the cell according to the fifth aspect, or the pharmaceutical composition according to the sixth aspect or the method of the eleventh aspect, in the manufacture of a medicament for the treatment of a disorder of the immune system.

[0004m] In a thirteenth aspect, the present invention provides a method of treating a subject having a disorder of the immune system, comprising administering to the subject a therapeutically effective amount of the protein according to the first aspect, the CAR according to the second aspect, the nucleic acid of the third aspect, the vector of the fifth aspect, the cell according to the sixth aspect, or the pharmaceutical composition according to the seventh aspect.

[0004n] In a fourteenth aspect, the present invention provides use of an immune cell comprising a chimeric antigen receptor (CAR) in the manufacture of a medicament for the treatment of cancer, wherein the CAR comprises: a) a target binding domain comprising a DD that specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168; a transmembrane domain and an intracellular domain; wherein the intracellular domain comprises a signaling domain, and wherein, upon administration to a subject, the target binding

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domain specifically binds to the target of interest expressed by a cancer cell, and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell.

[0004o] In a fifteenth aspect, the present invention provides a method of treating cancer in a subject comprising administering an immune cell comprising a chimeric antigen receptor (CAR) to the subject, wherein the CAR comprises: a) a target binding domain comprising a DD that specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168; b) a transmembrane domain and an intracellular domain; wherein the intracellular domain comprises a signaling domain, and wherein, upon administration to a subject, the target binding domain specifically binds to the target of interest expressed by a cancer cell, and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell.

[0005] In some embodiments, the disclosure provides a protein comprising a D Domain (DD) target binding domain (DDpp) wherein the DD specifically binds a target of interest selected from the group consisting of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), CS1 (SEQ ID NO: 965), HER2 (SEQ ID NO: 967), AFP (SEQ ID NO: 9), AFP p26 (SEQ ID NO: 10), or a fragment thereof. In some embodiments, the DDpp are monovalent or multivalent. In some embodiments, the DDpp are monospecific or multispecific. In further embodiments, the monospecific and multivalent. In other embodiments, the DDpp are multispecific and multivalent. Fusion proteins comprising one or more DD are also provided, as are methods of making and using the fusion proteins. Nucleic acids encoding the DDpps and vectors and host cells containing the nucleic acids are also provided. Non-limiting examples of such uses include, but are not limited to target analysis, and diagnostic and therapeutic applications.

[0006] In additional embodiments, the disclosure provides a protein comprising a D Domain (DD) target binding domain (DDpp) wherein the DD is a member selected from the group consisting of: (a) a DD that specifically binds BCMA (SEQ ID NO: 7) and comprises the amino acid sequence of SEQ ID NO: 11-305, or 306; (b) a DD that specifically binds CD123 (SEQ ID NO: 8) and comprises the amino acid sequence of SEQ ID NO: 307-739, or 740; (c) a DD that specifically binds AFP (SEQ ID NO: 9) or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895; (d) a DD that specifically binds AFP p26 (SEQ

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ID NO: 10) and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895, (e) a DD that specifically binds CS1 (SEQ ID NO: 965) or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 896-909, or 910, and (f) a DD that specifically binds HER2 or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 911-949, or 950. Proteins comprising variants of (a)-(f) that retain the ability to specifically bind their respective targets are also provided. In some embodiments, the DDpp is fused to a heterologous polypeptide. In some embodiments, the heterologous polypeptide comprises a full-length antibody or an antibody fragment. In some embodiments, the DD is fused to: the amino terminus of a full-length antibody heavy chain; the amino terminus of a full-length antibody light chain; the

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carboxyl terminus of a full-length antibody heavy chain; or the carboxyl terminus of a full-length antibody light chain. In other embodiments, the DD is fused to an antibody fragment which is an Fc. In additional embodiments, the heterologous polypeptide comprises a member selected from the group consisting of: (i) a transmembrane domain; (ii) a membrane associating domain; (iii) human serum albumin or a fragment thereof; (iv) AFP or a fragment thereof; (v) AFP p26 or a fragment thereof; (vi) the extracellular domain of a receptor or a fragment thereof; and (vii) the extracellular domain of an intracellular receptor (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the protein contains a heterologous polypeptide that comprises the extracellular domain, or a fragment of an extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8) or CD19 (SEQ ID NO: 3) or CS1 (SEQ ID NO: 965). In some embodiments, the protein contains a heterologous polypeptide that comprises the extracellular domain, or a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96. In some embodiments, the protein contains a heterologous polypeptide that comprises an antigenic portion of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the protein contains a heterologous polypeptide that comprises an antigenic portion of an intracellular protein (*e.g.,* a nuclear protein). In some embodiments, the protein is labeled. In further embodiments, the label is selected from the group consisting of an enzymatic label, a fluorescent label, a luminescent label, a bioluminescent label, and a biotin moiety. In additional embodiments, the protein is conjugated to a therapeutic or cytotoxic agent. In some embodiments, the protein contains a heterologous polypeptide that binds to one or more with major histocompatibility complex (MHC) class I or class II complexes.

[0007] In some embodiments, a DD of the DDpp specifically binds BCMA. In some embodiments, the DD specifically binds a BCMA protein having an amino acid sequence consisting of SEQ ID NO: 7. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that bind BCMA. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to

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different epitopes of BCMA. In some embodiments, the DDpp comprises a DD that specifically binds BCMA and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to BCMA or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds BCMA and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds BCMA and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0008] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds BCMA. In some embodiments, the DDpp fusion protein comprises a DD that specifically binds a BCMA protein having an amino acid sequence consisting of SEQ ID NO: 7. In some embodiments, the DDpp is a fusion protein comprising a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiment, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the BCMA-binding DDpp is an Fc fusion protein.

[0009] In some embodiments, the DDpp fusion protein comprises a BCMA-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp

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fusion protein comprises AFP or AFP p26, or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP (*e.g.,* SEQ ID NO: 9), or a fragment thereof. In other embodiments, the DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof.

[0010] In some embodiments, the DDpp fusion protein is a soluble protein comprising one or more target-binding DDpp and a p29 protein (e.g., having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974). Such fusion proteins containing p29 sequences have been discovered herein to have surprisingly long serum half-life. In some embodiments, the soluble DDpp fusion protein has a plasma half-life *in vivo* of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more. In some embodiments, the soluble fusion protein has an *in vivo* plasma half-life of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more hours 65 hours, or 1-10 hours, 2-10 hours, 4-10 hours, 6-10 hours, or 6-9 hours in a mouse. In some embodiments, the soluble DDpp fusion protein has an *in vivo* plasma half-life of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more hours 65 hours, or 1-10 hours, 2-10 hours, 4-10 hours, 6-10 hours, or 6-9 hours, in a human.

[0011] In some embodiments, the BCMA-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In further embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of CD123 (SEQ ID NO: 8), or a fragment thereof. In some embodiments, the BCMA-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37, CS1, TSLPR, IL7R, and gp96, or a fragment thereof.

[0012] In additional embodiments, the BCMA-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the BCMA-binding DDpp fusion protein comprises a

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fragment of a serum protein (*e.g.,* HSA, AFP, and AFP p26), an extracellular domain of a receptor (*e.g.,* BCMA, CD123, CS1, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0013] In some embodiments, a DD of the DDpp specifically binds CD123. In some embodiments, the DDpp specifically binds a CD123 protein having an amino acid sequence consisting of SEQ ID NO: 8. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that bind CD123. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to different epitopes of CD123. In some embodiments, the DDpp comprises a DD that specifically binds CD123 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to BCMA or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds CD123 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds CD123 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0014] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds CD123. In some embodiments, the DD specifically binds a CD123 protein having an amino acid sequence consisting of SEQ ID NO: 8. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from

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the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN8828. In other embodiments, the CD123-binding DDpp is an Fc fusion protein.

[0015] In some embodiments, the DDpp fusion protein comprises a CD123-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP or AFP p26, or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP (*e.g.,* SEQ ID NO: 9), or a fragment thereof. In other embodiments, the DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof.

[0016] In some embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the CD123-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In further embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8), or a fragment thereof. In further embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37, CS1, TSLPR, IL7R, and gp96, or a fragment thereof.

[0017] In additional embodiments, the CD123-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the CD123-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID

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NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740.

[0018] In some embodiments, the CD123-binding DDpp fusion protein comprises a fragment of a serum protein (*e.g.,* HSA, AFP, and AFP 26), an extracellular domain of a receptor (*e.g.,* BCMA, CS1, CD123, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0019] In some embodiments, a DD of the DDpp specifically binds CS1. In some embodiments, the DDpp specifically binds a CS1 protein having an amino acid sequence consisting of SEQ ID NO: 965. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that bind CS1. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to different epitopes of CS1. In some embodiments, the DDpp comprises a DD that specifically binds CS1 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to BCMA or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds CS1 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds CS1 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0020] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds CS1. In some embodiments, the DD specifically binds a CS1 protein having an amino acid sequence

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consisting of SEQ ID NO: 965. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN8828. In other embodiments, the CS1-binding DDpp is an Fc fusion protein.

[0021] In some embodiments, the DDpp fusion protein comprises a CS1-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP or AFP p26, or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP (*e.g.,* SEQ ID NO: 9), or a fragment thereof. In other embodiments, the DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof.

[0022] In some embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the CS1-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In further embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37, CS-1, TSLPR, IL7R, and gp96, or a fragment thereof.

[0023] In additional embodiments, the CS1-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the CS1-binding DDpp

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fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910.

[0024] In some embodiments, the CS1-binding DDpp fusion protein comprises a fragment of a serum protein (*e.g.,* HSA, AFP, and AFP 26), an extracellular domain of a receptor (*e.g.,* BCMA, CS1, CD123, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0025] In some embodiments, a DD of the DDpp specifically binds AFP or a fragment thereof. In some embodiments, the DDpp specifically binds an AFP protein having an amino acid sequence consisting of SEQ ID NO: 9 or a fragment thereof. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that bind AFP or a fragment thereof. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to different epitopes of AFP or a fragment thereof. In some embodiments, the DDpp comprises a DD that specifically binds AFP or a fragment thereof and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to AFP, an AFP fragment, or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds AFP or a fragment thereof and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

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[0026] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP, or a fragment thereof. In some embodiments, the DD specifically binds an AFP protein having an amino acid sequence consisting of SEQ ID NO: 9, or a fragment thereof. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the fusion protein comprises an AFP-binding DD operably linked to a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882. In some embodiments, the AFP-binding DDpp is an Fc fusion protein.

[0027] In some embodiments, the DDpp fusion protein comprises a DD that specifically binds AFP or an AFP fragment, operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof.

[0028] In some embodiments, the DDpp fusion protein comprises a DD that specifically binds AFP or an AFP fragment and further comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8), or a fragment thereof. In some embodiments, the DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

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[0029] In additional embodiments, the DDpp fusion protein comprises a DD that specifically binds AFP or an AFP fragment and further comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0030] In some embodiments, the AFP-binding DDpp fusion protein comprises a fragment of a serum protein (*e.g.,* HSA), an extracellular domain of a receptor (*e.g.,* BCMA, CS1, CD123, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0031] In some embodiments, a DD of the DDpp specifically binds AFP p26. In some embodiments, the DDpp specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10, or a fragment thereof. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DD specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10, but does not specifically bind AFP having an amino acid sequence consisting of SEQ ID NO: 9. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc.*). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that bind AFP p26. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to different epitopes of AFP p26. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to AFP p26 or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the

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DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0032] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP p26. In some embodiments, the DD specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, a DD of the DDpp fusion protein specifically binds AFP p26 but does not specifically bind AFP having an amino acid sequence consisting of SEQ ID NO: 9. In further embodiments, the DDpp is a fusion protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp is an Fc fusion protein.

[0033] In some embodiments, the DDpp fusion protein comprises a DD that specifically binds AFP p26. In other embodiments, the DDpp fusion protein comprises an AFP p26-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof.

[0034] In some embodiments, the DDpp fusion protein comprises an AFP p26-binding DD and further comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8), or a fragment thereof. In some

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embodiments, the DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0035] In additional embodiments, the DDpp fusion protein comprises an AFP p26-binding DD and further comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the AFP p26-binding DDpp fusion protein comprises a fragment of a serum protein (*e.g.,* HSA), an extracellular domain of a receptor (*e.g.,* BCMA, CS1, CD123, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0036] In some embodiments, a DD of the DDpp specifically binds HER2. In some embodiments, the DDpp specifically binds a HER2 protein having an amino acid sequence consisting of SEQ ID NO: 967. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp comprises multiple target-binding domains (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that bind HER2. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD, that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that bind to different epitopes of HER2. In some embodiments, the DDpp comprises a DD that specifically binds HER2 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that bind to BCMA or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds HER2 and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds HER2 and

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further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0037] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds HER2. In some embodiments, the DD specifically binds a HER2 protein having an amino acid sequence consisting of SEQ ID NO: 967. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp comprises a commercially approved therapeutic antibody. In other embodiments, the HER2-binding DDpp is an Fc fusion protein.

[0038] In some embodiments, the DDpp fusion protein comprises a HER2-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP or AFP p26, or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP (*e.g.,* SEQ ID NO: 9), or a fragment thereof. In other embodiments, the DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof.

[0039] In some embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the HER2-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of

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an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In further embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37, CS-1, TSLPR, IL7R, and gp96, or a fragment thereof.

[0040] In additional embodiments, the HER2-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the HER2-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950.

[0041] In some embodiments, the HER2-binding DDpp fusion protein comprises a fragment of a serum protein (*e.g.,* HSA, AFP, and AFP 26), an extracellular domain of a receptor (*e.g.,* BCMA, CS1, CD123, and CD19), or an intracellular protein (*e.g.,* a nuclear protein), consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues.

[0042] In some embodiments, the DDpp fusion protein comprises a full length antibody. In further embodiments, the DDpp is a fusion protein comprising a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp is a fusion protein comprising a full length antibody, wherein the antibody specifically binds a cancer antigen believed to be expressed by the cancer of the subject to which the DDpp fusion protein is administered.

[0043] In some embodiments, the disclosed DDpp (*e.g.,* a DDpp fusion protein) is labeled. Labels that can be used to label the DDpp include but are not limited to an enzymatic label, a fluorescent label, a luminescent label, and a bioluminescent label. In some embodiments, the label is a biotin moiety. In some embodiments, the label is a streptavidin moiety. In some embodiments, the label is a His-tag or a FLAG tag. In some embodiments, the label is luciferase, green fluorescent protein, red fluorescent protein, or other similar agent.

[0044] In other embodiments, the DDpp fusion protein is attached to a solid support. In some embodiments, the solid support is selected from the group consisting of: a bead, a glass slide, a chip, a gelatin, and an agarose.

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[0045] In some embodiments, the DDpp (*e.g.,* a DDpp fusion protein) is associated with a liposome. In some embodiments, the DDpp is associated with the liposome through covalent binding. In some embodiments, DDpp is a fusion protein. In further embodiments, the DDpp is a CAR. In additional embodiments, the DDpp is associated with the liposome through ionic binding but not covalent binding.

[0046] In some embodiments, the target-binding DDpp is conjugated to a therapeutic or cytotoxic agent (*e.g.,* a chemotherapeutic agent or a radiotherapeutic agent).

[0047] In additional embodiments, the disclosure provides a chimeric antigen receptor (CAR) which comprises a target binding domain comprising a DD disclosed herein (*e.g.,* a DD comprising the amino acid sequence of SEQ ID NO: 11-949, or 950). In some embodiments, the DD binds BCMA and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DD binds CD123 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DD binds AFP and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DD binds AFP p26 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the CAR comprises, a target binding domain, a transmembrane domain, and an intracellular signaling domain. In some embodiments, the CAR transmembrane domain comprises a 41BB or CD28 transmembrane domain. In some embodiments the CAR comprises an intracellular signaling domain selected from the group consisting of a domain of a human T cell receptor alpha, beta, or zeta chain; a human 41BB domain; a human CD28 domain; and any combination thereof. In some embodiments, the CAR intracellular signaling domain comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4lBB, OX40, CD30, CD40, PD1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, and any combination thereof. In some embodiments the CAR further comprises a second target binding domain having the same or a different target than the DD target binding domain. In some embodiments, the CAR is expressed in an immune cell. In some embodiments, the immune cell is a T cell (CAR-T cell) or a natural killer (NK) cell (CAR-NK cell). In some embodiments, the CAR is associated with a liposome.

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[0048] In some embodiments, the CAR comprises 2, 3, 4, 5, or more than 5, DD and/or other binding domains (*e.g.,* scFv) that specifically bind a target of interest (*e.g.,* BCMA or CD123) expressed on the surface of the cancer cell. In additional embodiments, the CAR comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically bind a second, different target of interest, expressed on the surface of the cancer cell. In additional embodiments, the administered CAR further comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically binds a second, different target of interest, expressed by a second, different cancer cell or a vascular endothelial cell.

[0049] Nucleic acids encoding the disclosed DDpp (*e.g.*, DDpp fusion proteins) are also provided. Additionally provided are vectors (*e.g.,* plasmids, viral vectors, and non-viral vectors) containing nucleic acids encoding the DDpp (*e.g.,* DDpp fusion proteins) and host cells containing the nucleic acids and vectors. In some embodiments, the vector comprises a nucleotide sequence which regulates the expression of the polypeptide encoded by the nucleic acid molecule. In further embodiments, the vector comprises an inducible promoter sequence. In additional embodiments, the vector includes one or more additional standard components for expression of a protein encoded a nucleic acid (*e.g.,* promoters, packaging components, *etc.*). In some embodiments, the vector is a lentiviral vector.

[0050] The disclosure also provides host cells that comprise the nucleic acid molecules encoding a target-binding DDpp disclosed herein. In some embodiments, the host cells (*e.g.,* cells of a cell line) are engineered to express a protein containing a DD disclosed herein (*e.g.,* a DD having the amino acid sequence of SEQ ID NO: 11-949, or 950). In some embodiments, the expression of the DDpp by the host cells allows production and isolation of the DDpp. In some embodiments, the expression results in the DDpp being expressed on the surface and/or integral to the membrane of the host cells. In some embodiments, the host cell is a viral particle, or a bacterial, yeast, fungal, or plant cell. In other embodiments, the host cell is a mammalian cell. In a further embodiment, the mammalian cell is an immune cell. In one embodiment, the host cell is a human immune cell. In some embodiments, the human immune cell is a T cell. In other embodiments, the human immune cell is a natural killer (NK) cell. In some embodiments, the human immune cell displays the DDpp on its cell surface.

[0051] The disclosure further provides a host cell expressing a protein comprising a DD disclosed herein. In some embodiments, the host cell expresses a chimeric antigen receptor (CAR) comprising a DD disclosed herein. In some embodiments, the CAR comprises a target binding domain that

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comprises a DD that comprising an amino acid sequence selected from SEQ ID NO: 11-305, and 306; SEQ ID NO: 307-739, and 740; SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950 and a transmembrane domain. In some embodiments, the CAR further comprise an intracellular domain (comprising a signaling domain). In some embodiments, the CAR immune cell is a T cell. In some embodiments, the CAR immune cell is a NK cell. In some embodiments, the CAR immune cell is not a T cell or an NK cell. In some embodiments, the host cell is an immune cell that further comprises a second CAR polypeptide having a DD or other binding domain (*e.g.,* scFv) that specifically binds the same or a different target (*e.g.,* a different epitope of the same target, or a second target of interest) expressed by the cancer cell) as the first CAR expressed by the host immune cell.

[0052] Also provided are mammalian cells that generate membrane-bound virus-like particles (VLPs), wherein the mammalian cell is engineered to express a fusion protein comprising D domain polypeptide (DDpp) fused to a chimeric antigen receptor (CAR), the fusion protein being expressed on the generated VLPs (*e.g.,* as transmembrane proteins). Depending on the embodiments, the VLPs produced by the mammalian cells are suitable for use as immunogens for antibody generation.

[0053] Pharmaceutical compositions containing a protein comprising a DD disclosed herein, nucleic acids encoding the proteins, vectors containing the nucleic acids, and host cells containing the nucleic acids and or vectors are also provided. As are kits containing one or more of the disclosed target-binding DDpps (*e.g.,* DDpp fusion proteins such as DD-Fc and DD-CAR), nucleic acid molecules, vectors, and host cells (*e.g.,* a therapeutic kit, a diagnostic kit, a kit for research use, *etc.*).

[0054] DDpp provided herein possess activities that include but are not limited to the ability to specifically bind a target of interest (*e.g.,* a therapeutic target and/or diagnostic target such as BCMA, CD123, CS1, HER2, AFP, and AFP p26, a peptide tag, and a serum protein such as alpha-fetoprotein, human serum albumin (HSA) or an immunoglobulin) *in vitro* or *in vivo* and the ability to serve as a reactive site for linking or associating a protein such as a DDpp fusion protein with one or more additional moieties (*e.g.,* a solid support), and/or other modifications. The DDpp provided herein can also possess additional desirable properties and/or functionalities useful in manufacturing, formulation and biological, diagnostic, and therapeutic applications.

[0055] In some embodiments, the DDpp is used to bind, detect, and/or quantitate, a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) in a sample containing the target. In one

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embodiment, the disclosure provides a method for detecting a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) in a sample, comprising: (a) contacting the sample with a DDpp containing a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, that specifically binds the target, under conditions suitable for specific binding of the DDpp to the target, to form a target/DDpp complex, and (b) detecting the presence of the complex and/or captured target. In some embodiments, the DDpp is immobilized on a solid support. In some embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305 or 306, and the DDpp us used to bind, detect, and/or quantitate, BCMA or a fusion protein comprising BCMA in a sample. In some embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739 or 740, and the DDpp us used to bind, detect, and/or quantitate, CD123 or a fusion protein comprising CD123 in a sample. In some embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874 or 886-895, and the DDpp us used to bind, detect, and/or quantitate, AFP p26, or a fusion protein comprising AFP p26 in a sample. In some embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909 or 910, and the DDpp us used to bind, detect, and/or quantitate, CS1, or a fusion protein comprising CS1 in a sample. In some embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949 or 950, and the DDpp us used to bind, detect, and/or quantitate, HER2, or a fusion protein comprising HER2 in a sample.

[0056] Also provided is a method for quantifying a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) in a sample containing the target, comprising: (a) contacting the sample with a DDpp containing a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, that specifically binds the target and that is immobilized on a solid support, under conditions suitable for specific binding of the DDpp to the target, to form a target/DDpp complex and (b) detecting the presence of the target/DDpp complex and/or captured target, wherein quantitative detection of the product indicates, or is otherwise able to be correlated with, the quantity of the target or a fusion protein containing the target in the sample.

[0057] In additional embodiments, the provided DDpps are used in protein analytics. In some embodiments, the DDpps are conjugated to a detectable agent and/or tag. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305,

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and 306; SEQ ID NO: 307-739, and 740; SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306; SEQ ID NO: 307-739, and 740; or SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp is conjugated to a detectable agent. In one embodiment, the detectable agent comprises a chromogen. In another embodiment, the detectable agent comprises a fluorescent dye. In and additional embodiment, the detectable agent comprises a radionuclide. In some embodiments, the DDpp is conjugated to the detectable agent by covalent binding. In some embodiments, the DDpp is a fusion protein. In additional embodiments, the DDpp is multimeric. In additional embodiments, the DDpp is conjugated to a tag. In some embodiments, the tag is a member selected from the group consisting of: a polyhistidyl tag, a myc tag, and a FLAG tag. In further embodiments, the DDpp is conjugated to a combination of tags (*e.g.,* a polyhistidyl tag and a FLAG tag). In some embodiments, the DDpp is conjugated to the tag(s) by covalent binding. In some embodiments, the DDpp is a fusion protein. In some embodiments, the DDpp is multimeric.

[0058] In additional embodiments, the DDpp is conjugated to a solid support or tag. In some embodiments, the solid support is a chromatography bead, resin, glass slide, chip, gelatin, or agarose.

[0059] Methods of using DDpp in diagnostic and therapeutic applications are also provided. In one embodiment, the disclosure provides a method of treating a disease or disorder comprising administering a therapeutically effective amount of a DDpp (*e.g.,* a DDpp fusion protein) that specifically binds a therapeutic target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) to a subject in need thereof. In some embodiments, the disease or disorder is cancer, a B cell malignancy, a disease or disorder of the immune system, or an infection. Methods of treating a disease or disorder that comprises co-administering an additional therapeutic agent along with a disclosed DDpp are also provided. In some embodiments, the disease or disorder is multiple myeloma. In some embodiments, the disease or disorder is breast cancer or ovarian cancer.

[0060] The target binding DDpps disclosed herein have uses that include diagnostic and therapeutic applications. In some embodiments, the DDpps are useful in a therapeutic context, *e.g.,* for treatment and/or diagnosis of a disease, such as a cancer (*e.g.,* a solid or hematologic malignancy).

[0061] In some embodiments, the disclosure provides a method of treating a subject having cancer, the method comprising: administering to the subject a therapeutically effective amount of: a protein

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(*i.e.,* DDpp) containing a DD disclosed herein (*e.g.,* disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, the DDpp comprises a DD amino acid sequence that specifically binds BCMA. In some embodiments, a DD of the DDpp specifically binds BCMA having an amino acid sequence consisting of SEQ ID NO: 7. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp comprises a DD amino acid sequence that specifically binds CD123. In some embodiments, a DD of the DDpp specifically binds CD123 having an amino acid sequence consisting of SEQ ID NO: 8. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp comprises a DD amino acid sequence that specifically binds CS1. In some embodiments, a DD of the DDpp specifically binds CS1 having an amino acid sequence consisting of SEQ ID NO: 965. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp comprises a DD amino acid sequence that specifically binds HER2. In some embodiments, a DD of the DDpp specifically binds HER2 having an amino acid sequence consisting of SEQ ID NO: 967. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp comprises a DD amino acid sequence that specifically binds AFP. In some embodiments, a DD of the DDpp specifically binds AFP having an amino acid sequence consisting of SEQ ID NO: 9. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874 and 886-895. In some embodiments, the DDpp specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874 and 886-895. In some embodiments, a DD of the DDpp specifically binds AFP p26 but does not specifically bind AFP having an amino acid sequence consisting of SEQ ID NO: 9. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874 and 886-895.

[0062] In some embodiments, the disclosure provides a method of treating a subject having a B cell malignancy, said method comprising: administering to the subject an effective amount of: a protein containing a DD disclosed herein (*e.g.,* disclosed in Table 1, or having the amino acid sequence of

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SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, the B cell malignancy is selected from the group consisting of: a lymphoma (*e.g.,* a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, and a myeloma. In some embodiments, the B cell malignancy is selected from the group consisting of: acute lymphocytic leukemia, chronic lymphocytic leukemia, follicular lymphoma, mantle cell lymphoma, and diffuse large B-cell lymphoma, plasmacytoma, and multiple myeloma.

[0063] In some embodiments, the disclosure provides a method of treating a subject having cancer, the method comprising: administering to the subject an immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises: a target binding domain comprising a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, wherein the polypeptide specifically binds a target of interest and a transmembrane domain. In further embodiments, the target of interest is expressed by a cancer cell. In some embodiments, the DD specifically binds BCMA having an amino acid sequence consisting of SEQ ID NO: 7. In further embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DD specifically binds CD123 having an amino acid sequence consisting of SEQ ID NO: 8. In further embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DD specifically binds CS1 having an amino acid sequence consisting of SEQ ID NO: 965. In further embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DD specifically binds HER2 having an amino acid sequence consisting of SEQ ID NO: 967. In further embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DD specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10. In further embodiments, the DD comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the CAR comprises an intracellular domain. In further embodiments, the intracellular domain comprises a signaling domain, wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest expressed by a cancer cell (*e.g.,* BCMA and CD123), and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that

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result in cytotoxic effects on the cancer cell. In some embodiments, the immune cell is a T cell. In other embodiments, the immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject. In some embodiments, the immune cell administration is intravenous. In some embodiments, a combination of different CAR immune cell types is administered intravenously to the subject. In some embodiments, the cancer is multiple myeloma. In some embodiments, the cancer is breast cancer or ovarian cancer.

[0064] In some embodiments, the disclosure provides a method of treating a subject having a B cell malignancy, said method comprising: administering to the subject an immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises: a target binding domain comprising a polypeptide having an amino acid sequence comprising, the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, wherein the polypeptide specifically binds a target of interest expressed by a cancer cell, a transmembrane domain and an intracellular domain. In some embodiments, the target binding domain specifically binds BCMA having an amino acid sequence consisting of SEQ ID NO: 7. In further embodiments, the target binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the target binding domain specifically binds CD123 having an amino acid sequence consisting of SEQ ID NO: 8. In further embodiments, the target binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the target binding domain specifically binds CS1 having an amino acid sequence consisting of SEQ ID NO: 965. In further embodiments, the target binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the CAR comprises an intracellular domain. In further embodiments, the intracellular domain comprises a signaling domain, wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest expressed by a malignant B cell (*e.g.,* BCMA, CS1, and CD123), and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the malignant B cancer cell. In some embodiments, the B cell malignancy is selected from the group consisting of: a lymphoma (*e.g.,* a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, and a myeloma. In some embodiments, the B cell malignancy is selected from the group

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consisting of: acute lymphocytic leukemia, chronic lymphocytic leukemia, follicular lymphoma, mantle cell lymphoma, diffuse large B-cell lymphoma, plasmacytoma and multiple myeloma. In some embodiments, the B cell malignancy is multiple myeloma. In some embodiments, the immune cell is a T cell. In other embodiments, the immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject. In some embodiments, the immune cell administration is intravenous. In some embodiments, a combination of different CAR immune cell types is administered intravenously to the subject.

[0065] In some embodiments, the disclosure provides a method of treating a subject having a B cell associated disorder, said method comprising: administering to the subject an effective amount of: a protein containing a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector.

[0066] In some embodiments, the disclosure provides a method of treating a subject having a disorder of the immune system, said method comprising: administering to the subject an effective amount of: a protein comprising a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, the disorder of the immune system is an autoimmune disease such as rheumatoid arthritis.

[0067] In some embodiments, the disclosure provides for the use of a composition for treating cancer, wherein the composition comprises: a protein containing a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, the cancer is a B cell malignancy. In some embodiments, the B cell malignancy is selected from the group consisting of: a lymphoma (*e.g.,* a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, and a myeloma. In some embodiments, the B cell malignancy is selected from the group consisting of: acute lymphocytic leukemia, chronic lymphocytic leukemia, follicular lymphoma, mantle cell lymphoma, diffuse large

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B-cell lymphoma, plasmacytoma, and multiple myeloma. In some embodiments, the cancer is multiple myeloma. In some embodiments, the cancer is breast cancer or ovarian cancer.

[0068] In some embodiments, the disclosure provides for the use of a composition for treating a B cell malignancy, wherein the composition comprises: a protein containing a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, the B cell malignancy is selected from the group consisting of: a lymphoma (*e.g.,* a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, and a myeloma. In some embodiments, the B cell malignancy is selected from the group consisting of: acute lymphocytic leukemia, chronic lymphocytic leukemia, follicular lymphoma, mantle cell lymphoma, diffuse large B-cell lymphoma, plasmacytoma and multiple myeloma**.** In some embodiments, the B cell malignancy is multiple myeloma**.**

[0069] In some embodiments, the disclosure provides for the use of a composition for the treatment of a B cell associated disorder, wherein the composition comprises: a protein containing a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector.

[0070] In some embodiments, the disclosure provides for the use of a composition for the treatment of a disorder of the immune system, wherein the composition comprises: a protein containing a DD disclosed herein (*e.g.,* a DD having an amino acid sequence disclosed in Table 1, or having the amino acid sequence of SEQ ID NO: 11-949, or 950); a nucleic acid encoding the protein; a vector containing the nucleic acid; or a host cell containing the nucleic acid or vector. In some embodiments, disorder of the immune system is an autoimmune disease such as rheumatoid arthritis.

[0071] In additional embodiments, the disclosure provides for use of an immune cell comprising a chimeric antigen receptor (CAR) for the treatment of cancer, wherein the CAR comprises: a target binding domain comprising a polypeptide having an amino acid sequence comprising, the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, wherein the polypeptide specifically binds a target of interest expressed by a cancer cell, a transmembrane domain and an intracellular domain, wherein the intracellular domain comprises a signaling domain, wherein, upon administration to a subject having cancer, the target binding domain

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specifically binds to the target of interest expressed by a cancer cell, and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell. In some embodiments, the immune cell is a T cell or a natural killer (NK) cell. In some embodiments, the immune cell is a T cell. In some embodiments, the immune cell is a natural killer (NK) cell. In some embodiments, the immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* T cells and NK cells) is used. In some embodiments, the cancer is multiple myeloma. In some embodiments, the cancer is breast cancer or ovarian cancer.

[0072] In additional embodiments, the disclosure provides for use of an immune cell comprising a chimeric antigen receptor (CAR) for the treatment of a B cell malignancy, wherein the CAR comprises: a target binding domain comprising a polypeptide having an amino acid sequence comprising, the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, or 950, wherein the polypeptide specifically binds a target of interest (e.g., a target expressed by a malignant B cell, such as BCMA, CS1, or CD123, wherein the target binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-306, 307-740, and 896-910), a transmembrane domain and an intracellular domain, wherein the intracellular domain comprises a signaling domain, wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest expressed by a malignant B cell, and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the malignant B cell. In some embodiments, the immune cell is a T cell or a natural killer (NK) cell. In some embodiments, the immune cell is a T cell. In some embodiments, the immune cell is a natural killer (NK) cell. In some embodiments, the immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* T cells and NK cells) is used. In some embodiments, the B cell malignancy is multiple myeloma**.**

[0073] In additional embodiments, the disclosure provides for use of an immune cell comprising a chimeric antigen receptor (CAR) for the treatment of a disorder of the immune system, wherein the CAR comprises: a target binding domain comprising a polypeptide having an amino acid sequence comprising, the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, wherein the polypeptide specifically binds a target of interest expressed by the immune cell to be targeted, a transmembrane domain and an intracellular domain, wherein the

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intracellular domain comprises a signaling domain, wherein, upon administration to a subject having the disorder of the immune system, the target binding domain specifically binds to the target of interest expressed by the targeted immune cell, and wherein the binding of the target of interest induces the recombinant immune cell to generate cytotoxic signals that result in cytotoxic effects on the targeted immune cell. In some embodiments, the immune cell is a T cell or a natural killer (NK) cell. In some embodiments, the immune cell is not a T cell or an NK cell. In some embodiments, the immune cell is a natural killer (NK) cell. In some embodiments, the immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* T cells and NK cells) is used.

[0074] The methods summarized above and/or set forth herein describe certain actions taken by a practitioner; however, it should be understood that they can also include the instruction of those actions by another party. Thus, actions such as "administering a T cell comprising a target specific binding polypeptide-CAR" include "instructing the administration of a T cell comprising a target specific binding polypeptide-CAR."

[0075] In some embodiments, the disclosure provides:

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[1.] A protein comprising a D Domain (DD) target binding domain wherein the DD is a member selected from the group consisting of:

(a) a DD that specifically binds BCMA and comprises the amino acid sequence of SEQ ID NO: 11-305, or 306;

(b) a DD that specifically binds CD123 and comprises the amino acid sequence of SEQ ID NO: 307-739, or 740;

(c) a DD that specifically binds AFP and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895;

(d) a DD that specifically binds AFP p26 and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895;

(e) a DD that specifically binds CS1 and comprises the amino acid sequence of SEQ ID NO: 896-909, or 910; and

(f) a DD that specifically binds HER2 and comprises the amino acid sequence of SEQ ID NO: 911-949, or 950;

[2.] the protein of [1], wherein the DD is fused to a heterologous polypeptide;

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[3.] the protein of [2], wherein the heterologous polypeptide comprises a full-length antibody or an antibody fragment;

[4.] the protein of [2], wherein the heterologous polypeptide comprises a member selected from the group consisting of;

(a) a transmembrane domain;

(b) a membrane associating domain;

(c) human serum albumin or a fragment thereof;

(d) AFP or a fragment thereof;

(e) AFP p26 or a fragment thereof; and

(f) the extracellular domain of a receptor or a fragment thereof;

[5.] the protein of [3], wherein the DD is fused to: the amino terminus of a full-length antibody heavy chain; the amino terminus of a full-length antibody light chain; the carboxyl terminus of a full-length antibody heavy chain; or the carboxyl terminus of a full-length antibody light chain;

[6.] the protein of [3], wherein the heterologous polypeptide is an Fc;

[7.] the protein of [2], wherein the heterologous polypeptide comprises the extracellular domain, or a fragment of an extracellular domain, of a receptor selected from the group consisting of: BCMA, CD123, CS1, and CD19;

[8.] the protein according to any one of [1]-[7], which is labeled;

[9.] the protein according to [9, wherein the label is selected from the group consisting of an enzymatic label, a fluorescent label, a luminescent label, a bioluminescent label and a biotin moiety;

[10.] a protein according to any one of [1]-[10], which conjugated to a therapeutic or cytotoxic agent;

[11.] a chimeric antigen receptor (CAR) which comprises a target binding domain comprising the protein according to any one of [1]-[5];

[12.] the CAR of [11], which comprises, a target binding domain, a transmembrane domain, and an intracellular signaling domain;

[13.] the CAR of [11] or [12], wherein transmembrane domain comprises a 41BB or CD28 transmembrane domain;

[14.] the CAR according to any one of [11]-[13], wherein the intracellular signaling domain is selected from the group consisting of a domain of a human T cell receptor alpha, beta, or zeta chain; a human 41BB domain; a human CD28 domain; and any combination thereof;

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[15.] a CAR according to any one of [11]-[14], wherein the intracellular signaling domain comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4lBB, OX40, CD30, CD40, PD1, lymphocyte function-associated antigen- 1 (LFA-1), CD2, CD7, LIGHT, NKG2C, NKG2D, B7-H3, a ligand that specifically binds with CD83, and any combination thereof;

[16.] a protein according to any on of [1]-[15], which further comprises a second target binding domain having the same or a different target than the DD target binding domain;

[17.] an isolated nucleic acid encoding the protein according to any one of [1]-[16];

[18.] a vector comprising the nucleic acid of [17];

[19.] the vector of [18], wherein the nucleic acid is operably linked with a nucleotide sequence which regulates the expression of the protein encoded by the nucleic acid;

[20.] the vector of [19] which is a lentiviral vector;

[21.] a host cell comprising the nucleic acid acording to [17] or the vector according to any one of [18-21;

[22.] a cell engineered to express the protein according to any one of [1]-[16];

[23.] a cell according to [21] or [22], wherein the cell is a T cell or a natural killer (NK) cell;

[24.] a pharmaceutical composition comprising the protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], or the cell according to any one of [21]-[23];

[25.] a kit comprising the protein according to any one of [1]-[16];

[26.] a method of treating a subject having cancer, the method comprising:

administering to the subject an effective amount of a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], the cell according to any one of [21]-[23], or the pharmaceutical composition according to [24];

[26.] the method of [26], wherein the cancer is a B cell malignancy selected from the group consisting of: a lymphoma (e.g., a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, a plasmacytoma and a myeloma;

[28.] the method of [27], wherein the B cell malignancy is selected from the group consisting of: chronic lymphocytic leukaemia, follicular lymphoma, mantle cell lymphoma, and diffuse large B-cell lymphoma, plasmacytoma and multiple myeloma;

[27.] the method of [26], wherein the cancer is a myeloid malignancy selected from the group consisting of: chronic myeloid leukemia, acute myeloid leukemia, leukemia, plasmacytoma and myeloma;

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[29.] a method of treating a subject having a B cell associated disorder (e.g., monoclonal gammapathy of determined significance), (MGUS)), the method comprising: administering to the subject an effective amount of a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], the cell according to any one of [21]-[23], or the pharmaceutical composition according to [24];

[30.] a method of treating a subject having a disorder of the immune system, the method comprising: administering to the subject an effective amount of a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], the cell according to any one of [21]-[23], or the pharmaceutical composition according to [24];

[31.] the method of [30], wherein the disorder of the immune system is an autoimmune disease such as rheumatoid arthritis;

[32.] a method of treating a subject having cancer, the method comprising:

administering an immune cell comprising a chimeric antigen receptor (CAR) to the subject, wherein the CAR comprises: a target binding domain comprising a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, optionally wherein the DD specifically binds a target of interest expressed by a cancer cell;

a transmembrane domain and an intracellular domain; wherein the intracellular domain comprises a signaling domain, and wherein, upon administration to a subject, the target binding domain specifically binds to the target of interest expressed by a cancer cell, and

wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell;

[33.] the method of [32], wherein the immune cell is a T cell;

[34.] the method of [32], wherein the immune cell is a NK cell;

[35.] the method of [32] wherein the administration is intravenous;

[36.] use of a composition for treating cancer, wherein the composition comprises: a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], or the cell according to any one of [21]-[23];

[37.] the use according to [36], wherein the cancer is a B cell malignancy;

[38.] the use according to [37], wherein the B cell malignancy is selected from the group consisting of: a lymphoma (e.g., a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, and a myeloma;

[39.] the use according to [38], wherein the B cell malignancy wherein the B cell malignancy is selected from the group consisting of: chronic lymphocytic leukaemia, follicular lymphoma, mantle cell lymphoma, and diffuse large B-cell lymphoma;

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[40.] use of a composition for the treatment of a B cell associated disorder, wherein the composition comprises: a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], the cell according to any one of [21]-[23], or the pharmaceutical composition according to [24]

[41.] use of a composition for the treatment of a disorder of the immune system, wherein the composition comprises: a protein according to any one of [1]-[16], the nucleic acid of [17], the vector of [18], [19] or [20], the cell according to any one of [21]-[23], or the pharmaceutical composition according to [24]

[42.] the use according to [41], wherein the disorder of the immune system is an autoimmune disease such as rheumatoid arthritis;

[43.] use of an immune cell comprising a chimeric antigen receptor (CAR) for the treatment of cancer, wherein the CAR comprises: a target binding domain comprising a DD comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, or 950, and optionally wherein the target binding domain specifically binds a target of interest expressed by a cancer cell,

a transmembrane domain and an intracellular domain, wherein the intracellular domain comprises a signaling domain, wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest expressed by a cancer cell, and

wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell;

[44.] the use according to [43], wherein the immune cell is a T cell or a natural killer (NK) cell.

BRIEF DESCRIPTION OF THE DRAWINGS

[0076] FIGS. 1A-1B, DDpp impart novel binding specificities to another molecule (*e.g.,* a full length antibody) as part of a fusion protein (*e.g.,* an antibody-DDpp fusion protein. DDpp-antibody fusions were created using an RSV-specific antibody (SYN) and either the target-less peptide of SEQ ID NO: 1 (DD) or the CD137-specific DDpp (bb10) (SEQ ID NO: 876). The DDpp are fused to the N-terminus (bb10-SYN and DD-SYN) or the C-terminus (SYN-bb10 and SYN-DD). All four antibody fusions bind to RSV (FIG. 1A). However, the fusion of bb10 to either the N-terminus (bb10-SYN) or C-terminus (SYN-bb10) of the antibody heavy chain imparts a novel CD137 binding specificity to an otherwise mono-specific antibody (FIG. 1B).

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[0077] FIGS. 2A-2F. CD123-DDpp-CAR T cells produce cytokines in response to target binding. FIGS. 2A and 2B show data related to the production of interferon gamma (IFNγ) by T cells expressing CD123-DDpp-CARs when co-cultured with CD123 negative tumor K562 and CD123 positive tumor BDCM, respectively. FIGS. 2C and 2D depicts similar data measuring the production of interleukin-2 (IL2) by CD123-DDpp-CAR T cells when co-cultured with K562 and BDCM, respectively. FIG. 2E and 2F show similar target-driven cytokine (IFNγ, IL2) by PD-L1-DDppCAR T cells when co-cultured with PDL1 expressing tumor cells (SUDHL-1).

[0078] FIGS. 3A-3B. T cells expressing DDpp-CARs do not undergo excessive exhaustion to a greater degree than scFv. FIG. 3A depicts expression of three exhaustion markers (LAG3, PD1, and TIM3) on T cells expressing various DDpp-CARs at similar levels of the expression of those markers on scFv-CAR 32716 (32716 (Du X1, Ho M, Pastan I. 2007. New immunotoxins targeting CD123, a stem cell antigen on acute myeloid leukemia cells. J Immunother. 30(6): 607-13). FIG. 3B shows flow cytometry data depicting similar exhaustion marker expression on DDpp-CAR T cells (expressing CD123 targeting cg06 DDpp) as compared to a CAR T cell expressing CD123-specific scFv (32716).

[0079] FIGS. 4A-4C. T cells expressing DDpp-CARs (CD123-targeting) undergo degranulation when co-cultured with target-expressing tumor cells (BDCM). FIGS 4A-4C show results obtained by culturing T cells alone (FIG. 4A) or in the presence of K562 (FIG. 4B) or BDCM (FIG. 4C) cells.

[0080] FIGS. 5A-5D. T cells expressing DDpp-CARs mediate target-specific tumor cytotoxicity. FIG. 5A shows data related to CD123-DDpp-CAR T cells kill percentage of K562 tumor cells that are negative for CD123. FIG. 5B shows kill percentages when the CD123 targeting DDpp-CAR T cells are co-cultured with CD123 positive BDCM cells. The data from FIGS. 5A and 5B were generated using T cells from a first donor blood sample. FIGS. 5C and 5D show similar data from T cells collected from a second donor.

[0081] FIGS. 6A-6E. Bi-specific DDpp-CAR T cells. FIG. 6A shows the percentage of T cells expressing CD123 targeting DDpp-CARs (cg06). FIG. 6B shows the percentage of T cells expressing PDL1 targeting DDpp-CARs (pb04). FIG. 6C shows the percentage of T cells expressing bi-specific CD123-PDL1 targeting DDpp-CARs (expressed with cg06 DDpp distal to the T cell membrane versus the pb04 DDpp). FIG. 6D shows the percentage of T cells expressing bi-specific PDL1-CD123 targeting DDpp-CARs (expressed with pb04 DDpp distal to the T cell membrane versus the cg06 DDpp). FIG. 6E depicts data related to the increased intracellular signaling of bispecific DDpp.

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[0082] FIGS. 7A and 7B show that dual-binding domain adaptor proteins drive enhanced signaling by CAR-expressing Jurkat NFAT-Luciferase reporter cells over single-binding domain adaptor proteins. In FIG. 7A, 50,000 reporter cells previously transduced with an AFP (p26 domain)-binding CAR (af03) were cultured for 5 hours in the presence of the CD123-specific Cg06-adaptor (Cg06-p26) or the Cg06-dual adaptor protein (Cg06-p26-Cg06 in the presence of 50,000 $CD123^+$ MOLM13 or CD123-deficient MOLM13 cells, then assessed for luciferase activity. CD123 deficient cells were generated using CRISPR/Cas9 genetic engineering technology. In FIG. 7B, 50,000 reporter cells previously transduced with an AFP (p26 domain)-binding CAR (af03) were cultured for 5 hours in the presence of the BCMA-specific Bc40-adaptor (Bc40-p26) or the Bc40-dual adaptor protein (Bc40-p26-Bc40) in the presence or absence of 50,000 $BCMA^+$ U266 cells, then assessed for luciferase activity.

[0083] FIG. 8. The BCMA-targeting DDpp-CAR comprising the bc40 DDpp (SEQ-ID NO: 164) eradicates the BCMA-expressing tumor, U226 in a mouse model of B cell cancer.

DETAILED DESCRIPTION

[0084] The section headings used herein are for organizational purposes only and are not to be construed as in any way limiting of the subject matter described.

Definition of Terms

[0085] It is understood that wherever embodiments, are described herein with the language "comprising" otherwise analogous embodiments, described in terms of "consisting of" and/or "consisting essentially of" are also provided. However, when used in the claims as transitional phrases, each should be interpreted separately and in the appropriate legal and factual context (*e.g.,* "comprising" is considered more of an open-ended phrase while "consisting of" is more exclusive and "consisting essentially of" achieves a middle ground).

[0086] As used herein, the singular form "a", "an", and "the" includes plural references unless indicated otherwise.

[0087] The term "and/or" as used in a phrase such as "A and/or B" herein is intended to include both A and B; A or B; A (alone); and B (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

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[0088] The terms "protein" and "polypeptide" are used interchangeably herein to refer to a biological polymer comprising units derived from amino acids linked via peptide bonds; a protein can be composed of two or more polypeptide chains.

[0089] The terms "antibody" or "immunoglobulin," as used interchangeably herein, include full-length antibodies and antibody fragments including any functional domain of an antibody such as an antigen-binding fragment or single chains thereof, an effector domain, salvage receptor binding epitope, or portion thereof. A typical antibody comprises at least two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2, and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region is comprised of one domain, Cl. The VH and VL regions can be further subdivided into regions of hypervariablity, termed Complementarity Determining Regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FW). Each VH and VL is composed of three CDRs and four FWs, arranged from amino-terminus to carboxyl-terminus in the following order: FW1, CDR1, FW2, CDR2, FW3, CDR3, FW4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies can mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.,* effector cells) and the first component (C1q) of the classical complement system. Examples of antibodies of the present disclosure include typical antibodies, scFvs, and combinations thereof where, for example, a DDpp is covalently linked (*e.g.,* via peptide bonds or via a chemical linker) to the N-terminus of either the heavy chain and/or the light chain of a typical whole (full-length) antibody, or intercalated in the H chain and/or the L chain of a full-length antibody.

[0090] The term "antibody fragment" refers to a portion of an intact antibody and refers to any functional domain of an antibody such as an antigen-binding fragment or single chains thereof, an effector domain or a portion thereof, and a salvage receptor binding epitope or a portion thereof. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, and Fv fragments, linear antibodies, single chain antibodies, and multi-specific antibodies formed from antibody fragments. "Antibody fragment" as used herein comprises an antigen-binding site or epitope binding site. In one embodiment, the DDpp fusion protein comprises an effector domain or portion thereof. In

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one embodiment, the DDpp fusion protein comprises a salvage receptor binding epitope, or portion thereof.

[0091] As used herein, the term, "Fc region" or simply "Fc" is understood to mean the carboxyl-terminal portion of an immunoglobulin chain constant region, preferably an immunoglobulin heavy chain constant region, or a portion thereof. For example, an immunoglobulin Fc region may comprise (1) a CH1 domain, a CH2 domain, and a CH3 domain, (2) a CH1 domain and a CH2 domain, (3) a CH1 domain and a CH3 domain, 4) a CH2 domain and a CH3 domain, or (5) a combination of two or more domains and an immunoglobulin hinge region. Thus, in various embodiments, Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM Fc may include the J chain. For IgG, Fc comprises immunoglobulin domains Cγ2 and Cγ3 and the hinge between Cγl and Cγ2. In a preferred embodiment the immunoglobulin Fc region comprises at least an immunoglobulin hinge region a CH2 domain and a CH3 domain, and preferably lacks the CH1 domain. In one embodiment, the class of immunoglobulin from which the heavy chain constant region is derived is IgG (Igγ) (γ subclasses 1, 2, 3, or 4). Other classes of immunoglobulin, IgA (Igα), IgD (Igδ), IgE (Igε) and IgM (Igμ), may be used. Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to comprise residues C226 or p260 to its carboxyl-terminus, wherein the numbering is according to the EU index as set forth in Kabat (Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, NIH, Bethesda, Md. (1991)). Fc may refer to this region in isolation, or this region in the context of a full-length antibody, antibody fragment, or Fc fusion protein. Polymorphisms have been observed at a number of different Fc positions, including but not limited to positions 270, 272, 312, 315, 356, and 358 as numbered by the EU index, and thus slight differences between the presented sequence and sequences in the prior art may exist. The choice of appropriate immunoglobulin heavy chain constant region is discussed in detail in U.S. Pat. Nos. 5,541,087, and 5,726,044, each of which is herein incorporated by reference in its entirety. The choice of particular immunoglobulin heavy chain constant region sequences from certain immunoglobulin classes and subclasses to achieve a particular result is considered to be within the level of skill in the art. The portion of the DNA construct encoding the immunoglobulin Fc region preferably comprises at least a portion of a hinge domain, and preferably at least a portion of a CH3 domain of Fc gamma or the homologous domains in any of IgA,

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IgD, IgE, or IgM. Furthermore, it is contemplated that substitution or deletion of amino acids within the immunoglobulin heavy chain constant regions may be useful in the practice of the methods and compositions disclosed herein. One example would be to introduce amino acid substitutions in the upper CH2 region to create an Fc variant with reduced affinity for Fc receptors (Cole, J. Immunol. 159: 3613 (1997)).

[0092] "Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refer to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (*e.g.,* Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis (or other cytotoxic effects) of the target cell. To assess ADCC activity of a molecule of interest, any in vitro ADCC assay known in the art can be used, such as that described in U.S. Pat. No. 5,500,362 or 5,821,337. Useful effector cells for such assays include, but are not limited to, peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest can be assessed *in vivo*, *e.g.,* in an animal model such as that disclosed in Clynes *et al.* PNAS 95: 652-656 (1998).

[0093] The terms "single chain variable fragment(s)," or "scFv" antibodies as used herein refer to forms of antibodies (*e.g.,* antibody fragments) comprising the variable regions of only the heavy and light chains, connected by a linker peptide. In one embodiment, a DDpp fusion protein comprises a DDpp and a scFv.

[0094] The term "linker" refers to a peptide or other chemical linkage located between a DDpp and another polypeptide of a DDpp fusion protein. Suitable linkers for coupling the two or more linked DDpp will be clear to the persons skilled in the art and non-limiting examples are described herein.

[0095] The term "operably linked," as used herein, indicates that two molecules are attached so as to each retain at least some level of functional activity that each molecule had alone (assuming that each molecule had a function activity). In embodiments, when one molecule was without functional activity, it is operably linked with another molecule if the other molecule retains at least some level of its functional activity. Operably linked can also refer to linkage of two non-functional molecules. Two molecules can be "operably linked" whether they are attached directly or indirectly (*e.g.,* via a linker).

[0096] The terms "specifically binds," "having selective affinity for," "binds," or "binding" are used interchangeably to mean that a binding agent such as a DDpp reacts or associates more frequently, more rapidly, with greater duration, with greater affinity, or with some combination of the above, to

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the epitope, protein, or target molecule than with alternative substances, including proteins unrelated to the target epitope, protein, or target molecule. Because of the sequence identity between homologous proteins in different species, specific binding can, in some embodiments, include a binding agent that recognizes a protein or target in more than one species. Likewise, because of homology within certain regions of polypeptide sequences of different proteins, specific binding can include a binding agent that recognizes more than one protein or target. It is understood that, in certain embodiments, a binding agent that specifically binds a first target may or may not specifically bind a second target. As such, "specific binding" does not necessarily require (although it can include) exclusive binding, *e.g.,* binding to a single target. Thus, a binding agent may, in certain embodiments, specifically bind more than one target. In certain embodiments, multiple targets may be bound by the same antigen-binding site on the binding agent.

[0097] "Target" refers to any molecule or combination of molecules that can be bound by a DDpp such as a DDpp fusion protein, or other component of the DDpp fusion protein such as an antibody or antibody variable domain fragment.

[0098] The terms "epitope" and "antigenic determinant" are used interchangeably herein and refer to that portion of any molecule (*e.g.,* a target of interest such as BCMA, CD123, AFP, or AFP p26) capable of being recognized and specifically bound by a particular binding agent (*e.g.,* an DDpp or antibody). When the recognized molecule is a polypeptide, epitopes can be formed from contiguous amino acids and noncontiguous amino acids and/or other chemically active surface groups of molecules (such as carbohydrates) juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained upon protein denaturing, whereas epitopes formed by tertiary folding are typically lost upon protein denaturing. An epitope typically includes at least 3 amino acids, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation.

[0099] A "peptide tag" as used herein refers to a peptide sequence that is part of or attached (for instance through genetic engineering) to another protein, to provide a function to the resultant fusion. Peptide tags are usually relatively short in comparison to a protein to which they are fused; by way of example, peptide tags are, in some embodiments, four or more amino acids in length, such as, 5, 6, 7, 8, 9, 10, 15, 20, or 25 or more amino acids. In some embodiments, the DDpp is a fusion protein that contains a peptide tag. In other embodiments, the DDpp specifically binds a peptide tag. Numerous peptide tags that have uses as provided herein are known in the art. Examples of peptide tags that may

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be a component of a DDpp fusion protein or a target bound by a DDpp (*e.g.,* a DDpp fusion protein) include but are not limited to HA (hemagglutinin), c-myc, the Herpes Simplex virus glycoprotein D (gD), T7, GST, GFP, MBP, Strep-tags, His-tags, Myc-tags, TAP-tags and FLAG® tag (Eastman Kodak, Rochester, N.Y.) Likewise, antibodies to the tag epitope allow detection and localization of the fusion protein using techniques known in the art, such as, Western blots, ELISA assays, and immunostaining of cells.

[00100] The term "naturally occurring" when used in connection with biological materials such as a nucleic acid molecules, polypeptides, and host cells, refers to those which are found in nature and not modified by a human being. Conversely, "non-natural" or "synthetic" when used in connection with biological materials refers to those materials which are not found in nature and have been modified by a human being.

[0100] As used herein "modifications" with respect to the sequence of a reference sequence includes substitutions, deletions insertions and/or additions of the sequence of the corresponding amino acid position of the reference sequence (*e.g.,* a DD disclosed herein).

[0101] A "substitution" with respect to the sequence of a reference sequence refers to a replacement of a particular amino acid residue with a different amino acid residue at a corresponding amino acid position of the reference sequence.

[0102] A "conservative" amino acid substitution is one in which one amino acid residue is replaced with another amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (*e.g.,* lysine (K), arginine (R), histidine (H)), acidic side chains (*e.g.,* aspartic acid (D), glutamic acid (E)), uncharged polar side chains (*e.g.,* glycine (G), asparagine (N), glutamine (Q), serine (S), threonine (T), tyrosine (Y), cysteine (C)), nonpolar side chains (*e.g.,* alanine (A), valine (V), leucine (L), isoleucine (I), proline (P), phenylalanine (F), methionine (M), tryptophan (W), beta-branched side chains (*e.g.,* threonine (T), valine (V), isoleucine (I)) and aromatic side chains (*e.g.,* tyrosine (Y), phenylalanine (F), tryptophan (W), histidine (H)). For example, substitution of a phenylalanine for a tyrosine is a conservative substitution. In particular embodiments, conservative substitutions in the sequences of the DDpp result in the altered or unaltered specific binding of the DDpp containing the substitution to the target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) to which it binds. In one embodiment, conservative substitutions in the sequences of the DDpp do not abrogate the binding of the DDpp

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containing the substitution to the target of interest to which it binds. Methods of identifying nucleotide and amino acid conservative substitutions and non-conservative substitutions which confer, alter or maintain selective binding affinity are known in the art (*see, e.g.,* Brummell, Biochem. 32: 1180-1187 (1993); Kobayashi, Protein Eng. 12(10): 879-884 (1999); and Burks, PNAS 94: 412-417 (1997)).

[0103] A "non-conservative" amino acid substitution is one in which one amino acid residue is replaced with another amino acid residue having a dissimilar side chain. In one embodiment, non-conservative substitutions in the sequences of the DDpp result in the specific binding of the DDpp containing the substitution to the target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) to which it binds. In one embodiment, non-conservative substitutions in the sequences of the DDpp do not abrogate the binding of the DDpp containing the substitution to the target of interest to which it binds.

[0104] "Non-natural amino acids," "amino acid analogs" and "non-standard amino acid residues" are used interchangeably herein. Non-natural amino acids that can be substituted in a DDpp as provided herein are known in the art. In one embodiment the non-natural amino acid is 4-hydroxyproline which can be substituted for proline; 5-hydroxylysine which can be substituted for lysine; 3-methylhistidine which can be substituted for histidine; homoserine which can be substituted for serine; and ornithine which can be substituted for lysine. Additional examples of non-natural amino acids that can be substituted in a DDpp disclosed herein include, but are not limited to molecules such as: D-isomers of the common amino acids, 2,4-diaminobutyric acid, alpha-amino isobutyric acid, A-aminobutyric acid, Abu, 2-amino butyric acid, gamma-Abu, epsilon-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, beta-alanine, lanthionine, dehydroalanine, γ-aminobutyric acid, selenocysteine and pyrrolysine fluoro-amino acids, designer amino acids such as beta-methyl amino acids, C alpha-methyl amino acids, and N alpha-methyl amino acids, or combinations of non-natural amino acids. Additional non-natural amino acids can include for example, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine, and/or D-isomers of amino acids. As discussed herein, in some embodiments, non-natural amino acids or amino acid analogs can include deletion of one or more amino acids from a sequence.

[0105] The terms "polynucleotide" and "nucleic acid," used interchangeably herein, refer to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. These

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terms include, but are not limited to, DNA, RNA, cDNA (complementary DNA), mRNA (messenger RNA), rRNA (ribosomal RNA), shRNA (small hairpin RNA), snRNA (small nuclear RNA), snoRNA (short nucleolar RNA), miRNA (microRNA), genomic DNA, synthetic DNA, synthetic RNA, and/or tRNA.

[0106] The term "naked DNA" as used herein refers to DNA (*e.g.,* histone free DNA) encoding a protein such as a DDpp (*e.g.,* a CAR) disclosed herein is a DNA that is cloned in a suitable expression vector in proper orientation for expression (*e.g.,* a plasmid). Viral vectors which can be used to carry and/or express DNA encoding the DDpp include but are not limited to SIN lentiviral vectors, retroviral vectors, foamy virus vectors, adenovirus vectors, adeno-associated virus (AAV) vectors, hybrid vectors and/or plasmid transposons (for example sleeping beauty transposon system) or integrase based vector systems. Other vectors that can be used in connection with making and using DDpp are described herein or otherwise known in the art.

[0107] The terms "vector", "cloning vector" and "expression vector" as used herein refer to the vehicle by which a nucleic acid sequence (*e.g.,* a disclosed DDpp coding sequence) can be maintained or amplified in a host cell (*e.g.,* cloning vector) or introduced into a host cell, so as to transform the host and promote expression (*e.g.,* transcription and translation) of the introduced sequence. Vectors include plasmids, phages, viruses, *etc.*

[0108] A "host cell" includes an individual cell or cell culture which can be or has been a recipient of nucleic acids encoding a disclosed DDpp. Host cells includes but are not limited to viral particles, phagemids, bacteria, yeast plant, animal, and mammalian cells. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation and/or change. A host cell includes cells transfected or infected *in vivo*, in vitro, or *ex vivo* with nucleic acids encoding a disclosed DDpp. In some examples, the host cell is capable of expressing and displaying a disclosed DDpp on its surface, such as for example, in phage display or a CAR T cell. "Expression" includes transcription and/or translation.

[0109] As used herein, the terms "solid support," "support," "matrices," and "resins" are used interchangeably and refer to, without limitation, any column (or column material), bead, test tube, microtiter dish, solid particle (for example, agarose or sepharose), microchip (for example, silicon, silicon-glass, or gold chip), or membrane (*e.g.,* biologic or filter membrane) to which a DDpp,

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antibody, or other protein may be attached (*e.g.,* coupled, linked, or adhered), either directly or indirectly (for example, through other binding partner intermediates such as other antibodies or Protein A), or in which a DDpp or antibody may be embedded (for example, through a receptor or channel). Reagents and techniques for attaching polypeptides to solid supports (*e.g.,* matrices, resins, plastic, *etc.*) are well known in the art. Suitable solid supports include, but are not limited to, a chromatographic resin or matrix (*e.g.,* SEPHAROSE-4 FF agarose beads), the wall or floor of a well in a plastic microtiter dish, a silica based biochip, polyacrylamide, agarose, silica, nitrocellulose, paper, plastic, nylon, metal, and combinations thereof. DDpp and other compositions may be attached on a support material by a non-covalent association or by covalent bonding, using reagents and techniques known in the art. In one embodiment, the DDpp is coupled to a chromatography material using a linker.

[0110] As used herein, the terms "pharmaceutically acceptable," or "physiologically tolerable" and grammatical variations thereof, as they refer to compositions, carriers, diluents and reagents, are used interchangeably and represent that the materials are capable of administration to or upon a human without the production of therapeutically prohibitive undesirable physiological effects such as nausea, dizziness, gastric upset and the like.

[0111] "Modulate," means adjustment or regulation of amplitude, frequency, degree, or activity. In another related aspect, such modulation may be positively modulated (*e.g.,* an increase in frequency, degree, or activity) or negatively modulated (*e.g.,* a decrease in frequency, degree, or activity). In some embodiments, modulation in a positive or negative direction is referenced as compared to the cell, tissue, or organ function prior to administration of a therapeutic. In additional embodiments, modulation in a positive or negative direction is referenced with respect to a normal, healthy cell, tissue or organ.

[0112] An "effective amount" of a DDpp such as a DDpp fusion protein as provided herein, is an amount sufficient to carry out a specifically stated purpose such as to bring about an observable change in the level of one or more biological activities related to the target to which the DDpp (*e.g.,* a DDpp fusion protein) binds. In certain embodiments, the change increases the level of target activity. In other embodiments, the change decreases the level of target activity. An "effective amount" can be determined empirically and in a routine manner, in relation to the stated purpose. The term "therapeutically effective amount" refers to an amount of a DDpp such as a DDpp fusion protein, or

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other therapeutic agent effective to "treat" (*e.g.,* reduce symptoms of) a disease or disorder in a subject (mammal). The term "therapeutically effective amount" also refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired prophylactic result.

[0113] "Patient," "subject," "animal" and "mammal" are used interchangeably and refer to mammals such as human patients and non-human primates, as well as experimental animals such as rabbits, rats, and mice, and other animals. Animals include all vertebrates, *e.g.,* mammals and non-mammals, such as chickens, amphibians, and reptiles. "Mammal" as used herein refers to any member of the class Mammalia, including, without limitation, humans and nonhuman primates such as chimpanzees and other apes and monkey species; farm animals such as cattle, sheep, pigs, goats and horses; domestic mammals such as dogs and cats; laboratory animals including rodents such as mice, rats and guinea pigs, and the like. In a particular embodiment, the patient is a human. The term does not denote a particular age or sex. Thus, adult and newborn subjects, as well as embryos and fetuses, whether male or female, are intended to be included within the scope of this term.

[0114] The terms "treat," "treatment," and "treating," as used herein refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen or delay) the symptoms, complications, or biochemical indicia of a disease, condition, or disorder, alleviating the symptoms or arresting or inhibiting further development of the disease, condition, or disorder. Treatment can be prophylactic (to prevent or delay the onset of the disease, or to prevent the manifestation of clinical or subclinical symptoms thereof) or therapeutic suppression or alleviation of symptoms after the manifestation of the disease, condition, or disorder targeted pathologic condition, prevent the pathologic condition, pursue or obtain beneficial results, or lower the chances of the individual developing the condition even if the treatment is ultimately unsuccessful. Those in need of treatment include those already with the condition as well as those prone to have the condition or those in whom the condition is to be prevented. Treatment can be with a DDpp fusion protein alone or in combination with an additional therapeutic agent.

[0115] "Cancer," "tumor," or "malignancy" are used as synonymous terms and refer to any of a number of diseases that are characterized by uncontrolled, abnormal proliferation of cells, the ability of affected cells to spread locally or through the bloodstream and lymphatic system to other parts of the body (metastasize) as well as any of a number of characteristic structural and/or molecular features. "Tumor," as used herein refers to all neoplastic cell growth and proliferation, whether malignant or

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benign, and all pre-cancerous and cancerous cells and tissues. A "cancerous tumor," or "malignant cell" is understood as a cell having specific structural properties, lacking differentiation and being capable of invasion and metastasis. Cancers that can be treated using DDpp fusion proteins provided herein include hematological tumors, such as leukemias and lymphomas, or solid tumors. In particular embodiments, the cancer to be treated is a leukemia or a lymphoma. Types of cancers to be treated with the DBDpp include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies e.g., sarcomas, carcinomas, and melanomas. Types of cancer and tumors that may be treated using DDpp-include without limitation, breast, lung, brain, bone, liver, kidney, colon, head and neck, ovarian, hematopoietic (*e.g.,* leukemia), and prostate cancer. In some embodiments, the cancer and tumors that may be treated using DDpp-include breast and ovarian cancer. Other types of cancer and tumors that may be treated using DDpp-containing antibodies are described herein or otherwise known in the art.

[0116] The terms tumor antigen or cancer antigen are used interchangeably herein. Tumor and cancer antigens may be tumor-specific antigen (TSA), cancer-specific antigens (CSA) tumor-associated antigen (TAA) or cancer-associated antigens (CAA). A TSA is an antigen that is unique to tumor cells and does not occur on other cells in the body. A TAA is an antigen that is found on both tumor and some normal cells. Because of the dynamic nature of tumors, in some instances, tumor cells may express unique antigens at certain stages, and at others also express antigens that are also expressed on non-tumor cells. Thus, inclusion of a certain marker as a TAA does not preclude it being considered a TSA.

[0117] The term "target cell" as used herein refers to a cell or cells which are involved in a disease and can be targeted by DDpp containing compositions. Other target cells include any cell in a subject (*e.g.,* a human or animal) that can be targeted by disclosed DDpp. The target cell can be a cell expressing or overexpressing a target specifically bound by a DDpp fusion protein.

[0118] The term "effector cells" as used herein refers to leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc(RIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred in certain embodiments. The effector cells can be isolated

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from native source thereof, *e.g.,* from blood or PBMCs as described herein or otherwise known in the art. In a specific embodiment, the effector cells are human effector cells.

[0119] The term "effector function" refers to the specialized immune function of a differentiated cell. Effector function of a T cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines.

[0120] The term "immune cell" as used herein refers to the cells of the mammalian immune system including but not limited to antigen presenting cells, B cells, basophils, cytotoxic T cells, dendritic cells, eosinophils, granulocytes, helper T cells, leukocytes, lymphocytes, macrophages, mast cells, memory cells, monocytes, natural killer cells, neutrophils, phagocytes, plasma cells and T cells.

[0121] The terms "T cell" and "T lymphocyte" are interchangeable and used synonymously herein. Examples include but are not limited to naive T cells, central memory T cells, effector memory T cells or combinations thereof.

[0122] The term "immune response" as used herein refers to immunities including but not limited to innate immunity, humoral immunity, cellular immunity, immunity, inflammatory response, acquired (adaptive) immunity, autoimmunity and/or overactive immunity.

[0123] The term "transduction" as used herein refers to the introduction of a foreign nucleic acid into a cell using a viral vector. "Transfection" as used herein refers to the introduction of a foreign nucleic acid into a cell using recombinant DNA technology. The term "transformation" means the introduction of a "foreign" (*e.g.,* extrinsic, extracellular, or otherwise non-endogenous) nucleic acid (DNA or RNA) sequence to a host cell, so that the host cell will express the introduced nucleic acid to produce a desired substance, such as a protein or enzyme coded by the introduced coding sequence. The introduced nucleic acid sequence can also be called a "cloned" or "foreign" gene or sequence, can include regulatory or control sequences, such as start, stop, promoter, signal, secretion, or other sequences used by a cell's genetic machinery. The nucleic acid sequence can include nonfunctional sequences or sequences with no known function. A host cell that receives and expresses introduced nucleic acid (*e.g.,* DNA or RNA) has been "transformed" and is a "transformant" or a "clone." The DNA or RNA introduced to a host cell can come from any source, including cells of the same genus or species as the host cell, or cells of a different genus or species or may be non-naturally occurring.

[0124] "Cell surface receptor" refers to molecules and complexes of molecules capable of receiving a signal and the transmission of such a signal across the plasma membrane of a cell. An

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example of a cell surface receptor provided herein is an activated integrin receptor, for example, an activated αvβ3 integrin receptor on a metastatic cell. As used herein, "cell surface receptor" also includes a molecule expressed on a cell surface that contains a DDpp capable of binding a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26). The term "receptor" denotes a cell-associated protein that binds to, or otherwise interacts with, a molecule (*e.g.,* a ligand) and mediates the effect of the ligand on the cell. In some embodiment, the molecule that interacts with a receptor is a bioactive molecule. Membrane-bound cell-surface receptors are typically characterized by a multi-domain structure comprising an extracellular ligand-binding domain, a membrane spanning domain, and an intracellular effector domain that is typically involved in signal transduction.

[0125] The term "CS1" as used herein refers to an NK cell receptor regulating immune functions that is also expressed on B cells, T cells, dendritic cells, NK-T cells, and monocytes. CS1 is overexpressed in multiple myeloma and has been successfully targeted for immunotherapy multiple myeloma. Malaer & Mathew, Am J Cancer Res. 7(8): 1637–1641 (2017). CS1 is also known as SLAM7, protein 19A, CRACC, and CD319. The term "CS1" includes variants, isoforms, homologues, orthologs and paralogs. CS1 is a transmembrane protein with various differentially spliced isoforms. In some embodiments, the amino acid sequence of human CS1, comprising a 22 amino acid residue N-terminal signal sequence (MAGSPTCLTLIYILWQLTGSAA, SEQ ID NO: 964) and an extracellular domain comprising the 226 N-terminal residues (SEQ ID NO: 965), has Genbank Accession No. NP_067004 (SEQ ID NO: 966). In some embodiments, the amino acid sequence of human CS1 has Genbank Accession No. NP_001269517, NP_001269518, NP_001269519, NP_001269520, NP_001269521, NP_001269522, NP_001269523, NP_001269524, or NP_001269525.

[0126] "Chimeric antigen receptor" or "CAR" or "CARs" as used herein refers to an engineered receptor, which grafts an antigen or target specificity onto a cell (for example T cells such as naive T cells, central memory T cells, effector memory T cells, NK cells, NKT cells or combination thereof). CARs are also known as artificial T cell receptors, chimeric T cell receptors or chimeric immunoreceptors.

D Domain Polypeptides (DDpp)

[0127] Unless otherwise indicated, the practice of the disclosed compositions and methods employs standard techniques of molecular biology (including recombinant techniques, tissue culture,

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and cell transformation), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are typically performed according to the manufacturer's specifications or as commonly accomplished using or routinely modifying known procedures such as, those set forth in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)); PCR Technology: Principles and Applications for DNA Amplification (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); Oligonucleotide Synthesis (Gait, ed., 1984); Animal Cell Culture (Freshney, ed., 1987); Handbook of Experimental Immunology (Weir *et al.*, eds.; Gene Transfer Vectors for Mammalian Cells (Miller, ed., 1987); Current Protocols in Molecular Biology (Ausubel., ed., 1987); PCR Protocols: A Guide to Methods and Applications (Innis, ed., Academic Press, San Diego, Calif., 1990); Mattila, *et al.*, Nucleic Acids Res. 19: 967 (1991); Eckert, *et al.*, PCR Methods and Applications 1: 17 (1991); PCR (McPherson, ed., IRL Press, Oxford); PCR: The Polymerase Chain Reaction, (Mullis, ed., 1994); Harlow, Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) and Kontermann, ed., "The Antibody Engineering Lab Manual" (Springer Verlag, Heidelberg/New York, 2000); Current Protocols in Immunology (Coligan, ed., 1991); The Immunoassay Handbook (Wild, ed., Stockton Press NY, 1994); and Methods of Immunological Analysis (Masseyeff., ed., Weinheim: VCH Verlags gesellschaft mbH, 1993); and Gennaro, *et al.* 2000, Remington: the Science and Practice of Pharmacy, 20th Ed. Lipincott Williams and Wilkins: Baltimore, Md., or as described herein. Unless specific definitions are provided, the nomenclature utilized in connection with, and the laboratory procedures and techniques of analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein, are those known and used in the art. Additionally, standard techniques can be used for chemical syntheses, chemical analyses, recombinant production, purification, pharmaceutical preparation, formulation, delivery, and treatment of patients.

[0128] According to various embodiments, the disclosure provides a DDpp that specifically binds a target of interest selected from the group consisting of BCMA, CD123, CS1, HER2, AFP, and AFP p26. In some embodiments, a DD of the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-949, and 950. In some embodiments, the DDpp comprises a D Domain (DD) selected from the group consisting of: (a) a DD that specifically binds BCMA and comprises the amino acid sequence of SEQ ID NO: 11-305, or 306; (b) a DD that specifically binds CD123 and comprises the amino acid sequence of SEQ ID NO: 307-739, or 740; (c) a DD that

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specifically binds AFP or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895; (d) a DD that specifically binds AFP p26 and comprises the amino acid sequence of SEQ ID NO: 741-874, or 886-895, (e) a DD that specifically binds CS1 (SEQ ID NO: 965) or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 896-909, or 910, (f) a DD that specifically binds HER2 or a fragment thereof, and comprises the amino acid sequence of SEQ ID NO: 911-949, or 950. Proteins comprising variants of (a)-(f) that retain the ability to specifically bind their respective targets are also provided.

[0129] In additional embodiments, a DD of the DDpp is a variant of a DD reference sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, that retains the ability to specifically bind the target of the reference DD. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 11-949, and 950, and the variant DD retains the ability to specifically bind the target of the reference DD sequence.

[0130] In some embodiments, a DD of the DDpp is a variant of a BCMA-binding DD reference sequence selected from the group consisting of SEQ ID NO: 11-305, and 306, that retains the ability to specifically bind BCMA. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 11-305, and 306, and the variant DD retains the ability to specifically bind BCMA.

[0131] In some embodiments, a DD of the DDpp is a variant of a CD123-binding DD reference sequence selected from the group consisting of SEQ ID NO: 307-739, and 740, that retains the ability to specifically bind CD123. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 307-739, and 740, and the variant DD retains the ability to specifically bind CD123.

[0132] In some embodiments, a DD of the DDpp is a variant of a CS1-binding DD reference sequence selected from the group consisting of SEQ ID NO: 896-909, and 910, that retains the ability to specifically bind CS1. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98%

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sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 896-909, and 910, and the variant DD retains the ability to specifically bind CS1.

[0133] In some embodiments, a DD of the DDpp is a variant of a HER2-binding DD reference sequence selected from the group consisting of SEQ ID NO: 911-949, and 950, that retains the ability to specifically bind HER2. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 911-949, and 950, and the variant DD retains the ability to specifically bind HER2.

[0134] In some embodiments, a DD of the DDpp is a variant of a AFP-binding DD reference sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895, that retains the ability to specifically bind AFP. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895, and the variant DD retains the ability to specifically bind AFP.

[0135] In some embodiments, a DD of the DDpp is a variant of a AFP p26-binding DD reference sequence selected from the group consisting of SEQ ID NO: 741-874, or 886-895, that retains the ability to specifically bind AFP p26. In some embodiments, the sequence of the variant DD comprises the amino acid sequence of a variant that has at least 75%, 80%, 85%, 87%, 89%, 90%, 92%, 94%, 96% or 98% sequence identity to a reference DD sequence selected from the group consisting of SEQ ID NO: 741-874, or 886-895, and the variant DD retains the ability to specifically bind AFP p26.

[0136] In particular embodiments, the identity between a variant DD (query) sequence and a reference DD sequence, also referred to as a global sequence alignment, is determined using the FASTDB computer program based on the algorithm of Brutlag et al. Comp. App. Biosci. 6: 237-245 (1990). Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter. According to this embodiment, if the reference DD sequence is shorter than the variant DD query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction is made to the results to take into consideration the fact that

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the FASTDB program does not account for N- and C-terminal truncations of the reference DD sequence when calculating global percent identity. For reference sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the reference sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. A determination of whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of this embodiment.

[0137] In some embodiments, the DDpp contains a variant DD containing an amino acid sequence that differs from a corresponding reference DD of SEQ ID NO: 11-949, or 950, in two or more categories of sequence modifications (*i.e.*, substitutions, deletions, insertions, and additions), and the variant DD retains the ability to bind the target of the respective reference DD (e.g., BCMA, CD123, CS1, HER2, AFP, and AFP p26). For example, the sequence of the variant DD may include combinations of amino acid deletions, insertions and substitutions compared to the sequence of the reference DD. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, amino acid substitutions compared to a reference DD sequence of SEQ ID NO: 11-949, or 950. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, conservative amino acid substitutions compared to a reference DD sequence of SEQ ID NO: 11-949, or 950. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, nonconservative amino acid substitutions compared to a reference DD sequence of SEQ ID NO: 11-949, or 950. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, conservative and nonconservative amino acid substitutions compared to a reference DD sequence of SEQ ID NO: 11-949, or 950. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, amino acid deletions compared to a reference DD sequence of SEQ ID NO: 11-949, or 950. In some embodiments, the sequence of the variant DD contains 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10, amino acid insertions in a reference DD sequence of SEQ ID NO: 11-949, or 950 and the variant DD retains the ability to bind the target of the reference DD. Additionally provided are DDpp comprising a variant DD in which amino acid residues have been deleted from the amino terminus, the carboxy

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terminus, or both the amino and carboxy termini of a corresponding reference DD of SEQ ID NO: 866, and 867 In some embodiments, the sequence of the variant DD contains a sequence with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, amino acid residues deleted from the amino terminus of a reference DD sequence of SEQ ID NO: 11-949, or 950 and the variant DD retains the ability to bind the target of the reference DD. In some embodiments, the sequence of the variant DD contains a sequence with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, amino acid residues deleted from the carboxy terminus of a reference DD of SEQ ID NO: 11-949, or 950 and the variant DD retains the ability to bind the target of the reference DD. In some embodiments, the sequence of the variant DD sequence contains 1-5, 1-10, or 1 to 15, amino acid residues deleted from the amino terminus of a reference DD sequence of SEQ ID NO: 11-949, or 950, the variant DD sequence has 1-5, 1-10, or 1 to 15, amino acid residues deleted from the carboxy terminus of the reference DD sequence, and the variant DD retains the ability to bind the target of the reference DD.

DDpp fusion proteins

[0138] A "fusion protein," "chimeric polypeptide," "chimeric protein," "chimeric antigen," and a DDpp that comprises/contains a heterologous polypeptide, is a polypeptide comprised of at least two polypeptides and optionally a linker to operatively link the two polypeptides into one continuous polypeptide produced, *e.g.,* by recombinant processes. The two polypeptides may be operably attached directly or indirectly.

[0139] A "DDpp fusion protein" provided herein comprises at least one DDpp disclosed herein that specifically binds a target of interest (*e.g.,* BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), CS1 (SEQ ID NO: 965), HER2 (SEQ ID NO: 967), AFP (SEQ ID NO: 9), AFP p26 (SEQ ID NO: 10), or a fragment thereof). In one embodiment, the DDpp fusion protein contains one DDpp.

[0140] In some embodiments, the DDpp fusion protein is a soluble protein comprising one or more target-binding DDpp and a p26 protein (e.g., having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974). Such fusion proteins containing p26 sequences have been discovered herein to have surprisingly long serum half-life. In some embodiments, the soluble DDpp fusion protein has a plasma half-life *in vivo* of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more. In some embodiments, the soluble fusion protein has an *in vivo* plasma half-life of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more hours 65 hours, or 1-10 hours, 2-

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10 hours, 4-10 hours, 6-10 hours, or 6-9 hours in a mouse. In some embodiments, the soluble DDpp fusion protein has an *in vivo* plasma half-life of at least 1 hour, at least 2 hours, at least 4 hours, at least 8 hours, at least 16 hours, at least 32 hours, at least 64 hours, or more hours 65 hours, or 1-10 hours, 2-10 hours, 4-10 hours, 6-10 hours, or 6-9 hours, in a human.

[0141] In some embodiments, the disclosure provides a method for modifying the *in vivo* half-life (e.g., in a mouse or human) of a soluble fusion protein comprising a p26 protein (e.g., having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974). In some embodiments, the soluble p26 fusion protein comprises one or more target-binding DDpp. In some embodiments, the half-life of the p26 soluble fusion protein is increased or decreased by substituting or deleting one or more amino acid residues normally found in the human p26 protein, or by inserting one or more amino acid residues not normally found in the human p26 protein. In another embodiment, the p26 sequence of the soluble fusion protein is modified through 1, 2, 3, 5, 5, 10, or 1-20, 1-10, 3-10, or 3-5, amino acid substitutions (conservative and/or nonconservative substitutions), deletions, and/or insertions so as to increase or decrease the *in vivo* half-life of the soluble fusion protein. In a particular embodiment, the amino acid residue corresponding to the glutamine (Gln, Q) at position 217 of SEQ ID NO: 10 of p26 is substituted with another amino acid residues. In a further embodiment the substitution is Gln217Pro.In another embodiment, the p26 sequence of the soluble fusion protein is modified through deletion of 1-150, 1-100, 1-50, 1-25 or 1-10 amino acid residues so as to increase or decrease the *in vivo* half-life of the soluble fusion protein. In additional embodiments, the p26 sequence of the soluble fusion protein is modified through 1, 2, 3, 5, 5, 10 or 1-20, 1-10, 3-10, or 3-5, amino acid substitutions (conservative and/or nonconservative substitutions), deletions, and/or insertions so as to increase or decrease the interaction of the soluble fusion protein with FcRn.

Multimeric DDpp fusion proteins

[0142] In one embodiment, the DDpp fusion protein comprises more than one DDpp, wherein two or more DDpp have the same or different specificities. In additional embodiments, the DDpp fusion protein comprises a tandem repeat of the same or different DD that allow a DDpp fusion protein to bind multiple targets and/or repeating epitopes or different epitopes on the same target. In some embodiments, the DDpp fusion protein comprises at least 2, 3, 4, or 5, or more than 5, DDpp. In some embodiments, the DDpp fusion protein contains 1-3, 1-4, 1-5, or more than 5, different DDpp. In some embodiments, the DDpp fusion protein contains at least 2, 3, 4, or 5, or more than 5, different DDpp.

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Thus, a DDpp fusion protein can be a monomeric DDpp (*i.e.*, containing one DDpp) or multimeric DDpp (*i.e.*, containing more than one DDpp in tandem optionally operably connected by a linker). In some embodiments, the use of multimeric DDpp provides enhanced (*e.g.,* synergistic) target binding. In additional embodiments, multimeric DDpp allows targeting of more than one target using a single DDpp construct (*e.g.,* bi-, tri-specific, *etc.*). The linkage of two or more identical DDpp results in a multivalent molecule that provides distinct advantages (*e.g.,* increased binding avidity, target clustering and receptor activation) over monovalent compositions. The linkage of two or more different DDpp results in a multivalent and multi-specific molecule that has the potential to bind more than one target antigen, either independently or simultaneously.

[0143] The multimeric DDpp fusion protein can be a DDpp homo-multimeric (*i.e.*, containing more than one of the same DDpp in tandem optionally connected by linker(s) (*e.g.,* homodimers, homotrimers, homotetramers *etc.*) or DDpp hetero-multimeric (*i.e.*, containing two or more DDpp in which there are at least two different DDpp protein. The number of monomeric DDpp included within a multimeric composition may vary, depending on the embodiment, and may be defined, at least in part, by the expression system in which the DDpp is produced. In some embodiments, however, the fusion proteins may comprises multimers of about 5 to about 10 DDpp subunits, about 10 to about 15 subunits, about 15 to about 20 subunits, about 20 to about 25 subunits, or about 25 to about 30 subunits (including numbers in between those listed as well as endpoints). Moreover, multiple tandem components of a DDpp fusion protein can contain the same or different DDpp. In some DDpp fusions, the DDpp are present as a monomer, or in homomultimers or heteromers such as, homodimers or heterodimers, homotrimers or heterotrimers, homotetramers or heterotetramers.

[0144] A DDpp fusion protein can be "monospecific" or "multi-specific." A DDpp fusion protein that is "multi-specific" (*e.g.,* bispecific, trispecific or of greater multi-specificity) recognizes and binds to two or more different epitopes present on one or more different molecules (*e.g.,* proteins, solid support structures, *etc.*).

[0145] In some embodiments, two or more DDs are fused together as a multivalent DDpp. The DD of the multivalent DDpp may be the same or different. Thus, the disclosure provides a DDpp homo-dimer (*i.e.*, a DDpp comprising two identical DD), a DDpp homo-multimer (*i.e.*, a DDpp comprising three or more identical DD), a DDpp hetero-dimer (*i.e.*, a DDpp comprising two different DD), and DDpp hetero-multimer (*i.e.*, a DDpp comprising three or more DD, wherein at least two of

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the DD are different) comprising any of the DD described herein, optionally attached by one or more linkers.

[0146] In some embodiments, two or more DDs are linked by a multimerization domain or attached via chemical linkage, to generate a multivalent DD complex. The DD of the multivalent DD complex may be the same or different. Thus, the disclosure provides a DD homo-dimer complex (*i.e.*, a DD complex comprising two identical DD), a DD homo-multimer complex (*i.e.*, a DD complex comprising three or more identical DD), a DD hetero-dimer complex (*i.e.*, a DD complex comprising two different DD), and DD hetero-multimer complex (*i.e.*, a DD complex comprising three or more DD, wherein at least two of the DD are different) comprising any of the DD described herein, optionally attached by one or more linkers.

[0147] In one embodiment, a multi-specific DDpp fusion protein contains at least two DDpp that bind to at least two different epitopes on a single target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26). In a further embodiment, the DDpp fusion is bispecific and specifically binds to two different targets expressed on the surface of two different cell types. In one embodiment the bispecific DDpp fusion protein specifically binds to a target on a cancer cell and a target on an immune effector cell. In one embodiment the bispecific DDpp fusion protein specifically binds a target expressed on a cancer cell (*e.g.,* BCMA, CS1, CD123, and CD19) and a target expressed on the surface of a T lymphocyte (*e.g.,* CD3). In one embodiment the bispecific DDpp fusion protein specifically binds BCMA and CS1.

[0148] In additional embodiments, a multi-specific DDpp fusion protein comprises at least one DDpp that specifically binds one epitope on a target of interest and at least one other domain or sequence conferring function (*e.g.,* an antibody fragment or domain such as an scFv) that specifically binds to a different epitope on the same target of interest. In one embodiment, a multi-specific DDpp fusion protein comprises at least one DDpp that specifically binds to an epitope on a target of interest and at least one domain or sequence conferring function *e.g.,* an antibody fragment or domain (*e.g.,* scFv), that specifically binds to an epitope on a different target of interest. In one embodiment, the multi-specific DDpp fusion protein comprises at least one DDpp that specifically binds to an epitope on a target of interest and at least one domain or sequence that specifically binds to an epitope on a different target on the same cell. In other embodiments, a DDpp fusion protein comprises at least one

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DDpp and at least one other DDpp or domain sequence conferring function, *e.g.,* an antibody fragment or domain that specifically binds to a solid support.

[0149] In a further embodiment, the multimeric DDpp fusion comprising 2 or more DDpp are in turn fused with other heterologous proteins (or their subdomains) and in so doing, impart the multivalent and multi-specific properties to the fusion partner. Examples of fusion partners of a DDpp include but are not limited to, antibodies, antibody subdomains (*e.g.,* scFv or Fc domains), serum albumin, serum albumin subdomains, cell surface receptors, an alpha chain of a T cell receptor (TCR), a beta chain of a T cell receptor, cell surface receptor subdomains, peptides, peptide tags (*e.g.,* FLAG or myc), fibronectin type III repeats, z-domains, elastin-like polypeptides. The number and location of DDpp and their respective positions within the fusion protein can vary. For example, DDpp(s) can be located at one or all termini of a fusion partner and/or interspersed within heterologous subunits within the DDpp fusion partner.

[0150] In additional embodiments, a DDpp fusion protein comprises a DDpp and a polypeptide sequence containing an additional domain. In some embodiments, the DDpp fusion protein comprises a DDpp and a member selected from: an antibody, an antibody fragment (*e.g.,* an antigen binding domain or portion thereof (*e.g.,* an scFv), an effector domain or portion thereof, an FcRn binding domain or portion thereof, and an Fc or a portion thereof), a serum protein (*e.g.,* albumin or a portion thereof), a cytokine, a growth factor, a hormone, an imaging agent, a labeling agent, and a peptide tag. In some embodiments, the DDpp fusion protein comprises an Fc domain of an immunoglobulin (*e.g.,* a human Fc domain) or a portion thereof. In further embodiments, the Fc domain is a variant human Fc domain.

[0151] In some embodiments, the DDpp is fused to a heterologous polypeptide. In some embodiments, the heterologous polypeptide comprises a full-length antibody or an antibody fragment. In some embodiments, the DD is fused to: the amino terminus of a full-length antibody heavy chain; the amino terminus of a full-length antibody light chain; the carboxyl terminus of a full-length antibody heavy chain; or the carboxyl terminus of a full-length antibody light chain. In other embodiments, the DD is fused to an antibody fragment which is an Fc. In additional embodiments, the heterologous polypeptide comprises a member selected from the group consisting of: (i) a transmembrane domain; (ii) a membrane associating domain; (iii) human serum albumin or a fragment thereof; (iv) AFP or a fragment thereof; (v) AFP p26 or a fragment thereof; (vi) the extracellular

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domain of a receptor or a fragment thereof; and (vii) the extracellular domain of an intracellular receptor (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp contains a heterologous polypeptide comprising the extracellular domain, or a fragment of an extracellular domain, of a cell surface receptor.

[0152] In some embodiments, the DDpp of a DDpp fusion protein is incorporated into a larger, multi-domain molecular complex (*e.g.,* a monomeric or multimeric DDpp fusion protein) and in so doing, imparts the functional attributes of the incorporated DDpp to the resultant fusion protein. In some embodiments, the DDpp fusion protein comprises a DDpp and a polypeptide sequence from an antibody, an antibody fragment, a serum protein (*e.g.,* human serum albumin) or serum protein fragment, or a cell surface receptor, an alpha chain of a T cell receptor (TCR), a beta chain of a T cell receptor, cytokine, growth factor, hormone, or enzyme, or fragment thereof. Incorporation of DD into multidomain and/or multifunctional complexes can routinely be achieved by way of recombinant fusion to another polypeptide, binding to another chemical moiety, and covalent chemical linkage to another polypeptide (or other desirable chemical compound) using techniques known in the art. DDpp fusion proteins can additionally contain other optional components such as linkers and other components described herein.

DDpp fusion proteins as CARs

[0153] In addition to the incorporation of DD into soluble multi-domain proteins, the present invention provides a means by which to create cell-associated DDpp, comprised of at least one DDpp designed to impart binding specificity a membrane bound fusion protein. DDpp-receptors may be expressed by any cell type.

[0154] In one embodiment, the DDpp-receptor fusion protein comprises a chimeric antigen receptor (CAR), or DDpp-CAR, that comprises: an extracellular targeting domain and a transmembrane domain. In another embodiment, the DDpp-CAR is composed of an extracellular targeting domain, a transmembrane domain, and a cytoplasmic domain wherein the cytoplasmic domain comprises the signaling domain. In a further embodiment the DDpp-CAR extracellular domain comprises one or more DDpp, in which each DDpp constitutes a specific binding domain with the same or different specificities. In some embodiments, the target-specific domain is directed to one (or more) of the cancer or tumor antigens disclosed herein, such as BCMA, CD123, CS1, HER2, AFP,

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and AFP p26, as non-limiting examples. In one embodiment, the intracellular domain (*e.g.,* the cytoplasmic domain) of the DDpp-CAR comprises the intracellular domain of CD3 zeta chain. In another embodiment the intracellular signaling domain of the DDpp is comprised of part of the intracellular domain of CD3 zeta chain. In a further embodiment, the intracellular domain of the DDpp-CAR comprises the intracellular domain of CD3 zeta chain and a costimulatory signaling region. The costimulatory signaling region refers to a portion of the DDpp-CAR comprising all or part of the intracellular domain of a costimulatory molecule. Costimulatory molecules are cell surface molecules other than antigens receptors or their ligands that are required for an efficient response of lymphocytes to antigen. Costimulatory molecules and portions of these molecules that are able to confer costimulatory properties to an AR are known in the art and can routinely be incorporated into the DDpp-CAR. In addition, truncations or mutation to these intracellular signaling and costimulatory domains may be incorporated to further enhance or reduce receptor signaling. In preferred embodiments, a T cell is genetically modified to stably express a DDpp-CAR. In such embodiments, the cytoplasmic domain of the DDpp-CAR can be designed to comprise the CD28 and/or 41BB signaling domain by itself or be combined with any other desired cytoplasmic domain(s) useful in the context of the disclosed embodiments. In one embodiment, the cytoplasmic domain of the DDpp-CAR can be designed to further comprise the signaling domain of CD3-zeta. In one embodiment, the DDpp-CAR comprises an extracellular targeting domain, an extracellular protein linker with a transmembrane domain that passes through the cellular membrane (such as found in T cells or NK cells), and a cytoplasmic domain, optionally comprising multiple signaling modules. In some embodiments, the DDpp-CAR may also comprise an epitope tag. In some embodiments, the cytoplasmic domain of the DDpp-CAR can include but is not limited to CD3-zeta, 41BB and CD28 signaling modules and combinations thereof.

[0155] In additional embodiments, the disclosure provides a chimeric antigen receptor (CAR), wherein the CAR includes a targeting domain comprising a DDpp disclosed herein, a transmembrane domain, and an intracellular signaling domain. In some embodiments, the intracellular signaling domain is selected from the group consisting of a human CD3 zeta domain, 41BB domain, a CD28 domain and/or any combination thereof. Depending on the embodiment, the costimulatory signaling region can comprise, for example, the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4lBB, OX40, CD30, CD40, PD1, lymphocyte function-

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associated antigen-1 (LFA 1), CD2, CD7, LIGHT, NKG2C, B7H3, a ligand that specifically binds with CD83, and any combination thereof. In some embodiments, the targeting domain of the CAR comprises a plurality of binding domains (*e.g.,* DDs, or one or more DD and a scFv) that includes an additional target-binding polypeptide. Nucleic acids encoding CARs that include the target-binding polypeptides as part (or all) of the targeting region are also provided.

[0156] The disclosure also provides cells comprising a nucleic acid sequence encoding a CAR, wherein the CAR comprises an antigen binding domain made up of, at least in part, a disclosed DDpp that binds a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, and AFP p26), a transmembrane domain, and a signaling domain. In some embodiments, the CAR binds specifically to a tumor antigen (and thus functions to deliver the cell expressing the CAR to the tumor. In some embodiments, the tumor antigen is associated with a hematologic malignancy. In some embodiments, the tumor antigen is BCMA. In some embodiments, the tumor antigen is CD123. In some embodiments, the tumor antigen is CS1. In additional embodiments, tumor antigen is associated with a solid tumor. In some embodiments, the tumor antigen is HER2. In some embodiments, both solid and hematologic tumors are targeted. In some embodiments, the cell expressing the CAR is a T cell, a natural killer (NK) cell or other immune cell type. In some embodiments, the cell expressing the CAR (whether T cell, NK cell or other cell type) exhibits an anti-tumor immunity when the polypeptide binds to its corresponding tumor antigen.

Extracellular Domain

[0157] Depending on the desired antigen to be targeted, the DDpp-CAR can be engineered to include an antigen binding DDpp that is specific to the desired antigen target. For example, if BCMA is the desired antigen that is to be targeted, one or more BCMA-binding DDpp can be incorporated into the target specific binding domain of the DDpp-CAR. Moreover, the DDpp-CAR can include more than one DDpp, imparting multispecificity or multivalency to the DDpp-CAR. In some embodiments, the DDpp-CAR comprises a BCMA-binding DDpp. In some embodiments, the DDpp-CAR comprises a CS1-binding DDpp. In some embodiments, the DDpp-CAR comprises a BCMA-binding DDpp and a CS1-binding DDpp.

[0158] The choice of DDpp incorporated into the extracellular domain of the DDpp receptor (*e.g.,* DDpp-CAR) depends upon the identity of the cell or cells to be targeted. For example, a DDpp-CAR may specifically bind to cell surface proteins such as a receptor on the same cell or another cell.

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In other embodiments, DDpp-CAR specifically binds to a soluble molecule, such as an immunoglobulin. In other embodiments, the targets of interest bound by the DDpp-CAR include those associated with viral, bacterial and parasitic infections, diseases and disorders of the immune system (*e.g.,* autoimmune disease).

[0159] In other embodiments, the DDpp-CAR may be chosen to recognize a ligand that acts as a cell surface marker on target cells associated with a cancer. A DDpp-CAR can in some embodiments, target and bind a tumor antigen (*e.g.,* a TAA or other tumor antigen described herein or otherwise known in the art. Accordingly, provided herein are methods for creating DDpp-CAR, their use in creating chimeric cells such as, human T cells and natural killer cells and the use of these chimeric T cells in adoptive immunotherapy.

[0160] In the context provided herein, "tumor antigen" refers to antigens that are common to specific hyperproliferative disorders such as cancer. Tumor antigens that can be specifically bound by a DDpp in a DDpp-CAR are disclosed herein. In one embodiment, a DDpp in a DDpp-CAR specifically binds a tumor-specific antigen (TSA) or a tumor-associated antigen (TAA). A TSA is unique to tumor cells and does not occur on other cells in the body. A TAA associated antigen is not unique to a tumor cell and instead is also expressed on a normal cell under conditions that fail to induce a state of immunologic tolerance to the antigen. The expression of the antigen on the tumor may occur under conditions that enable the immune system to respond to the antigen. TAAs may be antigens that are expressed on normal cells during fetal development when the immune system is immature and unable to respond or they may be antigens that are normally present at extremely low levels on normal cells but which are expressed at much higher levels on tumor cells.

[0161] In some embodiments, a DDpp in the antigen binding moiety portion of a DDpp-CAR specifically binds BCMA, CS1, HER2, or CD123. In some embodiments, the DDpp specifically binds a BCMA protein having an amino acid sequence consisting of SEQ ID NO: 7. In further embodiments, the DDpp specifically binds BCMA and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp specifically binds a CD123 protein having an amino acid sequence consisting of SEQ ID NO: 8. In further embodiments, the DDpp specifically binds CD123 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp specifically binds a CS1 protein having an amino acid sequence consisting of SEQ ID NO: 965. In further embodiments,

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the DDpp specifically binds CS1 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp specifically binds a CS1 and BCMA. In some embodiments, the DDpp specifically binds a HER2 protein having an amino acid sequence consisting of SEQ ID NO: 967. In further embodiments, the DDpp specifically binds HER2 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In additional embodiments, the antigen binding moiety portion of the DDpp-CAR further binds a target selected from: HVEM, BTLA, DR3, CD19, CD20, and CD22.

[0162] In one embodiment, a DDpp in a DDpp-CAR specifically binds a tumor antigen associated with a malignant tumor. In one embodiment, a DDpp of a DDpp-CAR binds to an antigen selected from: a B cell lymphoma-specific idiotype immunoglobulin; a B cell differentiation antigen such as CD19, CD20 and CD37; TSLPR and IL7R on myeloid cells, and heat shock protein gp96 on multiple myeloma cells.

[0163] In some embodiments, a DDpp in the antigen binding moiety portion of a DDpp-CAR specifically binds AFP, AFP p26, or a fragment thereof. In some embodiments, the DDpp specifically binds an AFP protein having an amino acid sequence consisting of SEQ ID NO: 9, or a fragment thereof. In some embodiments, the DDpp specifically binds an AFP p26 protein having an amino acid sequence consisting of SEQ ID NO: 10, or a fragment thereof. In further embodiments, the DDpp specifically comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the antigen binding moiety portion of the DDpp-CAR further binds a tumor antigen. In additional embodiments, the antigen binding moiety portion of the DDpp-CAR further binds a target selected from: BCMA, CD123, CS1, HER2, HVEM, BTLA, DR3, CD19, CD20, and CD22.

Transmembrane Domain

[0164] "Transmembrane domain" (TMD) as used herein refers to the region of a cell surface expressed DDpp fusion protein such as a DDpp-CAR, which crosses the plasma membrane. In some embodiments, the transmembrane domain of the DDpp-CAR is the transmembrane region of a transmembrane protein (for example Type I transmembrane proteins), an artificial hydrophobic sequence or a combination thereof. Other transmembrane domains will be apparent to those of skill in the art and may be used in connection with alternate embodiments provided herein.

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[0165] The DDpp receptor (*e.g.,* DDpp-CAR) can be designed to contain a transmembrane domain that is fused to the extracellular domain of the DDpp receptor. As described above, the fusion of the extracellular and transmembrane domains can be accomplished with or without a linker. In one embodiment, the transmembrane domain that is naturally associated with one of the domains in the DDpp-CAR is used. In a specific embodiment, the transmembrane domain in the DDpp-CAR is the CD8 transmembrane domain. In some instances, the transmembrane domain of the DDpp-CAR comprises the CD8 hinge domain. In some embodiments, the transmembrane domain is be selected or modified by amino acid substitution to promote or inhibit association with other surface membrane proteins.

[0166] The transmembrane domain can be derived either from a natural or from a synthetic source. Where the source is natural, the domain can be derived from any membrane-bound or transmembrane protein. Transmembrane regions of particular use for the purposes herein may be derived from (*i.e.*, comprise at least the transmembrane region(s) of) a member selected from the group: the alpha, beta or zeta chain of the T cell receptor; CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, and CD154. Alternatively the transmembrane domain can be synthetic, in which case the DDpp-CAR transmembrane domain will comprise predominantly hydrophobic residues such as leucine and valine. In further embodiments, the transmembrane domain comprises the triplet of phenylalanine, tryptophan and valine at each end of a synthetic transmembrane domain.

[0167] "Extracellular spacer domain" (ESD) as used herein refers to the hydrophilic region which is between the antigen-specific targeting region and the transmembrane domain. In some embodiments, the DDpp-CAR comprise an extracellular spacer domain. In other embodiments, the DDpp-CAR does not comprise an extracellular spacer domain. The extracellular spacer domains include but are not limited to Fc fragments of antibodies or fragments or derivatives thereof, hinge regions of antibodies or fragments or derivatives thereof, CH2 regions of antibodies, CH3 regions of antibodies, artificial spacer sequences or combinations thereof. Additional examples of extracellular spacer domains include but are not limited to CD8a hinge, and artificial spacers made of polypeptides which may be as small as, for example, Gly3 or CHI and CH3 domains of IgGs (such as human IgG4). In some embodiments, the extracellular spacer domain is any one or more of (i) a hinge, CH2 and CH3 regions of IgG4, (ii) a hinge region of IgG4, (iii) a hinge and CH2 of IgG4, (iv) a hinge region of

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CD8a, (v) a hinge, CH2 and CH3 regions of IgGl, (vi) a hinge region of IgGl or (vi) a hinge and CH2 region of IgGl. Other extracellular spacer domains will be apparent to those of skill in the art and may be used in connection with alternate embodiments, provided herein.

[0168] In some embodiments, a short oligo- or polypeptide linker, from about 1 to 100 amino acids in length, is used to link together any of the domains of a DDpp-CAR. Linkers can be composed of flexible residues like glycine and serine (or any other amino acid) so that the adjacent protein domains are free to move relative to one another. The amino acids sequence composition of the linker may be selected to minimize potential immunogenicity of the DDpp-CAR or DDpp fusion protein. Longer linkers can be used when it is desirable to ensure that two adjacent domains do not sterically interfere with one another. In some embodiments, preferably between 2 and 10 amino acids in length forms the linkage between the transmembrane domain and the cytoplasmic signaling domain of the DDpp-CAR. In further embodiments, the linker is between 10 and 15 amino acids in length, or between 15 and 20, or between 20 and 30, or between 30 and 60, or between 60 and 100 amino acids in length (or any range in between those listed). In further embodiments, the linker is a glycine-serine doublet sequence. Further embodiments employ a fragment of the hinge region derived from the human T cell surface glycoprotein CD8 alpha-chain (for example ranging from amino acid positions 138-182 CD8 alpha chain; Swiss-Prot accession number P01732). Further embodiments employ a fragment of the CD8 hinge region that has been further modified, through amino acid substitution, to improve expression function or immunogenicity. Further embodiments employ a fragment of the extracellular region derived from the human CD28 Further embodiments employ a fragment of the CD28 extracellular region that has been further modified, through amino acid substitution, to improve expression function or immunogenicity.

Intracellular Domain

[0169] "Intracellular signaling domain" (ISD) or "cytoplasmic domain" as used herein refer to the portion of the DDpp-CAR which transduces the effector function signal and directs the cell to perform its specialized function. The cytoplasmic domain (*i.e.*, intracellular signaling domain) of a DDpp-CAR is responsible for activation of at least one of the normal effector functions of an immune cell engineered to express a DDpp-CAR. The term "effector function" refers to a specialized function of a cell. The effector function of a T cell, for example, includes cytolytic activity and helper activity including the secretion of cytokines. Thus the term "intracellular signaling domain" refers to the

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portion of a DDpp-CAR protein which transduces the effector function signal and directs the cell to perform a specialized function. While typically the entire intracellular signaling domain corresponding to a naturally occurring receptor can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the intracellular signaling domain is used, such truncated portion can be used in place of the intact chain as long as it transduces the effector function signal. The term intracellular signaling domain is thus meant to include any truncated portion of the intracellular signaling domain sufficient to transduce the effector function signal. In one embodiment, an intracellular signaling domain in the DDpp-CAR includes the cytoplasmic sequences of the T cell receptor (TCR) and also the sequence of co-receptors that act in concert to initiate signal transduction following antigen receptor engagement, or any derivative or variant of these sequences that has functional capability. Examples of domains that transduce an effector function signal include but are not limited to the ζ chain of the T cell receptor complex or any of its homologs (*e.g.,* η chain, FcsRly and β chains, MB 1 (Iga) chain, B29 (Ig) chain, *etc.*), human CD3 zeta chain, CD3 polypeptides (Δ, δ and ε), syk family tyrosine kinases (Syk, ZAP 70, *etc.*), src family tyrosine kinases (Lck, Fyn, Lyn, *etc.*) and other molecules involved in T cell transduction, such as CD2, CD5 and CD28.

[0170] It is known that signals generated through the TCR alone are insufficient for full activation of the T cell and that a secondary or co-stimulatory signal is also required. Thus, T cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequence: those that initiate antigen-dependent primary activation through the TCR (primary cytoplasmic signaling sequences) and those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal (secondary cytoplasmic signaling sequences).

[0171] Primary cytoplasmic signaling sequences regulate primary activation of the TCR complex either in a stimulatory way, or in an inhibitory way. Primary cytoplasmic signaling sequences that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs (ITAMs).

[0172] Examples of ITAM containing primary cytoplasmic signaling sequences that are of particular use in the provided embodiments include those derived from TCR zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD22, CD79a, CD79b, and CD66d. It is particularly preferred that cytoplasmic signaling molecule in the CAR comprises a cytoplasmic signaling sequence derived from CD3 zeta.

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[0173] "Co-stimulatory domain" (CSD) as used herein refers to the portion of a CAR or DDpp-CAR which enhances the proliferation, survival and/or development of memory cells. The DDpp-CAR may comprise one or more co-stimulatory domains. Each co-stimulatory domain comprises the costimulatory domain of any one or more of, for example, a member of the TNFR superfamily, selected from CD28, CD137 (4-lBB), CD134 (OX40), Dap10, CD27, CD2, CD5, ICAM-1, LFA-1(CD1 la/CD18), Lck, TNFR-I, TNFR-II, Fas, CD30, and CD40 or a combination thereof. Other co-stimulatory domains (*e.g.,* from other proteins) will be apparent to those of skill in the art and may be used in connection with alternate embodiments encompassed by the disclosure.

[0174] In a preferred embodiment, the cytoplasmic domain of a DDpp-CAR comprises the CD3-zeta signaling domain by itself or combined with any other desired cytoplasmic domain(s) useful in the context of the DDpp-CAR. For example, the cytoplasmic domain of the DDpp-CAR can comprise a CD3 zeta chain portion and a costimulatory signaling region. The costimulatory signaling region refers to a portion of the CAR comprising the intracellular domain of a costimulatory molecule. A costimulatory molecule is a cell surface molecule other than an antigen receptor or their ligands that is required for an efficient response of lymphocytes to an antigen. Examples of such molecules include CD27, CD28, 41BB (CD 137), OX40, CD30, CD40, PD1, ICOS, lymphocyte function-associated antigen-1 (LFA1), CD2, CD7, LIGHT, NKG2C, B7H3, TIM1, and LAG3.

[0175] Polypeptide linkers may be positioned between adjacent elements of the DDpp-CAR. For example linkers may be positioned between adjacent DDpp or between DDpp and the transmembrane domain or between the transmembrane domain and the cytoplasmic domain or between adjacent cytoplasmic domains. The cytoplasmic signaling sequences within the cytoplasmic signaling portion of the DDpp-CAR may be linked to each other in a random or specified order. Optionally, a short linker, preferably between 2 and 10 amino acids in length may form the linkage. A glycine-serine doublet provides a particularly suitable linker.

[0176] In additional embodiments, the DDpp fusion protein is a chimeric antigen receptor (CAR) which comprises a target binding domain comprising a DD disclosed herein (*e.g.,* a DD comprising the amino acid sequence of SEQ ID NO: 11-949, or 950). In some embodiments, the DD binds BCMA and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DD binds CD123 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments,

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the DD binds CS1 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DD binds HER2 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DD binds AFP and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DD binds AFP p26 and comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the CAR comprises, a target binding domain, a transmembrane domain, and an intracellular signaling domain. In some embodiments, the CAR transmembrane domain comprises a 41BB or CD28 transmembrane domain. In some embodiments the CAR comprises an intracellular signaling domain selected from the group consisting of a domain of a human T cell receptor alpha, beta, or zeta chain; a human 41BB domain; a human CD28 domain; and any combination thereof. In some embodiments, the CAR intracellular signaling domain comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4lBB, OX40, CD30, CD40, PD1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, and any combination thereof. In some embodiments the CAR further comprises a second target binding domain having the same or a different target than the DD target binding domain. In some embodiments, the CAR comprises a first target binding domain that binds CS1 and a second target binding domain that binds BCMA. In some embodiments, the CAR is expressed in an immune cell. In some embodiments, the immune cell is a T cell (CAR-T cell) or a natural killer (NK) cell (CAR-NK cell). In some embodiments, the CAR is associated with a liposome. In some embodiments, the CAR comprises 2, 3, 4, 5, or more than 5, DD and/or other binding domains (*e.g.,* scFv) that specifically bind a target of interest (*e.g.,* BCMA, CS1, or CD123) expressed on the surface of the cancer cell. In additional embodiments, the CAR comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically bind a second, different target of interest, expressed on the surface of the cancer cell. In additional embodiments, the administered CAR further comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically binds a second, different target of interest, expressed by a second, different cancer cell or a vascular endothelial cell.

Additional DDpp fusion proteins

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[0177] In some embodiments, the DDpp contains a heterologous polypeptide comprising a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp contains a heterologous polypeptide that comprises the extracellular domain, or a fragment of an extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8). In some embodiments, the DDpp contains a heterologous polypeptide that comprises the extracellular domain, or a fragment of an extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a heterologous polypeptide that comprises the extracellular domain, or a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0178] In some embodiments, the protein contains a heterologous polypeptide that comprises a serum protein or an antigenic fragment of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the DDpp contains a heterologous polypeptide comprising a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein. In some embodiments, the protein contains a heterologous polypeptide that comprises an intracellular protein or an antigenic portion of an intracellular protein (*e.g.,* a nuclear protein). In some embodiments, the DDpp contains a heterologous polypeptide comprising a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an intracellular protein. In some embodiments, the DDpp contains a heterologous polypeptide having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974.

[0179] In some embodiments, the DDpp fusion protein specifically binds BCMA, CD123, CS1, HER2, AFP, and/or AFP p26, and further binds one or more additional targets of interest. The targets of interest specifically bound by a DDpp fusion protein can be any molecule for which it is desirable for a DDpp to bind. For example, the targets specifically bound by the DDpp fusion protein can be BCMA, CD123, CS1, HER2, AFP, and/or AFP p26, and additionally any additional target of manufacturing, formulation, therapeutic, diagnostic, or prognostic relevance or value. A number of exemplary additional targets are provided herein, by way of example, and are intended to be illustrative and not limiting. The additional target of interest bound by the DDpp fusion protein can be naturally occurring or synthetic. The additional target of interest can be an extracellular component or an

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intracellular component, a soluble factor (*e.g.,* an enzyme, hormone, cytokine, and growth factor, toxin, venom, pollutant, *etc.*), or a transmembrane protein (*e.g.,* a cell surface receptor). In some embodiments, the target of interest bound by the DDpp fusion protein is a human protein. In one embodiment, a DDpp (*e.g.,* a DDpp fusion protein) binds a human protein target of interest and its monkey (*e.g.,* cynomolgous monkey), mouse, rabbit, hamster and/or a rabbit ortholog.

[0180] In one embodiment a DDpp fusion protein specifically binds BCMA, CD123, CS1, HER2, AFP, and/or AFP p26, and a serum protein. In one embodiment, the DDpp fusion protein specifically binds a serum protein selected from: serum albumin (*e.g.,* human serum albumin (HSA)), thyroxin-binding protein, transferrin, fibrinogen, and an immunoglobulin (*e.g.,* IgG, IgE and IgM). Without being bound by theory, the binding of a DDpp to a carrier protein is believed to confer upon the DDpp (or a fusion thereof) an improved pharmacodynamic profile that includes, but is not limited to, improved tumor targeting, tumor penetration, diffusion within the tumor, and enhanced therapeutic activity compared to the DDpp fusion protein in which the carrier protein binding sequence is missing (*see, e.g.,* WO01/45746, the contents of which is herein incorporated by reference in its entirety).

Antibody-based DDpp fusion proteins

[0181] In some embodiments, the DDpp fusion protein comprises a full-length antibody or a fragment or subdomain of an antibody. In some embodiment, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the DDpp is an Fc fusion protein. In further embodiments, the Fc protein comprises a variant human Fc domain.

[0182] In some embodiments, the DDpp fusion protein comprises a full-length antibody or an antibody fragment or subdomain (*e.g.,* an IgG1 antibody, IgG3 antibody, antibody variable region, CDR3, scFv, Fc, FcRn binding subdomain, and other antibody subdomains). DDpp proteins can be operably linked to one another and/or to one or more termini of an antibody, antibody chain, antibody fragment, or antibody subdomain to form a DDpp fusion protein.

[0183] The antibody component of a DDpp fusion protein can be any suitable full-length immunoglobulin or antibody fragment (*e.g.,* an antigen binding domain and/or effector domain) or a

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fragment thereof. In one embodiment, the DDpp-antibody fusion protein retains the structural and functional properties of a traditional monoclonal antibody. Thus, in some embodiments, the DDpp-antibody fusion protein retains the epitope binding properties, but advantageously also incorporate, via the DDpp fusion, one or more additional target-binding specificities. Antibodies that can be used in the DDpp fusions include, but are not limited to, monoclonal, multi-specific, human, humanized, primatized, and chimeric antibodies. Immunoglobulin or antibody molecules provided herein can be of any type (*e.g.,* IgG, IgE, IgM, IgD, IgA, and IgY), class (*e.g.,* IgGl, IgG2, IgG3, IgG4, IgAl and IgA2) or subclass of immunoglobulin molecule. In specific embodiments, the antibodies are Fc optimized antibodies. Antibodies can be from or derived from any animal origin including birds and mammals or generated synthetically. The antibody component of the DDpp-antibody fusion protein can be naturally derived or the result of recombinant engineering (*e.g.,* phage display, xenomouse, and synthetic). In certain embodiments, the antibody component of the antibody-DDpp fusion enhances half-life, and increase or decrease antibody dependent cellular cytotoxicity (ADCC), and/or complement dependent cytotoxicity (CDC) activity. In some embodiments, the antibodies are human, murine, donkey, rabbit, goat, guinea pig, camel, llama, horse, or chicken antibodies. In specific embodiments, the antibodies are human.

[0184] It is generally understood that the constant region mediates several effector functions. For example, binding of the C1 component of complement to antibodies activates the complement system. Activation of complement is important in the opsonization and lysis of cell pathogens. The activation of complement also stimulates the inflammatory response and can also be involved in autoimmune hypersensitivity. Further, antibodies bind to cells via the Fc region, with an Fc receptor site on the antibody Fc region binding to an Fc receptor (FcR) on a cell. There are a number of Fc receptors that are specific for different classes of antibody, including IgG (gamma receptors), IgE (eta receptors), IgA (alpha receptors) and IgM (mu receptors). Binding of antibody to Fc receptors on cell surfaces triggers a number of important and diverse biological responses including engulfment and destruction of antibody-coated particles, clearance of immune complexes, lysis of antibody-coated target cells by killer cells (called antibody-dependent cell-mediated cytotoxicity, or ADCC), release of inflammatory mediators, placental transfer and control of immunoglobulin production.

[0185] In certain embodiments, the DDpp-Fc fusion protein has an altered effector function that, in turn, affects the biological profile of the administered DDpp-Fc fusion protein. For example,

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the deletion or inactivation (through point mutations or other means) of a constant region subdomain can reduce Fc receptor binding of the circulating modified antibody. In other cases the constant region modifications, can moderate complement binding and thus reduce the serum half-life and nonspecific association of a conjugated cytotoxin. Yet other modifications of the constant region can be used to eliminate disulfide linkages or oligosaccharide moieties that allow for enhanced localization due to increased antigen specificity or antibody flexibility. Similarly, modifications to the constant region in accordance with this disclosure can easily be made using biochemical or molecular engineering techniques known to those of ordinary skill in the art.

[0186] In some embodiments, the DDpp-Fc fusion protein does not have one or more effector functions. For instance, in some embodiments, the DDpp-Fc fusion protein has no antibody-dependent cellular cytoxicity (ADCC) activity and/or no complement-dependent cytoxicity (CDC) activity. In certain embodiments, the DDpp-Fc fusion protein does not bind to an Fc receptor and/or complement factors. In certain embodiments, the DDpp-Fc fusion protein has no effector function. Examples of Fc sequence engineering modifications that reduce or eliminate ADCC and/or CDC activity and Fc receptor and/or complement factor binding are described herein or otherwise know in the art, as are assays and procedures for testing the same.

[0187] In some embodiments, DDpp-Fc fusion protein is engineered to fuse the CH3 domain directly to the hinge region of the respective modified antibody. In other constructs a peptide spacer is inserted between the hinge region and the modified CH2 and/or CH3 domains. For example, compatible constructs can be expressed in which the CH2 domain has been deleted and the remaining CH3 domain (modified or unmodified) is joined to the hinge region with a 5-20 amino acid spacer. Such a spacer can be added, for instance, to ensure that the regulatory elements of the constant domain remain free and accessible or that the hinge region remains flexible. Amino acid spacers can, in some cases, prove to be immunogenic and elicit an unwanted immune response against the construct. Accordingly, in certain embodiments, any spacer added to the construct can be relatively non-immunogenic, or even omitted altogether, so as to maintain the desired biochemical qualities of the modified DDpp-Fc fusion protein.

[0188] In additional embodiments, the DDpp-Fc fusion protein is modified by the partial deletion or substitution of a few or even a single amino acid in a constant region. For example, the mutation of a single amino acid in selected areas of the CH2 domain can be enough to substantially

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reduce Fc binding and thereby. Similarly one or more constant region domains that control the effector function (*e.g.,* complement C1Q binding) can be fully or partially deleted. Such partial deletions of the constant regions can improve selected characteristics of the DDpp-Fc fusion protein (*e.g.,* serum half-life) while leaving other desirable functions associated with the corresponding constant region domain intact. In some embodiments, the constant region of the DDpp-Fc fusion protein is modified through the mutation or substitution of one or more amino acids that enhances the profile of the resulting construct. In this respect it is possible to disrupt the activity provided by a conserved binding site (*e.g.,* Fc binding) while substantially maintaining the configuration and immunogenic profile of the modified DDpp-Fc fusion protein. The disclosure also provides an DDpp-Fc fusion protein that contains the addition of one or more amino acids to the constant region to enhance desirable characteristics such, as decreasing or increasing effector function or providing attachments sites for one or more cytotoxin, labeling or carbohydrate moieties. In such embodiments, it can be desirable to insert or replicate specific sequences derived from selected constant region domains.

[0189] In some embodiments, the DDpp is operably linked to an antibody fragment or subdomain (*e.g.,* scFv, diabody, EP 404,097; WO93/111161; WO14/028776; and Holliger *et al.*, PNAS 90: 6444-6448 (1993), the contents of each of which is herein incorporated by reference in its entirety). The antibody fragment or subdomain can be any fragment or domain of an antibody. See for example, WO04/058820, WO99/42077 and WO05/017148, the contents of each of which is herein incorporated by reference in its entirety. For example, a DDpp fusion protein can contain an antibody effector domain or derivative of an antibody effector domain that confers one or more effector functions to the DDpp and/or confers upon the DDpp fusion protein the ability to bind to one or more Fc receptors. In some embodiments, a DDpp-antibody fusion protein contains an antigen-binding fragment of an antibody or a fragment thereof. In additional embodiments, a DDpp-antibody fusion protein contains an immunoglobulin effector domain that comprises one or more CH2 and or CH3 domains of an antibody having effector function provided by the CH2 and CH3 domains. Other sequences in the DDpp fusion that provide an effector function and that are encompassed by the invention will be clear to those skilled in the art and can routinely be chosen and designed into a DDpp fusion protein encompassed herein on the basis of the desired effector function(s).

[0190] In one embodiment, the DDpp fusion contains a full-length antibody or an antibody fragment that is an antigen-binding fragment. In a further embodiment, the antibody or antibody

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fragment binds a disease-related antigen. In one embodiment the DDpp fusion protein comprises an antibody or an antibody fragment that specifically binds a cancer antigen. In another embodiment, the DDpp fusion protein comprises an antibody or an antibody fragment that specifically binds a particular pathogen (*e.g.,* a bacterial cell (*e.g.,* tuberculosis, smallpox, anthrax)), a virus (*e.g.,* HIV), a parasite (*e.g.,* malaria, leishmaniosis), a fungal infection, a mold, a mycoplasm, a prion antigen, In another embodiment, the DDpp fusion protein comprises an antibody or an antibody fragment that specifically binds a particular pathogen (*e.g.,* a bacterial cell (*e.g.,* tuberculosis, smallpox, anthrax)), a virus (*e.g.,* HIV), a parasite (*e.g.,* malaria, leishmaniosis), a fungal infection, a mold, a mycoplasm, or a prion antigen. In another embodiment, the DDpp fusion protein comprises an antibody or an antibody fragment that specifically binds an antigen associated with a disease or disorder of the immune system.

[0191] In preferred embodiments, the DDpp fusion protein containing an antibody fragment or domain retains activities of the parent antibody. Thus, in certain embodiments, the DDpp fusion protein containing an antibody fragment or domain is capable of inducing complement dependent cytotoxicity. In certain embodiments, the DDpp fusion protein containing an antibody fragment or domain is capable of inducing antibody dependent cell mediated cytotoxicity (ADCC).

[0192] Accordingly, in some embodiments, the DDpp fusion protein comprises an antibody fragment that confers upon the DDpp fusion protein a biological or biochemical characteristic of an immunoglobulin. In some embodiments, the antibody fragment confers a characteristic selected from: the ability to non-covalently dimerize, the ability to localize at the site of a tumor, and an increased serum half-life when compared to the DDpp fusion protein in which said one or more DDpp have been deleted. In certain embodiments, the DDpp fusion protein is at least as stable as the corresponding antibody without the attached DDpp. In certain embodiments, the DDpp fusion protein is more stable than the corresponding antibody without the attached DDpp. DDpp fusion protein stability can be measured using established methods, including, for example, ELISA techniques. In some embodiments, the DDpp fusion protein is stable in whole blood (*in vivo* or *ex vivo*) at 37° C for at least about 10 hours, at least about 15 hours, at least about 20 hours, at least about 24 hours, at least about 25 hours, at least about 30 hours, at least about 35 hours, at least about 40 hours, at least about 45 hours, at least about 48 hours, at least about 50 hours, at least about 55 hours, at least about 60 hours, at least about 65 hours, at least about 70 hours, at least about 72 hours, at least about 75 hours, at least about 80 hours, at least about 85 hours, at least about 90 hours, at least about 95 hours, or at least about

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100 hours (including any time between those listed). In one embodiment, a DDpp fusion contains an immunoglobulin effector domain or half-life influencing domain that corresponds to an immunoglobulin domain or fragment in which at least a fraction of one or more of the constant region domains has been altered so as to provide desired biochemical characteristics such as reduced or increased effector functions, the ability to non-covalently dimerize, increased ability to localize at the site of a tumor, reduced serum half-life, or increased serum half-life when compared with an immunoglobulin fragment having the corresponding unaltered immunoglobulin sequence. These alterations of the constant region domains can be amino acid substitutions, insertions, or deletions.

[0193] In one embodiment, a DDpp fusion protein comprises an amino acid sequence of an immunoglobulin effector domain or a derivative of an immunoglobulin effector domain that confers antibody dependent cellular cytotoxicity (ADCC) to the DDpp fusion protein. In additional embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to increase ADCC (*see, e.g.,* Bruhns, Blood 113: 3716-3725 (2009); Shields, J. Biol. Chem. 276: 6591-6604 (2001); Lazar, PNAS 103: 4005-4010 (2006); Stavenhagen, Cancer Res. 67: 8882-8890 (2007); Horton, Cancer Res. 68: 8049-8057 (2008); Zalevsky, Blood 113: 3735-3743 (2009); Bruckheimer, Neoplasia 11: 509-517 (2009); WO06/020114; Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and WO04/074455; the contents of each of which is herein incorporated by reference in its entirety). Examples of immunoglobulin fragment engineering modifications contained in an amino acid sequence in a DDpp fusion protein that increases ADCC include immunoglobulin effector domain sequences having one or more modifications corresponding to: IgG1-S298A, E333A, K334A; IgG1-S239D, I332E; IgG1-S239D, A330L, I332E; IgG1-P247I, A339D or Q; IgG1-D280H, K290S with or without S298D or V; IgG1-F243L, R292P, Y300L; IgG1-F243L, R292P, Y300L, P396L; and IgG1-F243L, R292P, Y300L, V305I, P396L; wherein the numbering of the residues in the Fc region is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0194] In other embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to decrease ADCC (*see, e.g.,* Idusogie *et al.*, J. Immunol. 166: 2571-2575 (2001); Sazinsky *et al.*, PNAS 105: 20167-20172 (2008); Davis *et al.*, J. Rheumatol. 34: 2204-2210 (2007); Bolt *et al.*, Eur. J. Immunol. 23: 403-411 (1993); Alegre *et al.*,

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Transplantation 57: 1537-1543 (1994); Xu *et al.*, Cell Immunol. 200: 16-26 (2000); Cole *et al.*, Transplantation 68: 563-571 (1999); Hutchins *et al.*, PNAS 92: 11980-11984 (1995); Reddy *et al.*, J. Immunol. 164: 1925-1933 (2000); WO97/11971; WO07/106585; US 2007/0148167A1; McEarchern *et al.*, Blood 109: 1185-1192 (2007); Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Kumagai *et al.*, J. Clin. Pharmacol. 47: 1489-1497 (2007), the contents of each of which is herein incorporated by reference in its entirety). Examples of immunoglobulin fragment sequence engineering modifications contained in an amino acid sequence in a DDpp fusion protein that decreases ADCC include immunoglobulin effector domain sequences having one or more modifications corresponding to: IgG1-K326W, E333S; IgG2-E333S; IgG1-N297A; IgG1-L234A, L235A; IgG2-V234A, G237A; IgG4-L235A, G237A, E318A; IgG4-S228P, L236E; IgG2- 118-260; IgG4- 261-447; IgG2-H268Q, V309L, A330S, A331S; IgG1-C220S, C226S, C229S, p268S; IgG1-C226S, C229S, E233P, L234V, L235A; or IgG1-L234F, L235E, P331S; wherein the numbering of the residues is that of the EU index of Kabat (Kabat *et al.*, Sequences of Proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0195] In additional embodiments, a DDpp fusion protein comprises an amino acid sequence of an immunoglobulin effector domain, or a derivative of an immunoglobulin effector domain, that confers antibody-dependent cell phagocytosis (ADCP) to the DDpp fusion protein. In additional embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to increase antibody-dependent cell phagocytosis (ADCP); (*see, e.g.,* Shields *et al.*, J. Biol. Chem. 276: 6591-6604 (2001); Lazar *et al.*, PNAS 103: 4005-4010 (2006); Stavenhagen *et al.*, Cancer Res. 67: 8882-8890 (2007); Richards *et al.*, Mol. Cancer Ther. 7: 2517-2527 (2008); Horton *et al.*, Cancer Res. 68: 8049-8057 (2008), Zalevsky *et al.*, Blood 113: 3735-3743 (2009); Bruckheimer *et al.*, Neoplasia 11: 509-517 (2009); WO06/020114; Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and WO04/074455, the contents of each of which is herein incorporated by reference in its entirety). Examples of immunoglobulin fragment engineering modifications contained in an amino acid sequence in a DDpp fusion protein that increases ADCP include immunoglobulin effector domain sequences having one or more modifications corresponding to: IgG1-S298A, E333A, K334A; IgG1-S239D, I332E; IgG1-S239D, A330L, I332E; IgG1-P247I, A339D or Q; IgG1-D280H, K290S with or without S298D or V; IgG1-F243L, R292P, Y300L; IgG1-F243L, R292P, Y300L, P396L; IgG1-F243L, R292P, Y300L, V305I, P396L; and IgG1-G236A, S239D, I332E; wherein the

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numbering of the residues is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its eitrety).

[0196] In other embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to decrease ADCP (*see, e.g.,* Sazinsky *et al.*, PNAS 105: 20167-20172 (2008); Davis *et al.*, J. Rheumatol. 34: 2204-2210 (2007); Bolt *et al.*, Eur. J. Immunol. 23: 403-411 (1993); Alegre *et al.*, Transplantation 57: 1537-1543 (1994); Xu *et al.*, Cell Immunol. 200: 16-20 (2000); Cole *et al.*, Transplantation 68: 563-571 (1999); Hutchins *et al.*, PNAS 92: 11980-11984 (1995); Reddy *et al.*, J. Immunol. 164: 1925-1933 (2000); WO97/11971; WO07/106585; US 2007/0148167A1; McEarchern *et al.*, Blood 109: 1185-1192 (2007); Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Kumagai *et al.*, J. Clin. Pharmacol. 47: 1489-1497 (2007), the contents of each of which is herein incorporated by reference in its entirety). By way of example, DDpp fusion proteins can contain an antibody fragment or domain that contains one or more of the following modifications that decrease ADCC: IgG1-N297A; IgG1-L234A, L235A; IgG2-V234A, G237A; IgG4-L235A, G237A, E318A; IgG4-S228P, L236E; IgG2 EU sequence 118-260; IgG4-EU sequence 261-447; IgG2-H268Q, V309L, A330S, A331S; IgG1-C220S, C226S, C229S, p268S; IgG1-C226S, C229S, E233P, L234V, L235A; and IgG1-L234F, L235E, P331S; wherein the numbering of the residues is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0197] In additional embodiments, a DDpp fusion protein comprises an amino acid sequence of an immunoglobulin effector domain, or a derivative of an immunoglobulin effector domain, that confers complement-dependent cytotoxicity (CDC) to the DDpp fusion protein. In additional embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to increase complement-dependent cytotoxicity (CDC) (*see, e.g.,* Idusogie *et al.*, J. Immunol. 166: 2571-2575 (2001); Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Natsume *et al.*, Cancer Res. 68: 3863-3872 (2008), the contents of each of which is herein incorporated by reference in its entirety). By way of example, DDpp fusion proteins can contain an antibody fragment or domain that contains one or more of the following modifications that increase CDC: IgG1-K326A, E333A; IgG1-K326W, E333S, IgG2-E333S; wherein the numbering of the residues is that of

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the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0198] In additional embodiments, a DDpp fusion protein comprises an amino acid sequence of an immunoglobulin effector domain, or a derivative of an immunoglobulin effector domain, that confers the ability to bind FcgammaRIIb receptor to the DDpp fusion. In additional embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to increase inhibitory binding to FcgammaRIIb receptor (*see, e.g.,* Chu *et al.*, Mol. Immunol. 45: 3926-3933 (2008)). An example of an immunoglobulin fragment engineering modification contained in an amino acid sequence in a DDpp fusion protein that increases binding to inhibitory FcgammaRIIb receptor is IgG1- S267E, L328F.

[0199] In other embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to decrease CDC (*see, e.g.,* WO97/11971; WO07/106585; US 2007/0148167A1; McEarchern *et al.*, Blood 109: 1185-1192 (2007); Hayden-Ledbetter *et al.*, Clin. Cancer 15: 2739-2746 (2009); Lazar *et al.*, PNAS 103: 4005-4010 (2006); Bruckheimer *et al.*, Neoplasia 11: 509-517 (2009); Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Sazinsky *et al.*, PNAS 105: 20167-20172 (2008); the contents of each of which is herein incorporated by reference in its entirety). By way of example, DDpp fusion proteins can contain an antibody fragment or domain that contains one or more of the following modifications that decrease CDC: IgG1-S239D, A330L, I332E; IgG2- 118-260; IgG4- 261-447; IgG2-H268Q, V309L, A330S, A331S; IgG1-C226S, C229S, E233P, L234V, L235A; IgG1-L234F, L235E, P331S; and IgG1-C226S, p260S; wherein the numbering of the residues is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0200] The half-life of an IgG is mediated by its pH-dependent binding to the neonatal receptor FcRn. In certain embodiments, a DDpp fusion protein comprises an amino acid sequence of an immunoglobulin effector domain, or a derivative of an immunoglobulin effector domain, that confers the ability to bind neonatal receptor FcRn to the to the DDpp fusion. In certain embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin FcRn binding domain that has been modified to enhance binding to FcRn (*see, e.g.,* Petkova *et al.*, Int. Immunol. 18: 1759-1769 (2006); Dall'Acqua *et al.*, J. Immunol. 169: 5171-5180 (2002); Oganesyan *et al.*, Mol. Immunol. 46: 1750-

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1755 (2009); Dall'Acqua *et al.*, J. Biol. Chem. 281: 23514-23524 (2006); Hinton *et al.*, J. Immunol. 176: 346-356 (2006); Datta-Mannan *et al.*, Drug Metab. Dispos. 35: 86-94 (2007); Datta-Mannan *et al.*, J. Biol. Chem. 282: 1709-1717 (2007); WO06/130834; Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Yeung *et al.*, J. Immunol. 182: 7663-7671 (2009); the contents of each of which is herein incorporated by reference in its entirety).

[0201] In additional embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to have a selective affinity for FcRn at pH 6.0, but not pH 7.4. By way of example, DDpp fusion proteins can contain an antibody fragment or domain that contains one or more of the following modifications that increase half-life: IgG1-M252Y, S254T, T256E; IgG1-T250Q, M428L; IgG1-H433K, N434Y; IgG1-N434A; and IgG1-T307A, E380A, N434A; wherein the numbering of the residues is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of Proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0202] In other embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been modified to decrease binding to FcRn (*see, e.g.,* Petkova *et al.*, Int. Immunol. 18: 1759-1769 (2006); Datta-Mannan *et al.*, Drug Metab. Dispos. 35: 86-94 (2007); Datta-Mannan *et al.*, J. Biol. Chem. 282: 1709-1717 (2007); Strohl, Curr. Op. Biotechnol. 20: 685-691 (2009); and Vaccaro *et al.*, Nat. Biotechnol. 23: 1283-1288 (2005); the contents of each of which is herein incorporated by reference in its entirety). By way of example, DDpp fusion proteins can contain an antibody fragment or domain that contains one or more of the following modifications that decrease half-life: IgG1-M252Y, S254T, T256E; H433K, N434F, 436H; IgG1-I253A; and IgG1-P257I, N434H and D376V, N434H; wherein the numbering of the residues is that of the EU index of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety).

[0203] According to another embodiment, DDpp fusion protein comprises an amino acid sequence corresponding to a immunoglobulin effector domain that has been modified to contain at least one substitution in its sequence corresponding to the Fc region (*e.g.,* FC gamma) position selected from the group consisting of: 238, 239, 246, 248, 249, 252, 254, 255, 256, 258, 265, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 301, 303, 305, 307, 309, 312, 315, 320, 322, 324, 326, 327, 329, 330, 331, 332, 333, 334, 335, 337, 338, 340, 360, 373,

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376, 378, 382, 388, 389, 398, 414, 416, 419, 430, 434, 435, 437, 438 and 439, wherein the numbering of the residues in the Fc region is according to the EU numbering system; of Kabat *et al.* (Kabat *et al.*, Sequences of proteins of Immunological Interest, 1991 Fifth edition, the contents of which is herein incorporated by reference in its entirety). In a specific embodiment, the DDpp fusion protein comprises a sequence of an immunoglobulin effector domain derivative wherein at least one residue corresponding to position 434 is a residue selected from the group consisting of: A, W, Y, F and H. According to another embodiment, the DDpp fusion protein comprises a sequence of an immunoglobulin effector fragment derivative having the following respective substitutions S298A/E333A/K334A. In an additional embodiment, the DDpp fusion protein comprises an immunoglobulin effector domain derivative having a substitution corresponding to K322A. In another embodiment, the DDpp fusion protein comprises a sequence of an immunoglobulin effector domain derivative having one or any combination of the following substitutions K246H, H268D, E283L, S324G, S239D and I332E. According to yet another embodiment, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain derivative having substitutions corresponding to D265A/N297A.

[0204] In certain embodiments, a DDpp fusion protein comprises a sequence of an immunoglobulin effector domain that has been glycoengineered or mutated to increase effector function using techniques known in the art. For example, the inactivation (through point mutations or other means) of a constant region domain sequence contained in a DDpp may reduce Fc receptor binding of the circulating DDpp fusion protein thereby increasing tumor localization. In other cases it may be that constant region modifications consistent with certain provided embodiments, moderate complement binding and thus reduce the serum half-life and nonspecific association of a conjugated cytotoxin. Yet other modifications of the constant region may be used to modify disulfide linkages or oligosaccharide moieties that allow for enhanced localization due to increased antigen specificity or antibody flexibility. The resulting physiological profile, bioavailability and other biochemical effects of the modifications, such as tumor localization, biodistribution and serum half-life, can easily be measured and quantified using well know immunological techniques without undue experimentation.

[0205] In some embodiments, an immune effector cell comprises a cell surface receptor for an immunoglobulin or other peptide binding molecule, such as a receptor for an immunoglobulin constant region and including the class of receptors commonly referred to as "Fc receptors" ("FcR"s). A number

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of FcRs have been structurally and/or functionally characterized and are known in the art, including FcR having specific abilities to interact with a restricted subset of immunoglobulin heavy chain isotypes, or that interact with Fc domains with varying affinities, and/or which may be expressed on restricted subsets of immune effector cells under certain conditions (*e.g.,* Kijimoto-Ochichai *et al.*, Cell Mol. Life. Sci. 59: 648 (2002); Davis *et al.*, Curr. Top. Microbiol. Immunol. 266: 85 (2002); Pawankar, Curr. Opin. Allerg. Clin. Immunol. 1: 3 (2001); Radaev *et al.*, Mol. Immunol. 38: 1073 (2002); Wurzburg *et al.*, Mol. Immunol. 38: 1063 (2002); Sulica *et al.*, Int. Rev. Immunol. 20: 371 (2001); Underhill *et al.*, Ann. Rev. Immunol. 20: 825 (2002); Coggeshall, Curr. Dir. Autoimm. 5: 1 (2002); Mimura *et al.*, Adv. Exp. Med. Biol. 495: 49 (2001); Baumann *et al.*, Adv. Exp. Med. Biol. 495: 219 (2001); Santoso *et al.*, Ital. Heart J. 2: 811 (2001); Novak *et al.*, Curr. Opin. Immunol. 13: 721 (2001); Fossati *et al.*, Eur. J. Clin. Invest. 31: 821 (2001)); the contents of each of which is herein incorporated by reference in its entirety.

[0206] Cells that are capable of mediating ADCC are examples of immune effector cells. Other immune effector cells include Natural Killer cells, tumor-infiltrating T lymphocytes (TILs), cytotoxic T lymphocytes, and granulocytic cells such as cells that comprise allergic response mechanisms. Immune effector cells thus include, but are not limited to, cells of hematopoietic origin including cells at various stages of differentiation within myeloid and lymphoid lineages and which may (but need not) express one or more types of functional cell surface FcR, such as T lymphocytes, B lymphocytes, NK cells, monocytes, macrophages, dendritic cells, neutrophils, basophils, eosinophils, mast cells, platelets, erythrocytes, and precursors, progenitors (*e.g.,* hematopoietic stem cells), as well as quiescent, activated, and mature forms of such cells. Other immune effector cells may include cells of non-hematopoietic origin that are capable of mediating immune functions, for example, endothelial cells, keratinocytes, fibroblasts, osteoclasts, epithelial cells, and other cells. Immune effector cells can also include cells that mediate cytotoxic or cytostatic events, or endocytic, phagocytic, or pinocytotic events, or that effect induction of apoptosis, or that effect microbial immunity or neutralization of microbial infection, or cells that mediate allergic, inflammatory, hypersensitivity and/or autoimmune reactions.

DDpp fusion proteins with inceasaed half-life

[0207] The disclosed DDpp can be fused or complexed to a second peptide domain increases the half-life or stability of the DDpp.

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[0208] In one aspect, the DDpp further comprises one or more amino acids that facilitate synthesis, handling, or use of the peptide, including, but not limited to, one or two lysines at the N-terminus and/or C-terminus to increase solubility of the polypeptide. Suitable fusion proteins include, but are not limited to, proteins comprising a DDpp linked to one or more polypeptides, polypeptide fragments, or amino acids not generally recognized to be part of the protein sequence. In one aspect, a fusion peptide comprises the entire amino acid sequences of two or more peptides or, alternatively, comprises portions (fragments) of two or more peptides. In some aspects, a peptide (*e.g.,* Protein S-binding peptide) is operably linked to, for instance, one or more of the following: a marker protein, a peptide that facilitates purification, a peptide sequence that promotes formation of multimeric proteins, or a fragment of any of the foregoing. Suitable fusion partners include, but are not limited to, a His tag, a FLAG tag, a strep tag, and a myc tag.

[0209] In some embodiments, the DDpp is fused to one or more moieties that enhance the half-life of the polypeptide. Half-life can be increased by for example, increasing the molecular weight of the DDpp to avoid renal clearance and/or incorporating a binding domain for FcRn-mediated recycling pathway. In one embodiment, the DDpp is fused to, or chemically conjugated to, an albumin polypeptide or a fragment thereof (*e.g.,* human serum albumin (HSA)). In particular embodiments, the fused or chemically conjugated albumin fragment comprises 10%, 25%, 50%, or 75% of the full length albumin protein. In additional or alternative embodiments, the DDpp is fused to or complexed with an albumin binding domain or fatty acid that binds albumin when administered *in vivo*. An example of an albumin binding domain is "albu-tag," a moiety derived from on 4-(p-iodophenyl)-butanoic acid (Dumelin *et al.*, Angew Chem. Int. Ed Engl. 47: 3196-3201 (2008)).

[0210] In one embodiment, the DDpp is fused to, or chemically conjugated to, a transferrin polypeptide or a fragment thereof (*e.g.,* human transferrin). In particular embodiments, the fused or chemically conjugated transferrin fragment comprises 10%, 25%, 50%, or 75% of the full length transferrin protein. In additional or alternative embodiments, the DDpp is fused to or complexed with a transferrin binding domain that binds transferrin when administered *in vivo*.

[0211] In some embodiments, the DDpp is fused to, or chemically conjugated to a proline-alanine-serine multimer (PASylation; XL-Protein GmbH), a non-exact repeat peptide sequence (XTENylation, rPEG), a homopolymer of glycine residues (HAPylation), elastin-like repeat(s) sequences (ELPylation; see for example, U.S. Pat. Appl. No. 61/442,106, the contents of which is

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herein incorporated by reference in its entirety), an artificial GLK (GLK fusion; Huang *et al*., Eur. J. Pharm. Biopharm. 72: 435–41 (2010)), or a CTP peptide from human CG beta-subunit (CTP fusion).

Additional DDpp fusion proteins

[0212] In some embodiments, the DDpp fusion protein specifically binds BCMA, CD123, CS1, HER2, AFP, and/or AFP p26, and further binds a disease-related antigen. The disease-related antigen can be an antigen characteristic of a cancer, and/or of a particular cell type (*e.g.,* a hyperproliferative cell), and/or of a pathogen (*e.g.,* a bacterial cell (*e.g.,* tuberculosis, smallpox, and anthrax), a virus (*e.g.,* HIV), a parasite (*e.g.,* malaria and leishmaniosis), a fungal infection, a mold, a mycoplasm, a prion antigen, or an antigen associated with a disorder of the immune system. In further embodiments, the DDpp fusion protein is conjugated to a therapeutic or cytotoxic agent.

[0213] In an additional embodiment, a DDpp fusion protein is linked to one or more chemical moieties (e.g., labels) that facilitate detection, multimerization, binding with an interaction partner, or characterization of DDpp activity. An exemplary chemical moiety is biotin. Other moieties suitable for conjugation to the DDpp include, but are not limited to, a photosensitizer, a dye, a fluorescence dye, a radionuclide, a radionuclide-containing complex, an enzyme, a toxin, and a cytotoxic agent. Photosensitizers include, *e.g.,* Photofrin, Visudyne, Levulan, Foscan, Metvix, Hexvix.RTM., Cysview.TM., Laserphyrin, Antrin, Photochlor, Photosens, Photrex, Lumacan, Cevira, Visonac, BF-200 ALA, and Amphinex. In additional embodiments, a His tag, a FLAG tag, a strep tag, or a myc tag is conjugated to the DDpp.

[0214] In another embodiment, the DDpp fusion protein comprises a DD that binds BCMA, CD123, CS1, HER2, AFP, AFP p26, or a fragment thereof, and further binds a peptide tag present on a target of interest. Such peptide tags provide a useful means by which to detect and/or attach targets of interest containing the peptide tags. In one embodiment, the DDpp fusion protein specifically binds a peptide tag selected from the group: a hexahistidyl (His6) tag, a myc tag or a FLAG tag. Other peptide tags are described herein or otherwise known in the art.

DDpp fusion proteins with an epitope tag

[0215] In some embodiments, the DDpp fusion protein comprises a peptide epitope tag. In some embodiments, the peptide tag is selected from the group consisting of a hexahistidyl (His6) tag, a myc tag and a FLAG tag. In additional embodiments, peptide tags include, but are not limited to,

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avitag (allows biotinylation of the tag and isolation with streptavidin), calmodulin, E-tag, hemagglutinin (HA), S-tag, SBP-tag, softag 1, streptavidin, tetra or poly-cysteine, V5, VSV, and Xpress tag. Additionally polyhistidyl tags (other than 6 residues) can be used. In additional embodiments, covalent peptide tags, protein tags, and the like can be used. Covalent peptide tags include, but are not limited to, isopeptag (covalently binds pilinC protein), Spytag (covalently binds to the SpyCatcher protein), and Snooptag (covalently binds to the SnoopCatcher protein). In still additional embodiments, protein tags, including but not limited to biotin carboxyl carrier protein (BCCP), glutathione-s-transferase, green fluorescent protein (or other fluorophore), Halo tag, Nus tag, thioredoxin, and Fc tags may optionally be used. In still additional embodiments, multiple types of tags may be used. In still additional embodiments, no tag is used. In still additional embodiments, the DDpp fusion protein comprises a removable tag. Any combination of extracellular, transmembrane and intracellular domains disclosed herein may be used, depending on the embodiment.

DDpp Linkers

[0216] The terms "linker" and spacer are used interchangeably herein to refer to a peptide or other chemical linkage that functions to link otherwise independent functional domains. In one embodiment, a linker in a DDpp is located between a DDpp and another polypeptide component containing an otherwise independent functional domain. Suitable linkers for coupling the two or more linked DDpp will be clear to the persons skilled in the art and may generally be any linker used in the art to link peptides, proteins or other organic molecules. In particular embodiments, such a linker is suitable for constructing proteins or polypeptides that are intended for pharmaceutical use.

[0217] Suitable linkers for operably linking a DDpp and an additional component of a DDpp fusion protein in a single-chain amino acid sequence include but are not limited to, polypeptide linkers such as glycine linkers, serine linkers, mixed glycine/serine linkers, glycine- and serine-rich linkers or linkers composed of largely polar polypeptide fragments.

[0218] In one embodiment, the linker is made up of a majority of amino acids selected from glycine, alanine, proline, asparagine, glutamine, and lysine. In one embodiment, the linker is made up of a majority of amino acids selected from glycine, alanine, proline, asparagine, aspartic acid, threonine, glutamine, and lysine. In one embodiment, the DDpp fusion protein linker is made up of one or more of the amino acids selected from glycine, alanine, proline, asparagine, glutamine, and lysine. In one embodiment, the DDpp fusion protein linker is made up of one or more of the amino

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acids selected from glycine, alanine, proline, asparagine, aspartic acid, threonine, glutamine, and lysine. In another embodiment, the DDpp fusion protein linker is made up of a majority of amino acids that are sterically unhindered. In another embodiment, a linker in which the majority of amino acids are glycine, serine, and/or alanine. In some embodiments, the peptide linker is selected from polyglycines (such as $(Gly)_5$ (SEQ ID NO: 975), and $(Gly)_8$ (SEQ ID NO: 976), poly(Gly-Ala), and polyalanines. In some embodiments, the peptide linker contains the sequence of Gly-Gly-Gly-Gly-Thr-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 4). In some embodiments, the peptide linker contains the sequence of Gly-Gly-Gly-Gly-Asp-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 5).

[0219] In one embodiment, a DDpp fusion comprises a DDpp directly attached (*i.e.*, without a linker) to another component of the DDpp fusion protein. In one embodiment, a DDpp fusion comprises at least 2, at least 3, at least 4, DDpp directly attached to another component of the DDpp fusion.

[0220] In another embodiment, a DDpp can be operably linked to another component of a DDpp fusion protein through a linker. DDpp fusion proteins can contain a single linker, multiple linkers, or no linkers. In one embodiment, a DDpp fusion comprises a DDpp operably linked to another component of the DDpp fusion protein through a linker peptide. In one embodiment, a DDpp fusion comprises at least 2, 3, 4, or 5 DD operably linked to another component of the DDpp fusion protein through a linker peptide.

[0221] Linkers can be of any size or composition so long as they are able to operably link a DDpp in a manner that enables the DDpp to bind a target of interest such as BCMA, CD123, CS1, HER2, AFP, or AFP p26. In some embodiments, linkers are about 1 to about 100 amino acids, about 1 to 50 amino acids, about 1 to 20 amino acids, about 1 to 15 amino acids, about 1 to 10 amino acids, about 1 to 5 amino acids, about 2 to 20 amino acids, about 2 to 15 amino acids, about 2 to 10 amino acids, or about 2 to 5 amino acids. It should be clear that the length, the degree of flexibility and/or other properties of the linker(s) may have some influence on the properties of the provided DD containing proteins, including but not limited to the affinity, specificity or avidity for a target of interest, or for one or more other target proteins of interest. When two or more linkers are used in the DDpp fusion proteins, these linkers may be the same or different. In the context and disclosure provided herein, a person skilled in the art will be able to routinely determine the optimal linker

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composition and length for the purpose of operably linking a DDpp and other components of a DDpp fusion protein.

[0222] The linker can also be a non-peptide linker such as an alkyl linker, or a PEG linker. For example, alkyl linkers such as -NH-(CH2)s-C(0)-, wherein s=2-20 can be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (*e.g.,* C1-C6) lower acyl, halogen (*e.g.,* Cl, Br), CN, NH2, phenyl, *etc.* An exemplary non- peptide linker is a PEG linker. In certain embodiments, the PEG linker has a molecular weight of about 100 to 5000 kDa, or about 100 to 500 kDa.

[0223] Suitable linkers for coupling DDpp fusion protein components by chemical cross-linking include, but are not limited to, homo-bifunctional chemical cross-linking compounds such as glutaraldehyde, imidoesters such as dimethyl adipimidate (DMA), dimethyl suberimidate (DMS) and dimethyl pimelimidate (DMP) or N-hydroxysuccinimide (NHS) esters such as dithiobis(succinimidylpropionate) (DSP) and dithiobis (sulfosuccini-midylpropionate) (DTSSP). Examples of suitable linkers for coupling DDpp fusion protein components of hetero-bifunctional reagents for cross-linking include, but are not limited to, cross-linkers with one amine-reactive end and a sulfhydryl-reactive moiety at the other end, or with a NHS ester at one end and an SH-reactive group (*e.g.,* a maleimide or pyridyl).

[0224] In additional embodiments, one or more of the linkers in the DDpp fusion protein is cleavable. Examples of cleavable linkers include, without limitation, a peptide sequence recognized by proteases (in vitro or *in vivo*) of varying type, such as Tev, thrombin, factor Xa, plasmin (blood proteases), metalloproteases, cathepsins (*e.g.,* GFLG, *etc.*), and proteases found in other corporeal compartments.

[0225] In one embodiment, the linker is a "cleavable linker" that facilitates the release of a DDpp or cytotoxic agent in a cell. For example, an acid-labile linker (*e.g.,* hydrazone), protease-sensitive (*e.g.,* peptidase-sensitive) linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari, Can. Res. 52: 127-131 (1992); U.S. Pat. No. 5,208,020; U.S. Appl. Pub. No. 20090110753; the contents of each of which is herein incorporated by reference in its entirety) can be used wherein it is desirable that the covalent attachment between a DDpp or a cytotoxic agent and the fusion partner is intracellularly cleaved when the composition is internalized into the cell. The terms "intracellularly cleaved" and "intracellular cleavage" refer to a metabolic process or reaction inside a

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cell on an DDpp drug conjugate whereby the covalent attachment, *i.e.*, linked via a linker between the DDpp and cytotoxic agent, DDpp and fusion partner, or between two DDpp is broken, resulting in the free DDpp and/or cytotoxic agent dissociated inside the cell.

[0226] Linker optimization can be evaluated using techniques described herein and/or otherwise known in the art. In some embodiments, linkers do not disrupt the ability of a DDpp to bind a target molecule and/or another DDpp fusion protein component such as an antibody domain or fragment to bind an antigen.

DDpp as Chemical Conjugates

[0227] DDpp fusion proteins that promote specific binding to targets of interest can be chemically conjugated with a variety of compound such as fluorescent dyes, radioisotopes, chromatography compositions (*e.g.,* beads, resins, gels, *etc.*) and chemotherapeutic agents. DDpp conjugates have uses that include but are not limited to diagnostic, analytic, manufacturing and therapeutic applications.

[0228] The inherent lack of cysteines in the DD sequence provides the opportunity for introduction of unique cysteines for purposes of site-specific conjugation.

[0229] In some embodiments, the DDpp (*e.g.,* a DDpp fusion protein) contains at least one reactive residue. Reactive residues are useful, for example, as sites for the attachment of conjugates such as chemotherapeutic drugs. The reactive residue can be, for example, a cysteine, a lysine, or another reactive residue. Thus, a cysteine can be added to a DDpp at either the N- or C- terminus, or within the DDpp sequence. A cysteine can be substituted for another amino acid in the sequence of a DDpp. In addition, a lysine can be added to a DDpp at either end or within the DDpp sequence and/or a lysine can be substituted for another amino acid in the sequence of a DDpp. In one embodiment, a reactive residue (*e.g.,* cysteine, lysine, *etc.*) is located in a loop sequence of a DD (*e.g.,* amino aicd residues 22-24 and 46-49 of SEQ ID NOS: 11-949, and 950). In one embodiment, a reactive residue is located between components of a DDpp fusion, *e.g.,* in a linker located between a DDpp and other component of a DDpp fusion protein. The reactive residue (*e.g.,* cysteine, lysine, *etc.*) can also be located within the sequence of a DDpp, or other component of the DDpp fusion protein. In one embodiment, a DDpp or a DDpp fusion protein comprises at least one, at least two, at least three reactive residues. In one embodiment, a DDpp such as a DDpp fusion protein comprises at least one, at least two, or at least three, cysteine residues.

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BCMA-binding DDpp

[0230] In some embodiments, a DD of the DDpp specifically binds BCMA. In further embodiments, a DD of the DDpp specifically binds BCMA having an amino acid sequence consisting of SEQ ID NO: 7. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306.

[0231] In some embodiments, the BCMA-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc.*). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind BCMA and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of BCMA and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp comprises a DD that specifically binds BCMA and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to BCMA or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds BCMA (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds BCMA *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds BCMA (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds BCMA (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds BCMA (*e.g.,* a DD having an amino acid sequence

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selected from the group consisting of SEQ ID NO: 11-305, and 306) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds BCMA (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0232] In some embodiments, the DDpp comprises a variant of a BCMA-binding DD disclosed herein (reference DD) that retains the ability to specifically bind BCMA. In some embodiments, the sequence of the BCMA-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306.

[0233] In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference BCMA-DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306.

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[0234] In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference BCMA-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the sequence of the BCMA-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306.

[0235] In some embodiments, the disclosure provides a BCMA-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to BCMA, wherein the reference DD has an amino acid sequence selected from SEQ ID NO: 11-305, and 306. In other embodiments, the disclosure provides BCMA-binding DDpp that bind to the same epitope of BCMA as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 11-305, and 306.

[0236] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds BCMA. In some embodiments, the DD specifically binds a BCMA protein having an amino acid sequence consisting of SEQ ID NO: 7. In some embodiments, the BCMA-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab,

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belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the BCMA-binding DDpp is an Fc fusion protein. In further embodiments, the Fc protein comprises a variant human Fc domain.

[0237] In some embodiments, the DDpp fusion protein comprises a BCMA-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP or AFP p26, or a fragment thereof. In some embodiments, the DDpp fusion protein comprises AFP (*e.g.,* SEQ ID NO: 9), or a fragment thereof. In other embodiments, the DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a polypeptide having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic fragment of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

[0238] In some embodiments, the BCMA-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In further embodiments, the BCMA-binding DDpp fusion protein comprises the extracellular domain of CD123 (SEQ ID NO: 8), or a fragment thereof. In some embodiments, the BCMA-binding DDpp fusion protein comprises the extracellular domain of of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0239] In some embodiments, the BCMA-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-

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50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0240] In additional embodiments, the BCMA-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In other embodiments, the BCMA-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306. In some embodiments, the BCMA-binding DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

CD123-binding DDpp

[0241] In some embodiments, a DD of the DDpp specifically binds CD123. In further embodiments, the DD specifically binds CD123 having an amino acid sequence consisting of SEQ ID NO: 8. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: SEQ ID NO: 307-739, and 740. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: SEQ ID NO: 307-739, and 740.

[0242] In some embodiments, the CD123-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind CD123 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of CD123 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp comprises a DD that specifically binds CD123 and further

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comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to CD123 or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds CD123 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds CD123 *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds CD123 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds CD123 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds CD123 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds CD123 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0243] In some embodiments, the DDpp comprises a variant of a CD123-binding DD disclosed herein (reference DD) that retains the ability to specifically bind CD123. In some embodiments, the sequence of the CD123-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10,

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1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740.

[0244] In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 4307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CD123-DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740.

[0245] In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference CD123-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the sequence of the CD123-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740.

[0246] In some embodiments, the disclosure provides CD123-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to CD123, wherein the

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reference DD has an amino acid sequence selected from SEQ ID NO: 307-739, and 740. In other embodiments, the disclosure provides CD123-binding DDpp that bind to the same epitope of CD123as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 307-739, and 740.

[0247] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds CD123. In some embodiments, a DD of the DDpp fusion protein specifically binds CD123 having an amino acid sequence consisting of of SEQ ID NO: 8. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the CD123-binding DDpp is an Fc fusion protein.

[0248] In some embodiments, the DDpp is a fusion protein comprising a CD123-binding DD operably linked to a serum protein. In some embodiments, the CD123-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the CD123-binding DDpp fusion protein comprises all or a portion of human serum albumin. In some embodiments, the DDpp fusion protein comprises AFP (SEQ ID NO: 9), or a fragment thereof. In some embodiments, the CD123-binding DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof. In some embodiments, the CD123-bindng DDpp fusion protein comprises a polypeptide having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic fragment of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

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[0249] In some embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In further embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of CD123 (SEQ ID NO: 8), or a fragment thereof. In some embodiments, the CD123-binding DDpp fusion protein comprises the extracellular domain of of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0250] In some embodiments, the CD123-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0251] In additional embodiments, the CD123-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In other embodiments, the CD123-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740. In some embodiments, the CD123-binding DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

CS1-binding DDpp

[0252] In some embodiments, a DD of the DDpp specifically binds CS1. In further embodiments, the DD specifically binds CS1 having an amino acid sequence consisting of SEQ ID

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NO: 965. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910.

[0253] In some embodiments, the CS1-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc.*). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind CS1 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of CS1 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp comprises a DD that specifically binds CS1 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to CS1 or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds CS1 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds CS1 *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds CS1 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds CS1 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds CS1 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds CS1 (*e.g.,* a DD having an amino acid sequence selected from the group

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consisting of SEQ ID NO: 896-909, and 910) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0254] In some embodiments, the DDpp comprises a variant of a CS1-binding DD disclosed herein (reference DD) that retains the ability to specifically bind CS1. In some embodiments, the sequence of the CS1-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the sequence of the CS1-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the sequence of the CS1-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910.

[0255] In some embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CS1-DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910.

[0256] In some embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference CS1-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some

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embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the sequence of the CS1-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910.

[0257] In some embodiments, the disclosure provides CS1-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to CS1, wherein the reference DD has an amino acid sequence selected from SEQ ID NO: 896-909, and 910. In other embodiments, the disclosure provides CS1-binding DDpp that bind to the same epitope of CS1as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 896-909, and 910.

[0258] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds CS1. In some embodiments, a DD of the DDpp fusion protein specifically binds CS1 having an amino acid sequence consisting of of SEQ ID NO: 965. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the DDpp fusion protein comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the CS1-binding DDpp is an Fc fusion protein.

[0259] In some embodiments, the DDpp is a fusion protein comprising a CS1-binding DD operably linked to a serum protein. In some embodiments, the CS1-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and

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910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the CS1-binding DDpp fusion protein comprises all or a portion of human serum albumin. In some embodiments, the DDpp fusion protein comprises AFP (SEQ ID NO: 9), or a fragment thereof. In some embodiments, the CS1-binding DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof. In some embodiments, the CS1-bindng DDpp fusion protein comprises a polypeptide having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic fragment of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

[0260] In some embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In further embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the CS1-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0261] In some embodiments, the CS1-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

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[0262] In additional embodiments, the CS1-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In other embodiments, the CS1-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910. In some embodiments, the CS1-binding DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

HER2-binding DDpp

[0263] In some embodiments, a DD of the DDpp specifically binds HER2. In further embodiments, the DD specifically binds HER2 having an amino acid sequence consisting of SEQ ID NO: 967. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950.

[0264] In some embodiments, the HER2-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc*.). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind HER2 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of HER2 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp comprises a DD that specifically binds HER2 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to HER2 or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds HER2 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds HER2 *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and further comprises one or more additional DDs or other target-binding binding

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domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds HER2 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds HER2 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds HER2 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds HER2 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0265] In some embodiments, the DDpp comprises a variant of a HER2-binding DD disclosed herein (reference DD) that retains the ability to specifically bind HER2. In some embodiments, the sequence of the HER2-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950.

[0266] In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference HER2-DD having an amino acid sequence selected

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from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950.

[0267] In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference HER2-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the sequence of the HER2-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950.

[0268] In some embodiments, the disclosure provides HER2-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to HER2, wherein the reference DD has an amino acid sequence selected from SEQ ID NO: 911-949, and 950. In other embodiments, the disclosure provides HER2-binding DDpp that bind to the same epitope of HER2as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 911-949, and 950.

[0269] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds HER2. In some embodiments, a DD of the DDpp fusion protein specifically binds HER2 having an amino acid sequence consisting of SEQ ID NO: 967. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the DDpp fusion protein

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comprises a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the HER2-binding DDpp is an Fc fusion protein.

[0270] In some embodiments, the DDpp is a fusion protein comprising a HER2-binding DD operably linked to a serum protein. In some embodiments, the HER2-binding DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the HER2-binding DDpp fusion protein comprises all or a portion of human serum albumin. In some embodiments, the DDpp fusion protein comprises AFP (SEQ ID NO: 9), or a fragment thereof. In some embodiments, the HER2-binding DDpp fusion protein comprises AFP p26 (SEQ ID NO: 10), or a fragment thereof. In some embodiments, the HER2-bindng DDpp fusion protein comprises a polypeptide having the sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic fragment of a serum protein (*e.g.,* AFP, and AFP p26). In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

[0271] In some embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In further embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of HER2 (SEQ ID NO: 967), or a fragment thereof. In some embodiments, the HER2-binding DDpp fusion protein comprises the extracellular domain of a receptor selected from

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the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0272] In some embodiments, the HER2-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0273] In additional embodiments, the HER2-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In other embodiments, the HER2-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950. In some embodiments, the HER2-binding DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

AFP-binding DDpp

[0274] In some embodiments, a DD of the DDpp specifically binds AFP or a fragment thereof. In further embodiments, a DD of the DDpp specifically binds AFP having an amino acid sequence consisting of SEQ ID NO: 9 or a fragement thereof. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In additional embodiments, the AFP-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0275] In some embodiments, the AFP-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc.*). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind AFP and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some

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embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of AFP and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp comprises a DD that specifically binds AFP and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to AFP or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds AFP (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds AFP (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds AFP (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds AFP (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0276] In some embodiments, the DDpp comprises a variant of a AFP-binding DD disclosed herein (reference DD) that retains the ability to specifically bind AFP. In some embodiments, the sequence of the AFP-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In

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some embodiments, the sequence of the AFP-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0277] In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 4741-874, and 886-895. In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference AFP-DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0278] In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference AFP-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37,

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39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0279] In some embodiments, the disclosure provides an AFP-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to AFP, wherein the reference DD has an amino acid sequence selected from SEQ ID NO: 741 873, and 874. In other embodiments, the disclosure provides AFP-binding DDpp that bind to the same epitope of AFP as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 741 873, and 874.

[0280] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP. In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP having an amino acid sequence consisting of SEQ ID NO: 9. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the DDpp is a fusion protein comprising a AFP-binding DD that is a variant of a DD comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0281] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP operably linked to a full-length antibody or a portion (fragment) of an antibody. In some embodiments, the DDpp is an Fc fusion protein. In some embodiment, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the AFP-binding DDpp is an Fc fusion protein.

[0282] In some embodiments, the DDpp is a fusion protein comprising an AFP-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic

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fragment of a serum protein. In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

[0283] In some embodiments, the AFP-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the AFP-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8), or a fragment thereof. In further embodiments, the AFP-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the AFP-binding DDpp fusion protein comprises the extracellular domain of of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

[0284] In some embodiments, the AFP-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0285] In additional embodiments, the AFP-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the AFP-binding DDpp fusion protein

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comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

AFP p26-binding DDpp

[0286] In some embodiments, a DD of the DDpp specifically binds AFP p26. In further embodiments, a DD of the DDpp specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 10. In some embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In additional embodiments, the AFP p26-binding DDpp comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0287] In some embodiments, the AFP p26-binding DDpp comprises multiple target-binding domains that bind a single target (*e.g.,* dimers, trimers, *etc.*). In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that specifically bind AFP p26 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp comprises 2, 3, 4, 5, or more than 5, DD that have the same sequence. In some embodiments, the DDpp comprises 2, 3, 4, 5 or more than 5, DD that specifically bind to different epitopes of AFP p26 and that have an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 and further comprises 2, 3, 4, 5 or more than 5, additional different DDs or target-binding binding domains (*e.g.,* scFvs) that specifically bind to AFP p26 or a different target antigen. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more antigens expressed on the surface of a B cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 *e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and further comprises one or more additional DDs or other target-binding binding domains that bind one or more cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different targets. In further embodiments, the DDpp comprises a DD that specifically binds AFP p26 (*e.g.,* a DD having an amino acid sequence selected

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from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, different cancer antigens expressed on the surface of a cancer cell. In some embodiments, the DDpp comprises a DD that specifically binds AFP p26 (*e.g.,* a DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895) and specifically binds 2, 3, 4, 5, or more than 5, cancer antigens expressed on the surface of different cancer cells.

[0288] In some embodiments, the DDpp comprises a variant of a AFP p26-binding DD disclosed herein (reference DD) that retains the ability to specifically bind AFP p26. In some embodiments, the sequence of the AFP p26-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions compared to a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions compared to a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions compared to a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0289] In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 4741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues 1-22, 29-46, and 52-72, of a reference AFP p26-DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino

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acid residues 1-22, 29-46, and 52-72, of a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0290] In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative or non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference AFP p26-binding DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the sequence of the AFP p26-binding DD variant contains a total of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, 1-3, 1-5, or 1-10, non-conservative substitutions in positions corresponding to amino acid residues: 2-6, 8-10, 12, 13, 15-17, 19, 20, 29, 30, 32-34, 36, 37, 39-41, 43, 44, 52-55, 57-59, 61, 62, 64-66, and 68-70, of a reference DD having an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895.

[0291] In some embodiments, the disclosure provides an AFP p26-binding DDpp that completely or partially (*e.g.,* overlap with an epitope) block binding of a reference DD to AFP p26, wherein the reference DD has an amino acid sequence selected from SEQ ID NO: 741 873, and 874. In other embodiments, the disclosure provides AFP p26-binding DDpp that bind to the same epitope of AFP p26 as a a reference DD consisting of an amino acid sequence selected from SEQ ID NO: 741 873, and 874.

[0292] In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP p26. In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP p26 having an amino acid sequence consisting of SEQ ID NO: 9. In further embodiments, the DDpp comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the DDpp is a fusion protein comprising a AFP p26-binding DD that is a variant of a DD comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the DDpp is a fusion protein comprising a DD that specifically binds AFP p26 operably linked to a full-length antibody or a portion (fragment)

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of an antibody. In some embodiments, the DDpp is an Fc fusion protein. In some embodiment, the DDpp fusion protein comprises a full length IgG antibody (*e.g.,* IgG1, IgG2, IgG2, or IgG4). In further embodiments, the DDpp fusion protein comprises a full length antibody that specifically binds a cancer antigen. In further embodiments, the DDpp comprises a commercially approved therapeutic antibody (*e.g.,* rituximab, ofatumumab, ocrelizumab, veltuzumab, MEDI-551, epratuzumab, belimumab, tabalumab, AMG-557, MEDI-570, and NN882). In other embodiments, the AFP p26-binding DDpp is an Fc fusion protein. In further embodiments, the Fc fusion protein comprises a variant human Fc domain.

[0293] In some embodiments, the DDpp is a fusion protein comprising an AFP p26-binding DD operably linked to a serum protein. In some embodiments, the DDpp fusion protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the DDpp fusion protein comprises human serum albumin or a fragment thereof. In some embodiments, the DDpp fusion protein contains a fragment of a serum protein or an antigenic fragment of a serum protein. In some embodiments, the DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of a serum protein.

[0294] In some embodiments, the AFP p26-binding DDpp fusion protein comprises the extracellular domain of a receptor or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In further embodiments, the AFP p26-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8), or a fragment thereof. In further embodiments, the AFP p26-binding DDpp fusion protein comprises the extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965), or a fragment thereof. In some embodiments, the AFP p26-binding DDpp fusion protein comprises the extracellular domain of of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96, or a fragment thereof.

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[0295] In some embodiments, the AFP p26-binding DDpp fusion protein contains a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acids of an extracellular domain, of a cell surface receptor. In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7) or CD123 (SEQ ID NO: 8). In some embodiments, the DDpp fusion protein contains a fragment of an extracellular domain of BCMA (SEQ ID NO: 7), or CD123 (SEQ ID NO: 8), or CS1 (SEQ ID NO: 965). In some embodiments, the DDpp contains a fragment of an extracellular domain, of a receptor selected from the group consisting of: CD19, CD20, CD22, HVEM, BTLA, DR3, CD37; TSLPR, IL7R, and gp96.

[0296] In additional embodiments, the AFP p26-binding DDpp fusion protein comprises an intracellular protein (*e.g.,* a nuclear protein) or a fragment thereof. In some embodiments, the DDpp fusion protein comprises a DD that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In other embodiments, the AFP p26-binding DDpp fusion protein comprises a variant of an amino acid sequence selected from the group consisting of SEQ ID NO: 741-874, and 886-895. In some embodiments, the AFP p26-binding DDpp fusion protein comprises a fragment consisting of 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 10-500, 10-400, 10-300, 10-200, 10-100, or 10-50 amino acid residues of an intracellular protein (*e.g.,* a nuclear protein).

[0297] Nucleic acids encoding the DDpp and vectors containing the nucleic acids are also provided. Host cells (including viral particles) containing the nucleic acids and vectors are also provided. In some embodiments, the host cell is a prokaryote or a eukaryote that display the variant DD on its surface. In some embodiments, the host cell displays the variant DD on its surface. In a further embodiment, the host cell is a phage that displays the variant DD on its surface. In a further embodiment, the host cell is a human immune cell that expresses a variant DD fusion protein on its surface.

[0298] A DDpp agonist refers to a DDpp that in some way increases or enhances the biological activity of the DDpp target or has biological activity comparable to a known agonist of the DDpp target. In another embodiment, the DDpp is an antagonist of the target it binds. A DDpp antagonist refers to a DDpp that completely or partially blocks or in some way interferes with the biological activity of the DDpp target protein or has biological activity comparable to a known antagonist or inhibitor of the DDpp target protein.

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[0299] Expressions like "binding affinity for a target", "binding to a target" and the like refer to a property of a polypeptide which may be directly measured through the determination of the affinity constants, *e.g.,* the amount of DDpp that associates and dissociates at a given antigen concentration. Different methods can be used to characterize the molecular interaction, including but not limited to, competition analysis, equilibrium analysis and microcalorimetric analysis, and real-time interaction analysis based on surface plasmon resonance interaction (for example using a Biacore® instrument). These methods are known to the skilled person and are described, for example, in Neri *et al.,* Tibtech 14: 465-470 (1996) and Jansson *et al.,* J Biol Chem 272: 8189-8197 (1997).

[0300] Affinity requirements for a given DDpp binding event are contingent on a variety of factors including, but not limited to: the composition and complexity of the binding matrix, the valency and density of both the DDpp and target molecules, and the functional application of the DDpp. In one embodiment, DDpp bind a target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) with a dissociation constant (KD) of less than or equal to 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, or 10^{-5} M. In an additional embodiment, a DDpp binds a target of interest with a KD of less than or equal to 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7}M, 5×10^{-8} M, or 10^{-8} M. In additional embodiments, a DDpp binds a target of interest with a KD of less than or equal to 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10−15 M, or 10^{-15} M. In some embodiments, the provided DDpp has a dissociation constant selected from the group consisting of between 10^{-4} M and 10^{-5} M, between 10^{-5} M and 10^{-6} M, between 10^{-6} M and 10^{-7} M, between 10^{-7} M and 10^{-8} M, between 10^{-8} M and 10^{-9} M, between 10^{-9} M and 10^{-10} M, between 10^{-10} M and 10^{-11} M and between 10^{-11} M and 10^{-12} M.

[0301] In some embodiments, the DDpp binds a target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) in active form. In one embodiment the DDpp reversibly binds the target of interest in active form and also releases the bound target in active form. In some embodiments, the DDpp binds a target of interest in the native form. In specific embodiments, DDpp binds a target of interest with an off-rates or K_{off} of greater than or equal to 10^{-10} sec^{-1}, 5×10^{-9} sec^{-1}, 10^{-9} sec^{-1}, 5×10^{-8} sec^{-1}, 10^{-8} sec^{-1}, 5×10^{-7} sec^{-1}, 10^{-7} sec^{-1}, 5×10^{-6} sec^{-1}, 10^{-6} sec^{-1}, 5×10^{-5} sec^{-1}, 10^{-5} sec^{-1}, 5×10^{-4} sec^{-1}, 10^{-4} sec^{-1}, 5×10^{-3} sec^{-1}, 10^{-3} sec^{-1}, 5×10^{-2} sec^{-1}, 10^{-2} sec^{-1}, 5×10^{-1} sec^{-1}, or 10^{-1} sec^{-1}.

[0302] Binding experiments to determine KD and off-rates can routinely be performed in a number of conditions including, but not limited to, [pH 6.0, 0.01% Tween 2, [pH 6.0, 0.1% gelatin],

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[p H5.0, 0.01% Tween 2, [pH 9.0, 0.1% Tween 2, [pH 6.0, 15% ethylene glycol, 0.01% Tween 2, [pH 5.0, 15% ethylene glycol, 0.01% Tween 2, and [pH 9.0, 15% ethylene glycol, 0.01% Tween 2. The buffers in which to make these solutions can routinely be determined by one skilled in the art, and depend largely on the desired pH of the final solution. Low pH solutions (<pH 5.5) can be made, for example, in citrate buffer, glycine-HCl buffer, or in succinic acid buffer. High pH solutions can be made, for example, in Tris-HCl, phosphate buffers, or sodium bicarbonate buffers. A number of conditions may routinely be used by those skilled in the art to determine KD and off-rates for the purpose of determining, for example, optimal pH and/or salt concentrations.

[0303] In one embodiment, the DDpp specifically binds a target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) with a K_{Off} ranging from 0.1 to 10^{-7} sec^{-1}, 10^{-2} to 10^{-7} sec^{-1}, or 0.5 X 10^{-2} to 10^{-7} sec^{-1}. In a specific embodiment, the DDpp (*e.g.,* a DDpp fusion protein) binds a target of interest with an off rate (K_{Off}) of less than 5 X 10^{-2} sec^{-1}, 10^{-2} sec^{-1}, 5 X 10^{-3} sec^{-1}, or 10^{-3} sec^{-1}. In an additional embodiment, a DDpp, binds a target of interest with an off rate (K_{Off}) of less than 5 X 10^{-4} sec^{-1}, 10^{-4} sec^{-1}, 5 X 10^{-5} sec^{-1}, or 10^{-5} sec^{-1}, 5 X10^{-6} sec^{-1}, 10^{-6} sec^{-1}, 5 X 10^{-7} sec^{-1}, or 10^{-7} sec^{-1}.

[0304] In one embodiment, the DDpp specifically binds a target of interest (*e.g.,* BCMA, CD123, AFP, or AFP p26) with a K_{On} ranging from 10^3 to 10^7 $M^{-1}sec^{-1}$, 10^3 to 10^6 $M^{-1}sec^{-1}$, or 10^3 to 10^5 $M^{-1}sec^{-1}$. In a specific embodiment, the DDpp (*e.g.,* a DDpp fusion protein) binds the target of interest with an on rate (K_{On}) of greater than 10^3 $M^{-1}sec^{-1}$, 5 X 10^3 $M^{-1}sec^{-1}$, 10^4 $M^{-1}sec^{-1}$, or 5 X 10^4 $M^{-1}sec^{-1}$. In an additional embodiment, the DDpp, binds the target of interest with a K_{On} of greater than 10^5 $M^{-1}sec^{-1}$, 5 X 10^5 $M^{-1}sec^{-1}$, 10^6 M^{-1} sec^{-1}, or 5 X 10^6 $M^{-1}sec^{-1}$, or 10^7 M^{-1} sec^{-1}.

[0305] Nucleic acid molecules encoding the disclosed DDpp are encompassed herein, as are vectors containing these nucleic acids, host cells containing these nucleic acids vectors, and methods of making the DDpp-albumin fusion proteins and using these nucleic acids, vectors, and/or host cells. The invention also encompasses pharmaceutical formulations comprising a DDpp-albumin fusion protein and a pharmaceutically acceptable diluent or carrier. Such formulations can be used in methods of treating, preventing, ameliorating or diagnosing a disease or disease symptom in a patient, preferably a mammal, most preferably a human, comprising the step of administering the pharmaceutical formulation to the patient.

Production of DDpp

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[0306] The disclosed DDpp can routinely be made using commercially available reagents and techniques known in the art. In one embodiment, the DDpp are synthesized by solid phase synthesis techniques known in the art, such as, Merrifield, J. Am. Chem. Soc. 85: 2149 (1963); Davis *et al.*, Biochem. Intl. 10: 394-414 (1985); Larsen *et al.*, J. Am. Chem. Soc. 115: 6247 (1993); Smith *et al.*, J. Peptide Protein Res. 44: 183 (1994); O'Donnell *et al.*, J. Am. Chem. Soc. 118: 6070 (1996); Stewart and Young, Solid Phase Peptide Synthesis, Freeman (1969); Finn *et al.*, The Proteins, 3.sup.rd ed., 2: 105-253 (1976); and Erickson *et al.*, The Proteins, 3.sup.rd ed., 2: 257-527 (1976). The disclosure contemplates synthetic peptides. Alternatively, the peptide is expressed recombinantly by introducing a nucleic acid encoding the disclosed DDpp into host cells, which are cultured to express the peptide. Such peptides are purified from the culture media or cell pellets.

[0307] The production of the DDpp, useful in practicing the provided methods, may be carried out using a variety of standard techniques for chemical synthesis, semi-synthetic methods, and recombinant DNA methodologies known in the art. Also provided is a method for producing a DDpp, individually or as part of multi-domain fusion protein, as soluble agents and cell associated proteins.

[0308] Optionally, the reference sequence and/or the modified polypeptides (*e.g.,* DDpp) can be de-immunized. For example, residues or motifs that are potentially immunogenic can be identified and modified in order to reduce or eliminate potential immune responses to the DDpp. Additional details regarding various embodiments, of the production, selection, and isolation of DDpp are provided in more detail below.

Recombinant expression of DDpp

[0309] In some embodiments, a DDpp such as a DDpp fusion protein is "recombinantly produced," (*i.e.*, produced using recombinant DNA technology). Exemplary recombinant methods available for synthesizing DDpp fusion proteins, include, but are not limited to polymerase chain reaction (PCR) based synthesis, concatemerization, seamless cloning, and recursive directional ligation (RDL) (*see, e.g.,* Meyer *et al.*, Biomacromolecules 3: 357-367 (2002); Kurihara *et al.*, Biotechnol. Lett. 27: 665-670 (2005); Haider *et al.*, Mol. Pharm. 2: 139-150 (2005); and McMillan *et al.*, 32: 3643-3646 (1999); the contents of each of which is herein incorporated by reference in its entirety).

[0310] Nucleic acids comprising a polynucleotide sequence encoding a DDpp are also provided. Such polynucleotides optionally further comprise, one or more expression control elements.

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For example, the polynucleotide can comprise one or more promoters or transcriptional enhancers, ribosomal binding sites, transcription termination signals, and polyadenylation signals, as expression control elements. The polynucleotide can be inserted within any suitable vector, which can be contained within any suitable host cell for expression.

[0311] The expression of nucleic acids encoding DDpp is typically achieved by operably linking a nucleic acid encoding the DDpp to a promoter in an expression vector. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the desired nucleic acid sequence. Methods known in the art can be used to routinely construct expression vectors containing the nucleic acid sequence encoding a DDpp along with appropriate transcriptional/ translational control signals. These methods include, but are not limited to in vitro recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. The expression of the polynucleotide can be performed in any suitable expression host known in the art including, but not limited to bacterial cells, yeast cells, insect cells, plant cells or mammalian cells. In one embodiment, a nucleic acid sequence encoding a DDpp is operably linked to a suitable promoter sequence such that the nucleic acid sequence is transcribed and/or translated into DDpp in a host. Promoters useful for expression in E. coli, include but are not limited to, the T7 promoter.

[0312] In one embodiment, a vector comprising a DDpp encoding nucleic acid is introduced into a host cell (*e.g.,* phagemid) for expression of a DDpp. The vector can remain episomal or become chromosomally integrated, as long as the insert encoding therapeutic agent can be transcribed. Vectors can be constructed by standard recombinant DNA technology. Vectors can be plasmids, phages, cosmids, phagemids, viruses, or any other types known in the art, which are used for replication and expression in prokaryotic or eukaryotic cells. It will be appreciated by one of skill in the art that a wide variety of components known in the art (such as expression control elements) can be included in such vectors, including a wide variety of transcription signals, such as promoters and other sequences that regulate the binding of RNA polymerase onto the promoter. Any promoter known or demonstrated to be effective in the cells in which the vector will be expressed can be used to initiate expression of the DDpp. Suitable promoters can be inducible (*e.g.,* regulated) or constitutive. Non-limiting examples of suitable promoters include the SV40 early promoter region, the promoter contained in the 3' long terminal repeat of Rous sarcoma virus, the HSV-1 (herpes simplex virus-1) thymidine kinase

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promoter, the regulatory sequences of the metallothionein gene, *etc.*, as well as the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells; insulin gene control region which is active in pancreatic beta cells, mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells, albumin gene control region which is active in liver, alpha-fetoprotein gene control region which is active in liver, alpha 1-antitrypsin gene control region which is active in the liver, beta-globin gene control region which is active in erythroid cells, myelin basic protein gene control region which is active in oligodendrocyte cells in the brain, myosin light chain-2 gene control region which is active in skeletal muscle, and gonadotropin releasing hormone gene control region which is active in the hypothalamus. In a particular embodiment, the promoter is an immunoglobulin gene control region which is active in lymphoid cells.

[0313] In one embodiment, one or several nucleic acids encoding a DDpp is expressed under the control of a constitutive promoter or, alternately, a regulated expression system. Suitable regulated expression systems include, but are not limited to, a tetracycline-regulated expression system, an ecdysone inducible expression system, a lac-switch expression system, a glucocorticoid-inducible expression system, a temperature-inducible promoter system, and a metallothionein metal-inducible expression system. If several different nucleic acids encoding a DDpp are contained within the host cell system, some of the nucleic acids may be expressed under the control of a constitutive promoter, while others may be expressed under the control of a regulated promoter. Expression levels may be determined by methods known in the art, including Western blot analysis and Northern blot analysis.

[0314] A variety of host-expression vector systems can be utilized to express a nucleic acid encoding a DDpp. Vectors containing the nucleic acids encoding the DDpp (*e.g.,* individual DD subunits or DDpp fusions) or portions or fragments thereof, include plasmid vectors, a single and double-stranded phage vectors, as well as single and double-stranded RNA or DNA viral vectors. Phage and viral vectors may also be introduced into host cells in the form of packaged or encapsulated virus using known techniques for infection and transduction. Moreover, viral vectors may be replication competent or alternatively, replication defective. Alternatively, cell-free translation systems may also be used to produce the protein using RNAs derived from the DNA expression constructs (*see, e.g.,* WO86/05807 and WO89/01036; and U.S. Pat. No. 5,122,464; the contents of each of which is herein incorporated by reference in its entirety).

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[0315] Generally, any type of cells or cultured cell line can be used to express a DDpp provided herein. In some embodiments, the background cell line used to generate an engineered host cells is a phage, a bacterial cell, a yeast cell or a mammalian cell. A variety of host-expression vector systems may be used to express the coding sequence a DDpp fusion protein. Mammalian cells can be used as host cell systems transfected with recombinant plasmid DNA or cosmid DNA expression vectors containing the coding sequence of the target of interest and the coding sequence of the fusion polypeptide.

[0316] The cells can be primary isolates from organisms (including human), cultures, or cell lines of transformed or transgenic nature. In some embodiments, the host cell is a human cell. In some embodiments, the host cell is human T cell. In some embodiments, the host cell is derived from a human patient.

[0317] Useful host cells include but are not limited to microorganisms such as, bacteria (*e.g., E. coli, B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing DDpp coding sequences; yeast (*e.g., Saccharomyces, Pichia*) transformed with recombinant yeast expression vectors containing DDpp coding sequences; insect cell systems infected with recombinant virus expression vectors (*e.g.,* baculovirus) containing DDpp coding sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.,* cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.,* Ti plasmid) containing DDpp coding sequences. In particular embodiments, the mammalian cell systems are used to produce the DDpp. Mammalian cell systems typically utilize recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.,* metallothionein promoter) or from mammalian viruses (*e.g.,* the adenovirus late promoter; the vaccinia virus 7.5K promoter).

[0318] Prokaryotes useful as host cells in producing a DDpp such as DDpp fusion protein, include gram negative or gram positive organisms such as, E. coli and B. subtilis. Expression vectors for use in prokaryotic host cells generally contain one or more phenotypic selectable marker genes (*e.g.,* genes encoding proteins that confer antibiotic resistance or that supply an autotrophic requirement). Examples of useful prokaryotic host expression vectors include the pKK223-3 (Pharmacia, Uppsala, Sweden), pGEMl (Promega, Wis., USA), pET (Novagen, Wis., USA) and pRSET (Invitrogen, Calif., USA) series of vectors (*see, e.g.,* Studier, J. Mol. Biol. 219: 37 (1991) and

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Schoepfer, Gene 124: 83 (1993)). Exemplary promoter sequences frequently used in prokaryotic host cell expression vectors include T7, (Rosenberg *et al.*, Gene 56: 125-135 (1987)), beta-lactamase (penicillinase), lactose promoter system (Chang *et al.*, Nature 275: 615 (1978)); and Goeddel *et al.*, Nature 281: 544 (1979)), tryptophan (trp) promoter system (Goeddel *et al.*, Nucl. Acids Res. 8: 4057 (1980)), and tac promoter (Sambrook *et al.*, 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[0319] In one embodiment, a eukaryotic host cell systems is be used, including yeast cells transformed with recombinant yeast expression vectors containing the coding sequence of a DDpp, such as, the expression systems taught in U.S. Appl. No. 60/344,169 and WO03/056914 (methods for producing humanlike glycoprotein in a non-human eukaryotic host cell) (the contents of each of which is herein incorporated by reference in its entirety). Exemplary yeast that can be used to produce the provided compositions, such as, DD, include yeast from the genus Saccharomyces, Pichia, Actinomycetes and Kluyveromyces. Yeast vectors typically contain an origin of replication sequence from a 2mu yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Examples of promoter sequences in yeast expression constructs include, promoters from metallothionein, 3-phosphoglycerate kinase (Hitzeman, J. Biol. Chem. 255: 2073 (1980)) and other glycolytic enzymes, such as, enolase, glyceraldehyde-3 -phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phospho glycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Additional suitable vectors and promoters for use in yeast expression as well as yeast transformation protocols are known in the art. *See, e.g.,* Fleer, Gene 107: 285-195 (1991) and Hinnen, PNAS 75: 1929 (1978).

[0320] Insect and plant host cell culture systems are also useful for producing the compositions encompassed by the disclosure. Such host cell systems include for example, insect cell systems infected with recombinant virus expression vectors (*e.g.,* baculovirus) containing the coding sequence of a DD; plant cell systems infected with recombinant virus expression vectors (*e.g.,* cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.,* Ti plasmid) containing the coding sequence of a DD, including, but not limited to, the expression systems taught in U.S. Pat. No. 6,815,184; U.S. Publ. Nos. 60/365,769, and

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60/368,047; and WO04/057002, WO04/024927, and WO03/078614; the contents of each of which is herein incorporated by reference in its entirety.

[0321] In an additional embodiment the host cell systems may be used, including animal cell systems infected with recombinant virus expression vectors (*e.g.,* adenoviruses, retroviruses, adeno-associated viruses, herpes viruses, lentiviruses) including cell lines engineered to contain multiple copies of the DNA encoding a DDpp either stably amplified (CHO/dhfr) or unstably amplified in double-minute chromosomes (*e.g.,* murine cell lines). In one embodiment, the vector comprising the polynucleotide(s) encoding the DDpp is polycistronic. Exemplary mammalian cells useful for producing these compositions include 293 cells (*e.g.,* 293T and 293F), CHO cells, BHK cells, NS0 cells, SP2/0 cells, YO myeloma cells, P3X63 mouse myeloma cells, PER cells, PER.C6 (Crucell, Netherlands) cells VERY, Hela cells, COS cells, MDCK cells, 3T3 cells, W138 cells, BT483 cells, Hs578T cells, HTB2 cells, BT20 cells, T47D cells, CRL7O30 cells, HsS78Bst cells, hybridoma cells, and other mammalian cells. Additional exemplary mammalian host cells that are useful in practicing the the provided embodiments include but are not limited, to T cells. Some examples of expression systems and selection methods are described in the following references and references cited therein: Borth *et al.*, Biotechnol. Bioen. 71(4): 266-73 (2000), in Werner *et al.*, Arzneimittel-forschung/Drug Res. 48(8): 870-80 (1998), Andersen *et al.*, Curr. Op. Biotechnol. 13: 117-123 (2002), Chadd *et al.*, Curr. Op. Biotechnol. 12: 188-194 (2001), and Giddings, Curr. Op. Biotechnol. 12: 450-454 (2001). Additional examples of expression systems and selection methods are described in Logan *et al.*, PNAS 81: 355-359 (1984), Birtner *et al.,* Methods Enzymol. 153: 51-544 (1987)). Transcriptional and translational control sequences for mammalian host cell expression vectors are frequently derived from viral genomes. Commonly used promoter sequences and enhancer sequences in mammalian expression vectors include, sequences derived from Polyoma virus, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus (CMV). Exemplary commercially available expression vectors for use in mammalian host cells include pCEP4 (Invitrogen) and pcDNA3 (Invitrogen).

[0322] Physical methods for introducing a nucleic acid into a host cell (*e.g.,* a mammalian host cell) include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and the like. Methods for producing cells comprising vectors and/or exogenous nucleic acids are well-known in the art. *See*, for example, Sambrook *et al.* (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York).

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[0323] Biological methods for introducing a polynucleotide of interest into a host cell include the use of DNA and RNA vectors. Viral vectors, and especially retroviral vectors, have become the most widely used method for inserting genes into mammalian (*e.g.,* human) cells. Other viral vectors can be derived from lentivirus, poxviruses, herpes simplex virus I, adenoviruses and adeno-associated viruses, and the like. See, for example, U.S. Pat, Nos. 5,350,674 and 5,585,362, the contents of each of which is herein incorporated by reference in its entirety.

[0324] Methods for introducing a DNA and RNA polynucleotides of interest into a host cell include electroporation of cells, in which an electrical field is applied to cells in order to increase the permeability of the cell membrane, allowing chemicals, drugs, or polynucleotides to be introduced into the cell. DDpp containing DNA or RNA constructs may be introduced into mammalian or prokaryotic cells using electroporation.

[0325] In a preferred embodiment, electroporation of cells results in the expression of a DDpp-CAR on the surface of T cells, NK cells, NKT cells. Such expression may be transient or stable over the life of the cell. Electroporation may be accomplished with methods known in the art including MaxCyte GT® and STX® Transfection Systems (MaxCyte, Gaithersburg, MD, USA).

[0326] Chemical means for introducing a polynucleotide into a host cell include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oILin-water emulsions, micelles, mixed micelles, and liposomes. An exemplary colloidal system for use as a delivery vehicle in vitro and *in vivo* is a liposome (*e.g.,* an artificial membrane vesicle). In the case where a non-viral delivery system is utilized, an exemplary delivery vehicle is a liposome. The use of lipid formulations is contemplated for the introduction of the nucleic acids into a host cell (in vitro, *ex vivo* or *in vivo*). In another aspect, the nucleic acid can be associated with a lipid. The nucleic acid associated with a lipid can be encapsulated in the aqueous interior of a liposome, interspersed within the lipid bilayer of a liposome, attached to a liposome via a linking molecule that is associated with both the liposome and the oligonucleotide, entrapped in a liposome, complexed with a liposome, dispersed in a solution containing a lipid, mixed with a lipid, combined with a lipid, contained as a suspension in a lipid, contained or complexed with a micelle, or otherwise associated with a lipid. Lipid, lipid/DNA or lipid/expression vector associated compositions are not limited to any particular structure in solution. For example, they can be present in a bilayer structure, as micelles, or with a "collapsed" structure. They can also simply be interspersed in a

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solution, possibly forming aggregates that are not uniform in size or shape. Lipids are fatty substances which can be naturally occurring or synthetic lipids. For example, lipids include the fatty droplets that naturally occur in the cytoplasm as well as the class of compounds which contain long-chain aliphatic hydrocarbons and their derivatives, such as fatty acids, alcohols, amines, amino alcohols, and aldehydes.

[0327] Lipids suitable for use can be obtained from commercial sources. For example, dimyristoyl phosphatidylcholine ("DMPC") can be obtained from Sigma, St. Louis, MO; dicetyl phosphate ("DCP") can be obtained from K & K Laboratories (Plainview, NY); cholesterol ("Choi") can be obtained from Calbiochem-Behring; dimyristoyl phosphatidylglycerol ("DMPG") and other lipids may be obtained from Avanti Polar Lipids, Inc. (Birmingham, AL). Stock solutions of lipids in chloroform or chloroform/methanol can be stored at about -20°C. Chloroform may be used as the only solvent since it is more readily evaporated than methanol. "Liposome" is a generic term encompassing a variety of single and multilamellar lipid vehicles formed by the generation of enclosed lipid bilayers or aggregates. Liposomes can be characterized as having vesicular structures with a phospholipid bilayer membrane and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers (Ghosh *et al.*, Glycobiology 5: 505-510 (1991)). However, compositions that have different structures in solution than the normal vesicular structure are also encompassed. For example, the lipids can assume a micellar structure or merely exist as non-uniform aggregates of lipid molecules. Also contemplated are lipofectamine-nucleic acid complexes.

[0328] Regardless of the method used to introduce exogenous nucleic acids into a host cell, or the presence of the recombinant nucleic acid sequence in the host cell can routinely be confirmed through a variety of assays known in the art. Such assays include, for example, "molecular biological" assays known in the art, such as Southern and Northern blotting, RT-PCR and PCR; "biochemical" assays, such as detecting the presence or absence of a particular peptide, *e.g.,* by immunological means (ELISAs and Western blots) or by assays described herein to identify agents falling within the scope of the provided embodiments.

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[0329] Reporter genes are used for identifying potentially transfected cells and for evaluating the functionality of regulatory sequences. In general, a reporter gene is a gene that is not present in or expressed by the recipient organism, tissue, or cell and that encodes a polypeptide whose expression is manifested by some easily detectable property, *e.g.,* enzymatic activity. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells. A non-limiting list of suitable reporter genes can include genes encoding luciferase, beta-galactosidase, chloramphenicol acetyl transferase, secreted alkaline phosphatase, or the green fluorescent protein gene (*e.g.,* Ui-Tei *et al.*, FEBS Lett. 479: 79-82 (2000)). Suitable expression systems are known in the art and can be prepared using known techniques or obtained commercially. In general, the construct with the minimal 5' flanking region showing the highest level of expression of reporter gene is identified as the promoter. Such promoter regions can routinely be linked to a reporter gene and used to evaluate agents for the ability to modulate promoter-driven transcription.

[0330] A number of selection systems can be used in mammalian host-vector expression systems, including, but not limited to, the herpes simplex virus thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase and adenine phosphoribosyltransferase (Lowy *et al.*, Cell 22: 817 (1980)) genes, which can be employed in tk^-, $hgprt^-$ or $aprt^-$ cells, respectively. Additionally, antimetabolite resistance can be used as the basis of selection for *e.g.,* dhfr, gpt, neo, hygro, trpB, hisD, ODC (ornithine decarboxylase), and the glutamine synthase system.

Expression of Cell Associated DDpp

[0331] In another embodiment, the production of DDpp results in cell associated DDpp compositions. For example, the expression of recombinant vectors that encode DDpp operably linked to a cell membrane anchor or transmembrane domain have the potential to remain cell associated. DDpp comprising chimeric antigen receptors are intentionally cell associated and used in the context of the cell in which they are expressed. One particular embodiment relates to a strategy of adoptive cell transfer of T cells which have been transduced to express a DDpp chimeric antigen receptor (CAR). Preferably, the cell can be genetically modified to stably express a DDpp on its surface, conferring novel target specificity that is MHC independent.

[0332] A variety of viral-derived vectors can be used in applications in which viruses are used for transfection and integration into a mammalian cell genome. Viruses, which are useful as vectors include, but are not limited to, retroviruses, adenoviruses, adeno-associated viruses, herpes viruses,

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and lentiviruses. Lentiviral vectors are particularly suitable to achieving long-term gene transfer (*e.g.,* adoptive T cell immune therapy) since they allow long-term, stable integration of a transgene and its propagation in daughter cells. Lentiviral vectors have the added advantage over vectors derived from onco-retroviruses such as murine leukemia viruses in that they can transduce non-proliferating cells, such as hepatocytes. They also have the added advantage of low immunogenicity. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers, (*e.g.,* WO01/96584 and WO01/29058; and U.S. Pat. No. 6,326,193). Several vector promoter sequences are available for expression of the transgenes. One example of a suitable promoter is the immediate early cytomegalovirus (CMV) promoter sequence. This promoter sequence is a strong constitutive promoter sequence capable of driving high levels of expression of any polynucleotide sequence operatively linked thereto. Another example of a suitable promoter is EF1a. However, other constitutive promoter sequences can also be used, including, but not limited to the simian virus 40 (SV40) early promoter, mouse mammary tumor virus (MMTV), human immunodeficiency virus (HIV) long terminal repeat (LTR) promoter, MoMuLV promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, as well as human gene promoters such as, but not limited to, the actin promoter, the myosin promoter, the hemoglobin promoter, and the creatine kinase promoter. Inducible promoters include, but are not limited to a metallothionein promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

[0333] In order to assess the expression of a DDpp-CAR polypeptide or portions thereof, the expression vector to be introduced into a cell can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the population of cells sought to be transfected or infected through viral vectors, in other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co- transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as neo and the like.

[0334] Prior to expansion and genetic modification of the T cells, a source of T cells is obtained from a subject. T cells can be obtained from a number of sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of

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infection, ascites, pleural effusion, spleen tissue, and tumors. In varoius embodiments, any number of T cell lines available in the art, may be used.

[0335] A full discussion of T cell isolation, culturing, activation and expansion methods may be found in WO/12079000, the contents of which is herein incorporated by reference in its entirety.

[0336] Additionally provided is a host cell comprising nucleic acids encoding a DDpp described herein. Compositions comprising a nucleic acid sequence encoding the DDpp are also provided.

[0337] "Co-express" as used herein refers to simultaneous expression of two or more protein coding sequences. The coding sequences may be nucleic acids encoding, for example, a single protein or a chimeric protein as a single polypeptide chain.

Chemical Synthesis of DDpp

[0338] In addition to recombinant methods, DDpp production may also be carried out using organic chemical synthesis of the desired polypeptide using a variety of liquid and solid phase chemical processes known in the art. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Tam *et al.*, J. Am. Chem. Soc. 105: 6442 (1983); Merrifield, Science 232: 341-347 (1986); Barany and Merrifield, The Peptides, Gross and Meienhofer, eds, Academic Press, New York, 1- 284; Barany *et al.*, Int. J. Pep. Protein Res. 30: 705-739 (1987); Kelley *et al.* in Genetic Engineering Principles and Methods, Setlow, J. K., ed. Plenum Press, NY. 1990, vol. 12, pp. 1-19; Stewart *et al.*, Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, 1989. One advantage of these methodologies is that they allow for the incorporation of non-natural amino acid residues into the sequence of the DDpp.

[0339] The DDpp that are used in the methods ecompassed herein may be modified during or after synthesis or translation, *e.g.,* by glycosylation, acetylation, benzylation, phosphorylation, amidation, pegylation, formylation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, ubiquitination, *etc.* (*See, e.g.,* Creighton, Proteins: Structures and Molecular Properties, 2d Ed. (W.H. Freeman and Co., N.Y., 1992); Postranslational Covalent Modification of Proteins, Johnson, ed. (Academic Press, New York, 1983), pp. 1-12; Seifter, Meth. Enzymol. 182:

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626-646 (1990); Rattan, Ann. NY Acad. Sci. 663: 48-62 (1992).) In specific embodiments, the peptides are acetylated at the N-terminus and/or amidated at the C-terminus.

[0340] The disclosure also provides DDpp derivatives and include polypeptides that have been chemically modified in some manner distinct from addition, deletion, or substitution of amino acids. In this regard, a DDpp is chemically bonded with polymers, lipids, other organic moieties, and/or inorganic moieties. Examplary polypeptide modifications are provided in Hermanson, Bioconjugate Techniques, Academic Press, (1996). The DDpp optionally comprise a functional group that facilitates conjugation to another moiety (*e.g.,* a peptide moiety). Exemplary functional groups include, but are not limited to, isothiocyanate, isocyanate, acyl azide, NHS ester, sulfonyl chloride, aldehyde, epoxide, oxirane, carbonate, arylating agent, imidoester, carbodiimide, anhydride, alkyl halide derivatives (*e.g.,* haloacetyl derivatives), maleimide, aziridine, acryloyl derivatives, arylating agents, thiol-disulfide exchange reagents (*e.g.,* pyridyl disulfides or TNB thiol), diazoalkane, carboyldiimadazole, N,N'-Disuccinyl carbonate, N-Hydroxysuccinimidyl chloroformate, and hydrazine derivatives. Maleimide is useful, for example, for generating a DDpp that binds albumin *in vivo*.

[0341] In some embodiments, the DDpp is covalently modified to include one or more water soluble polymer attachments. The water soluble polymer (or other chemical moiety) is attached to any amino acid residue, although attachment to the N- or C-terminus is preferred in some embodiments. Useful polymers include, but are not limited to, PEG (*e.g.,* PEG approximately 40 kD, 30 kD, 20 kD, 10 kD, 5 kD, or 1 kD in size), polyoxyethylene glycol, polypropylene glycol, monomethoxy-polyethylene glycol, dextran, hydroxyethyl starch, cellulose, poly-(N-vinyl pyrrolidone)-polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polysialic acid (PSA), polyoxyethylated polyols (*e.g.,* glycerol) and polyvinyl alcohol, as well as mixtures of any of the foregoing. In one embodiment, the DDpp is PEGylated. PEG moieties are available in different shapes, *e.g.,* linear or branched. For further discussion of water soluble polymer attachments, see U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; and 4,179,337. Other moieties useful for improving peptide half-life or stability are described herein and include, for instance, albumin (optionally modified to allow conjugation to the DDpp), fatty acid chains (*e.g.,* C12-C18 fatty acid, such as a C14 fatty acid, or dicarboxylic acids, such as octadecane dicarboxylic acid (oddc)), an antibody or fragment thereof (*e.g.,* an Fc portion of an antibody), and proline-alanine-serine multimers.

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[0342] In some embodiments, the DDpp is conjugated to a polyethylene glycol (PEG) moiety, human serum albumin (HSA), an antibody or antibody fragment, hydroxyethyl starch, a proline-alanine-serine multimer (PASylation), a C12-C18 fatty acid, or polysialic acid.

[0343] In some embodiments, the DDpp are acylated at the N-terminal amino acid of the peptide. In another aspect, the DDpp are amidated at the C-terminal amino acid of the polypeptide. In a still further aspect, the peptides are acylated at the N-terminal amino acid of the peptide and are amidated at the C-terminal amino acid of the peptide.

[0344] In some embodiments, the DDpp comprises one or more modified or non-proteinogenic amino acids or a modified linker group (*see, e.g.,* Grant, Synthetic Peptides: A User's Guide, Oxford University Press (1992)). Modified amino acids include, for example, amino acids wherein the amino and/or carboxyl group is replaced by another group. Non-limiting examples include modified amino acids incorporating thioamides, ureas, thioureas, acylhydrazides, esters, olefines, sulfonamides, phosphoric acid amides, ketones, alcohols, boronic acid amides, benzodiazepines and other aromatic or non-aromatic heterocycles (*see*, Estiarte *et al.*, Burgers Medicinal Chemistry, 6.sup.th edition, Volume 1, Part 4, John Wiley & Sons, New York (2002)). Non-proteinogenic amino acids include, but are not limited, to beta-alanine (Bal), norvaline (Nva), norleucine (Nle), 4-aminobutyric acid (gamma-Abu), 2-aminoisobutyric acid (Aib), 6-aminohexanoic acid (epsilon-Ahx), ornithine (Orn), hydroxyproline (Hyp), taurine, sarcosine, citrulline (Cit), cysteic acid (Coh), cyclohexylalanine (Cha), methioninesulfoxide (Meo), methioninesulfone (Moo), homoserine-methylester (Hsm), propargylglycine (Eag), 5-fluorotryptophan (5Fw), 6-fluorotryptophan (6Fw), 3',4'-dimethoxyphenyl-alanine (Ear), 3',4'-difluorophenylalanine (Dff), 4'-fluorophenyl-alanine (Pff), 1-naphthyl-alanine (1Ni), 2-Naphthylalanine (2Ni), 1-methyltryptophan (1Mw), penicillamine (Pen), homoserine (Hse), t-butylglycine, t-butylalanine, phenylglycine (Phg), benzothienylalanine (Bta), L-homo-cysteine (Hcy), N-methyl-phenylalanine (Nmf), 2-thienylalanine (Thi), 3,3-diphenylalanine (Ebw), L-alpha-t-Butylglycine (Tle), Bpa, homophenylalanine (Hfe), and S-benzyl-L-cysteine (Ece). These and other non-proteinogenic amino acids may exist as D- or L-isomers. Examples of modified linkers include but are not limited to the flexible linker 4,7,10-trioxa-1,13-tridecanediamine (Ttds), glycine, 6-aminohexanoic acid, beta-alanine (Bal), pentynoic acid (Pyn), and combinations of Ttds, glycine, 6-aminohexanoic acid and Bal.

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[0345] Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to acetylation, formylation, *etc.* Additionally, the derivative may contain one or more non-classical amino acids.

***Table* 1 – Exemplary target-specific binding DDs**

SEQ NO:	D-Domain Sequence	Target	ELISA_avg
11	MGSWYEFSWRLQAIHQRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRAYAAGIRGALQAYRHN	BCMA	9.48683
12	MGSWHEFTWRLIAIQQRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRAYAAGIRHHLQAYRHN	BCMA	17.125
13	MGSWREFAWRLVAINSRLKALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHYAASIRDGLQAYRHN	BCMA	9.66
14	MGSWHEFAWRLQAINQRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHYAAHIRNGLQAYRHN	BCMA	13.14
15	MGSWNEFAWRLTAIEQRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHYAAGIRDNLQAYRHN	BCMA	18.28
16	MGSWTEFAWRLQAIHQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRVYAAKIRISLQAYRHN	BCMA	18.71
17	MGSWIEFAWRLQAIHQRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLREYAANIRDSLQAYRHN	BCMA	18.97
18	MGSWHEFTWRLVAIQQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRKFAAKIRYELQAYRHN	BCMA	19.51
19	MGSWHEFTWRLIAIRERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREYAASIRNMLQAYRHN	BCMA	12.99
20	MGSWIEFSWRLEAIRQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRSYAARIRQELQAYRHN	BCMA	9.92
21	MGSWVEFSWRLEAIRQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRSYAARIRQELQAYRHN	BCMA	19.14
22	MGSWVEFSWRLEAIRQRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRKYAARIRGELQAYRHN	BCMA	21.3
23	MGSWVEFAWRLTAIDQRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRFYAAKIRSHLQAYRHN	BCMA	8.43
24	MGSWVEFAWRLEAIKQRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRLYAAKIRRVLQAYRHN	BCMA	8.9
25	MGSWVEFAWRLTAIHTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRKYAAKIRKQLQAYRHN	BCMA	6.08
26	MGSWTEFAWRLEAINQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGKPEVEALRAYAAKIRTRLQAYRHN	BCMA	15.1475
27	MGSWSEFAWRLEAIHQRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRLFAAQIRENLQAYRHN	BCMA	18.04
28	MGSWNEFAWRLIAINQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRHFAANIRNDLQAYRHN	BCMA	11.53
29	MGSWTEFAWRLIAIDQRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILRELAAEIRFHLQAYRHN	BCMA	8.55
30	MGSWSEFMNRLDAITYRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRHYAAQIRDSLQAYRHN	BCMA	12.9

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
31	MGSWTEFMERLDAISYRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDYAAIIRNSLQAYRHN	BCMA	9.87
32	MGSWAEFMDRLDAITYRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRGYAAIIRSELQAYRHN	BCMA	10.83
33	MGSWIEFQERLDAIFYRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRDAAATIRRQLQAYRHN	BCMA	18.58
34	MGSWIEFQQRLDAIFYRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRDMAAIIRKQLQAYRHN	BCMA	20.02
35	MGSWYEFQSRLDAIFYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREAAASIRTQLQAYRHN	BCMA	14.08
36	MGSWSEFIDRLDAITYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRWYAGVIREQLQAYRHN	BCMA	10.18
37	MGSWSEFYDRLYAINQRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAAFIRAQLQAYRHN	BCMA	5.98
38	MGSWYEFYDRLDAIVHRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRWYAAMIRVRLQAYRHN	BCMA	14.68
39	MGSWVEFQDRLEAITDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAAMIRVILQAYRHN	BCMA	8.87825
40	MGSWVEFQERLMAISDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWQAAMIRYTLQAYRHN	BCMA	6.7
41	MGSWFEFQHRLEAISMRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWQAAYIRVVLQAYRHN	BCMA	4.05
42	MGSWVEFQSRLEAIATRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWQAAWIRMMLQAYRHN	BCMA	18.0075
43	MGSWEEFQYRLGAIAARLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWQAAMIRFMLQAYRHN	BCMA	3.11
44	MGSWYEFQVRLQAISWRLKALGGSEAELAAFEKEIAAFESE LQAYKGKGNHEVEELRIQAALIRVMLQAYRHN	BCMA	14.23
45	MGSWVEFRSRLEAISNRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRTTAALIRVYLQAYRHN	BCMA	3.04
46	MGSWVEFKARLEAISSRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRVYLQAYRHN	BCMA	8.70714
47	MGSWSEFYTRLEAINNRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYTAALIRIYLQAYRHN	BCMA	3.66
48	MGSWAEFYHRLDAISSRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYTAALIRIYLQAYRHN	BCMA	4.31
49	MGSWTEFASRLVAIRQRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAAIIRVMLQAYRHN	BCMA	7.99
50	MGSWSEFDQRLAAIYQRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRVMLQAYRHN	BCMA	7.72
51	MGSWVEFHNRLSAISDRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRVMLQAYRHN	BCMA	7.36
52	MGSWNEFEDRLSAISARLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRVMLQAYRHN	BCMA	4.09
53	MGSWVEFEYRLVAIFDRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYQAALIRVMLQAYRHN	BCMA	7.63
54	MGSWVEFQGRLGAIHERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRVFLQAYRHN	BCMA	3.83429

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
55	MGSWYEFSMRLSAIWERLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYQAALIRFYLQAYRHN	BCMA	7.12
56	MGSWTEFSQRLGAISERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRFMLQAYRHN	BCMA	4.15
57	MGSWTEFHDRLEAITHRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALLRVFLQAYRHN	BCMA	5.79
58	MGSWTEFEHRLEAIAGRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAALIRFWLQAYRHN	BCMA	6.34
59	MGSWTEFANRLEAINARLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFSAALIRVYLQAYRHN	BCMA	6.42
60	MGSWEEFDRRLYAIARRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYQAALIRVWLQAYRHN	BCMA	8.85
61	MGSWIEFHQRLEAIVTRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYQAALIRVFLQAYRHN	BCMA	8
62	MGSWSEFYDRLKAIADRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRTEAAIIRVYLQAYRHN	BCMA	8.215
63	MGSWWEFEDRLSAIMERLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYRAAIIRVYLQAYRHN	BCMA	10.39
64	MGSWVEFEERLAAIATRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWRAAIIRVYLQAYRHN	BCMA	16.29
65	MGSWSEFRGRLQAIHSRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYSAAIIRIYLQAYRHN	BCMA	7.585
66	MGSWTEFRDRLGAIYHRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYQAAIIRVYLQAYRHN	BCMA	6.7
67	MGSWVEFYHRLEAIRYRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYVAAVIRYRLQAYRHN	BCMA	7.8
68	MGSWVEFYDRLEAIRYRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYIAAVIRYRLQAYRHN	BCMA	5.636
69	MGSWVEFYDRLAAIRKRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFRAALIRIWLQAYRHN	BCMA	9.76
70	MGSWEEFSERLEAISIRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRVSAAIIRVWLQAYRHN	BCMA	11.26
71	MGSWSEFSDRLHAISDRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRIQAAIIRVWLQAYRHN	BCMA	6.3725
72	MGSWIEFSHRLEAIVDRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRNTAAIIRVYLQAYRHN	BCMA	18.67
73	MGSWEEFSDRLEAILRRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRFAAAIIRVQLQAYRHN	BCMA	9.08
74	MGSWMEFSHRLDAIHERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRFAAAIIRVQLQAYRHN	BCMA	6.3
75	MGSWSEFQQRLHAIRTRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFEAAIIRVMLQAYRHN	BCMA	11.615
76	MGSWYEFQNRLGAINRRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFEAAIIRVMLQAYRHN	BCMA	4.68
77	MGSWQEFTGRLHAIRHRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFEAAYIRVWLQAYRHN	BCMA	3.315
78	MGSWTEFDHRLGAIWERLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFHAAIIRIFLQAYRHN	BCMA	9.54

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
79	MGSWTEFHVRLSAIWDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFHAAIIRIVLQAYRHN	BCMA	23.62
80	MGSWNEFDNRLQAIWDRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFHAAMIRITLQAYRHN	BCMA	9.87
81	MGSWTEFHERLQAIWFRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFRAAIIRLYLQAYRHN	BCMA	12.0656
82	MGSWNEFSGRLTAIKDRLAALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRFRAAVIRLWLQAYRHN	BCMA	3.39
83	MGSWVEFDERLVAIWFRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRARAAYIRIWLQAYRHN	BCMA	8.96
84	MGSWSEFGQRLSAIWERLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRADAAFIRIWLQAYRHN	BCMA	14.01
85	MGSWYEFEDRLVAIWIRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYNAAFIRGALQAYRHN	BCMA	4.93
86	MGSWYEFGDRLSAIWERLAALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRTHAAEIRTILQAYRHN	BCMA	8.895
87	MGSWHEFYYRLEAIEQRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRFDAALIRIYLQAYRHN	BCMA	3.73
88	MGSWSEFEERLAAIGSRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRFDAALIRIYLQAYRHN	BCMA	4.85
89	MGSWLEFHYRLHAIQFRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRHIAALIRNQLQAYRHN	BCMA	12.7486
90	MGSWQEFYNRLEAIHMRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEGLRSDAAPIRDVLQAYRHN	BCMA	6.47
91	MGSWNEFHHRLWAIFDRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRKMAAGIRGGLQAYRHN	BCMA	3.88
92	MGSWYEFHYRLKAINDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRYSAAMIRHKLQAYRHN	BCMA	6.04
93	MGSWTEFHQRLGAIHARLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFSAAFIRLKLQAYRHN	BCMA	8.87
94	MGSWFEFQYRLEAIFYRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGKPEVEELRVRAALIRHLLQAYRHN	BCMA	17.31
95	MGSWVEFHARLDAIYTRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRVLAAHIRISLQAYRHN	BCMA	3.8
96	MGSWVEFGTRLSAIYNRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRFEAAIIRIMLQAYRHN	BCMA	15.425
97	MGSWVEFTHRLDAIYIRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHEAAVIREELQAYRHN	BCMA	13.9167
98	MGSWVEFHGRLAAIYVRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRYHAAMIRRNLQAYRHN	BCMA	4
99	MGSWVEFDRRLVAIYIRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRDDAALIRLLLQAYRHN	BCMA	8.93
100	MGSWVEFDRRLVAIYIRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYDAATIRETLQAYRHN	BCMA	8
101	MGSWLEFDRRLTAIYLRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALREDAAMIRDMLQAYRHN	BCMA	9.82
102	MGSWIEFDRRLLAIHVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRADAAKIRMELQAYRHN	BCMA	13.72

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
103	MGSWIEFDRRLIAIWIRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRSDAADIRQKLQAYRHN	BCMA	9.45
104	MGSWVEFDRRLIAIWVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRSDAAMIREHLQAYRHN	BCMA	5.77
105	MGSWYEFHTRLIAIYVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRGDAAKIRGYLQAYRHN	BCMA	4.06
106	MGSWSEFSTRLSAIYVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRNKAASIRKTLQAYRHN	BCMA	5.35
107	MGSWVEFRYRLGAIYHRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDRAATIRRLLQAYRHN	BCMA	10.81
108	MGSWNEFRNRLGAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRAHAAIIRSVLQAYRHN	BCMA	4.69667
109	MGSWHEFRNRLGAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRARAAMIRSVLQAYRHN	BCMA	3.49359
110	MGSWTEFYQRLEAINFRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDKAALIRLMLQAYRHN	BCMA	6.955
111	MGSWNEFYNRLHAINLRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLREHAAIIRQALQAYRHN	BCMA	3.00395
112	MGSWEEFYGRLSAIQDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRMHAAVIRRALQAYRHN	BCMA	3.28
113	MGSWGEFNLRLVAIHVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRSQAANIRAQLQAYRHN	BCMA	12.81
114	MGSWGEFSDRLEAINERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRWQAAFIRANLQAYRHN	BCMA	4.26
115	MGSWMEFQGRLPAILARLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDKAAYIRWMLQAYRHN	BCMA	8.32
116	MGSWMEFEGRLPAILARLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDKAAYIRWMLQAYRHN	BCMA	3.93
117	MGSWFEFQNRLQAILFRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRDKAAYIRLMLQAYRHN	BCMA	5.39333
118	MGSWVEFDMRLQAILERLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDSAAYIRLMLQAYRHN	BCMA	23.525
119	MGSWVEFNARLDAILFRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDQAAYIRLMLQAYRHN	BCMA	13.52
120	MGSWMEFNVRLRAILDRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRDKAAYIRFMLQAYRHN	BCMA	15.59
121	MGSWIEFDTRLAAIVHRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRDKAAYIRYMLQAYRHN	BCMA	13.9475
122	MGSWIEFDYRLKAILHRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEGLRDKAAYIRFLLQAYRHN	BCMA	11.8767
123	MGSWYEFEDRLLAIKVRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRDQAAYIRFMLQAYRHN	BCMA	17.6133
124	MGSWYEFQDRLSAITTRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRDKAAYIRFMLQAYRHN	BCMA	10.085
125	MGSWEEFDDRLNAIVYRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRDQAAYIRLMLQAYRHN	BCMA	18.64
126	MGSWVEFEQRLHAIVVRLRALGGSEAELAAFEKEIAAFESE LQAYKGGGNPEVENLRDQAAYIRFMLQAYRHN	BCMA	17.7467

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
127	MGSWVEFEWRLEAIVVRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDKAAYIRYMLQAYRHN	BCMA	14.95
128	MGSWYEFEHRLKAIVSRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDKAAYIRYMLQAYRHN	BCMA	4.55
129	MGSWMEFKHRLAAITFRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRDKAAYIRLLLQAYRHN	BCMA	6.06
130	MGSWMEFEGRLHAIKRRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDQAAYIRLLLQAYRHN	BCMA	7.335
131	MGSWSEFVFRLDTIKSRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRDQAAYIRLMLQAYRHN	BCMA	19.86
132	MGSWYEFDERLSAIKLRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRAQAAYIRAILQAYRHN	BCMA	16.94
133	MGSWMEFDERLWAIKKRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRHQAAYIRMLLQAYRHN	BCMA	9.526
134	MGSWHEFDGRLSAIKRRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRDQAAYIRYMLQAYRHN	BCMA	5.4
135	MGSWYEFDGRLQAIIARLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRFRAAYIRWILQAYRHN	BCMA	3.29
136	MGSWFEFDKRLYAIIHRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYKAAIIRLYLQAYRHN	BCMA	11.82
137	MGSWVEFDNRLYAIVDRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRQKAAYIRLILQAYRHN	BCMA	11.7167
138	MGSWIEFHQRLNAIFNRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRHHAAYIREMLQAYRHN	BCMA	7.34167
139	MGSWNEFRLRLWAITERLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVECLRAEAAWIRTMLQAYRHN	BCMA	3.87179
140	MGSWYEFWLRLSAISYRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRKEAAEIRSWLQAYRHN	BCMA	14.4653
141	MGSWYEFQLRLWAIHWRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRMRAAEIRNELQAYRHN	BCMA	20.59
142	MGSWYEFAHRLEAIEWRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRQYAAAIRNYLQAYRHN	BCMA	9.48
143	MGSWYEFDTRLGAIRNRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRFQAAYIRFLLQAYRHN	BCMA	13.934
144	MGSWYEFWVRLTAIRWRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREQAASIRWVLQAYRHN	BCMA	5.72
145	MGSWFEFDRRLKAIDRRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRMQAAIIRNYLQAYRHN	BCMA	6.1625
146	MGSWVEFWERLDAIDNRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRWHAAYIRGYLQAYRHN	BCMA	11.42
147	MGSWAEFWDRLDAIDSRLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREWAAYIRGYLQAYRHN	BCMA	18.22
148	MGSWAEFDLRLRAIAKRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRLDAAYIRGVLQAYRHN	BCMA	4.09
149	MGSWSEFWDRLYAIRIRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRSVAARIRNWLQAYRHN	BCMA	12.52
150	MGSWSEFWFRLGAIRNRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRDVAAHIRHWLQAYRHN	BCMA	14.93

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
151	MGSWSEFNDRLDAIRWRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRQVAATIRYRLQAYRHN	BCMA	13.59
152	MGSWVEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAAAIRHYLQAYRHN	BCMA	5.22
153	MGSWAEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAAAIRHYLQAYRHN	BCMA	
154	MGSWTEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAAAIRHYLQAYRHN	BCMA	
155	MGSWVEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLKYTAAAIRHYLQAYRHN	BCMA	
156	MGSWVEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLQYTAAAIRHYLQAYRHN	BCMA	
157	MGSWVEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAAAIKHYLQAYRHN	BCMA	
158	MGSWAEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLQYTAAAIKHYLQAYRHN	BCMA	
159	MGSWTEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLQYTAAAIKHYLQAYRHN	BCMA	
160	MGSWVEFWDRLGAIRERLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYVAAVIRHRLQAYRHN	BCMA	4.18
161	MGSWVEFWDRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRASAAAIRIALQAYRHN	BCMA	3.07
162	MGSWVEFWDRLGAIRDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRNTAAYIRTFLQAYRHN	BCMA	16.034
163	MGSWSEFWVRLGAIRDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRVTAAQIRHYLQAYRHN	BCMA	23.5
164	MGSWSEFWVRLGAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAATIRRFLQAYRHN	BCMA	7.55667
165	MGSWSEFWARLGAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAATIRRFLQAYRHN	BCMA	
166	MGSWSEFWVRLGAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAGTIRRFLQAYRHN	BCMA	
167	MGSWSEFWVRLGAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAATIKRFLQAYRHN	BCMA	
168	MGSWSEFWARLGAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAGTIKRFLQAYRHN	BCMA	
169	MGSWSEFWDRLTAIRVRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRYTAAHIRKFLQAYRHN	BCMA	16.14
170	MGSWTEFWTRLNAIYERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRFTAASIRMYLQAYRHN	BCMA	8.43
171	MGSWFEFWDRLAAIRDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRYVAAKIRVRLQAYRHN	BCMA	12.78
172	MGSWTEFWVRLNAIRDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRHTAAIIRNYLQAYRHN	BCMA	12.53
173	MGSWVEFWHRLGAIYDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRRTAALIRQTLQAYRHN	BCMA	19.904
174	MGSWVEFWNRLGAIYDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRHTAAVIRLYLQAYRHN	BCMA	14.55

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
175	MGSWSEFWERLEAIYDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRRTAATIRSFLQAYRHN	BCMA	18.78
176	MGSWEEFDNRLEAIFDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREFAATIRITLQAYRHN	BCMA	3.93
177	MGSWMEFWDRLYAIEFRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRRVAATIRNELQAYRHN	BCMA	11.6925
178	MGSWTEFWERLYAIEYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRSVAATIRYELQAYRHN	BCMA	12.7
179	MGSWNEFWERLYAIELRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRMTAAYIRNELQAYRHN	BCMA	9.945
180	MGSWYEFWKRLYAIEYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRKVAAKIREQLQAYRHN	BCMA	14.785
181	MGSWTEFWARLYAIEMRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRRVAALIREQLQAYRHN	BCMA	12.46
182	MGSWHEFWDRLYAIEFRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRQVAAKIRWHLQAYRHN	BCMA	7.3
183	MGSWDEFEFRLGALRWRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFGAAHIRHILQAYRHN	BCMA	9.2
184	MGSWTEFYHRLYAIRERLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFGAAHIRHLLQAYRHN	BCMA	9.6275
185	MGSWVEFETRLDAIRMRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFGAAHIRALLQAYRHN	BCMA	14.0717
186	MGSWGEFDVRLFAIRERLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRGYAAQIRSFLQAYRHN	BCMA	7.35333
187	MGSWVEFDERLSAIRERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRLYAAQIRVFLQAYRHN	BCMA	5.61
188	MGSWSEFDGRLGAIWDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRDRAAQIREFLQAYRHN	BCMA	10.0305
189	MGSWGEFEGRLHAIRSRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRGYAAWIRALLQAYRHN	BCMA	6.17
190	MGSWGEFNGRLGAIRERLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRAYAASIRAVLQAYRHN	BCMA	4.95333
191	MGSWWEFTFRLAAIEFRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRAIAAEIRKSLQAYRHN	BCMA	5.75
192	MGSWDEFQFRLAAIGFRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRRQAARIRHLLQAYRHN	BCMA	6.155
193	MGSWYEFVTRLHAIDHRLKALGGSEADLAAFEKEIAAFESE LQAYKGKGNPEVEWLRFYAAGIRMNLQAYRHN	BCMA	4.12
194	MGSWSIEFWRLEAIKFRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRVEAAAIRRVLQAYRHN	BCMA	8.43
195	MGSWGEFEHRLDPSTCVWLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRRGAAVIRHWLQAYRHN	BCMA	4.05
196	MGSWIEFAMRLEAIENRLTALGGSEAELAIFESMIAHFEEL LQNYKGKGNPEVEALIHEAFAIHKELWAYRHN	BCMA	10.73
197	MGSWNEFYQRLEAIENRLQALGGSEAELAMFEVRIALFEDM LQGYKGKGNPEVEALKQEAIAILRELIAYRHN	BCMA	6.01
198	MGSWNEFYDRLRAIKKRLYALGGSEAELADFEEDIAQFEVD LQDYKGKGNPEVEALHREAHAITHELWAYRHN	BCMA	12.36

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
199	MGSWGEFKHRLALIKWYLEALGGSEAELAHFEDWIAVFEVQ LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	17.09
200	MGSWYEFKHRLAIIKWYLEALGGSEAELAKFEAWIAEFEMI LQRYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	5.505
201	MGSWYEFKHRLAIIKWYLEALGGSEAELAHFEQYIADFEGT LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.8333
202	MGSWYNFKHRLAIIKWYLEALGGSEAELARFENFIANFETQ LQLYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.7615
203	MGSWFQFKHRLAIIKWQLEALGGSEAELAWFEQWIADFEHQ LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.39
204	MGSWYNFKHRLAIIKWFLEALGGSEAELAVFEVWIADFEHQ LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	16.38
205	MGSWDAFKHRLALIKWYLEALGGSEAELAHFEEYIAEFESN LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.98
206	MGSWDGFKHRLALIKWYLEALGGSEAELANFENWIAEFEQR LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	23.62
207	MGSWNGFKHRLAIIKWYLEALGGSEAELASFESYIAEFESG LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	16.53
208	MGSWNSFKHRLALIKWYLEALGGSEAELATFEWYIASFESE LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.34
209	MGSWSDFKYRLAVIKFYLEALGGSEAELASFESFIAHFEDD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.04
210	MGSWSGFKYRLAVIKFYLEALGGSEAELASFELFIAKFEID LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.066
211	MGSWYGFKYRLAVIKWYLEALGGSEAELASFEKYIAHFEHD LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.05
212	MGSWYGFKYRLAVIKWYLEALGGSEAELASFEKYIAQFEHD LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.63333
213	MGSWYGFKYRLALIKWYLEALGGSEAELASFETYIADFEDL LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.03
214	MGSWSTFKYHLAVIKWYLEALGGSEAELASFEDYIAQFETD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.65
215	MGSWHEFKYRLALIKWYLEALGGSEAELATFEHHIAQFEWD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	16.19
216	MGSWNMFKYRLAHIKWYLEALGGSEAELATFEAYIADFEVD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	16.33
217	MGSWHGFKYRLAIIKWWLEALGGSEAELAFFEEWIASFERD LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.025
218	MGSWHGFKYRLAVIKWYLEALGGSEAELAMFEGWIAQFEIT LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	5.99
219	MGSWQGFKYRLAVIKWMLEALGGSEAELAFFENWIAEFETK LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.75
220	MGSWSGFKYRLAVIKWYLEALGGSEAELATFEEWIAEFETE LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.975
221	MGSWGYFKYRLAMIKWYLEALGGSEAELASFESWIAEFEGS LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.018
222	MGSWHAFKYKLAMIKWYLEALGGSEAELAHFEEWIAEFEAL LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.63

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
223	MGSWQHFKYRLAIIKWYLEALGGSEAELAFFESFIAKFEHD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	8.91
224	MGSWNDFKYRLAIIKYYLEALGGSEAELAHFESYIASFEHD LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.1233
225	MGSWGAFKYRLAIIKFYLEALGGSEAELARFEEFIANFEHD LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.88
226	MGSWYNFKYRLAIIKFYLEALGGSEAELAQFEIWIAEFEHD LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	19.91
227	MGSWEQFKYRLAIIKYMLEALGGSEAELAWFESWIANFESD LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.01
228	MGSWQQFKYRLAIIKYYLEALGGSEAELAGFETYIAKFEEV LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.12
229	MGSWAGFKYRLAVIKYYLEALGGSEAELAHFEQWIAHFEGM LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.68
230	MGSWTAFKYRLAIIKFYLEALGGSEAELAHFESYIAHFEDM LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.43
231	MGSWAHFKYRLAIIKFWLEALGGSEAELANFEEYIAEFEST LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.12
232	MGSWANFKYRLALIKWHLEALGGSEAELASFEIWIADFEES LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.2878
233	MGSWATFKYRLALIKWHLEALGGSEAELADFEEYIAGFEEG LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.07
234	MGSWTHFKYRLALIKWWLEALGGSEAELAGFEVHIADFEAQ LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.36692
235	MGSWNTFKYHLAVIKFMLEALGGSEAELAFFEQWIAEFEVT LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.6006
236	MGSWTQFKYHLAVIKWYLEALGGSEAELAGFEQWIAEFEKT LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	21.1178
237	MGSWNQFKYRLAVIKFYLEALGGSEAELAHFETWIAAFEEQ LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.85
238	MGSWNEFKYHLAVIKFYLEALGGSEAELAHFETWIAEFEYE LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.68
239	MGSWVQFKYHLAVIKFYLEALGGSEAELAHFETWIAEFEVA LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.6957
240	MGSWVDFKYHLAVIKFWLEALGGSEAELANFETWIANFEQE LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.22
241	MGSWVDFKYHLAVIKWYLEALGGSEAELADFENWIAHFESI LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.43
242	MGSWVEFKYHLAVIKFTLEALGGSEAELADFEEEIARFEMI LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.92
243	MGSWSHFKYHLALIKWYLEALGGSEAELAKFEFWIAEFEHN LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.93
244	MGSWYHFKYHLALIKWYLEALGGSEAELAHFEHWIAEFEWT LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	8.85
245	MGSWQGFKYHLALIKFYLEALGGSEAELAHFEHWLAEFEHD LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	21.2
246	MGSWLSFKHHLALIKWYLEALGGSEAELASFEAWIALFEHQ LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.305

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
247	MGSWSEFKYKLALIKWYLEALGGSEAELAHFEGWIANFETT LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.2875
248	MGSWIEFKYKLAIIKFYLEALGGSEAELAHFEHWIADFEFV LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.88
249	MGSWQNFKYHLAMIKWYLEALGGSEAELANFEEFIAQFEIN LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.55
250	MGSWYNFKYHLAIIKWWLEALGGSEAELADFEHYIADFERN LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	8.62636
251	MGSWYQFKYHLAIIKWYLEALGGSEAELAGFENYIATFEQE LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.41
252	MGSWSHFKYHLAIIKFYLEALGGSEAELAGFEIWIAKFEDE LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.34
253	MGSWVGFKAHLAIIKWYLEALGGSEAELAGFEIFIADFEAL LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.71
254	MGSWVNFKYKLAIIKYMLEALGGSEAELAFFEDWIAEFERT LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.38951
255	MGSWSNFKYRLAVIKYMLEALGGSEAELAFFEDWIADFELH LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.34
256	MGSWTNFKYKLAVIKFMLEALGGSEAELAFFEDWIAGFEID LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.4075
257	MGSWTGFKYRLAIIKFMLEALGGSEAELAFFEQWIADFENE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.89
258	MGSWHNFKYRLAIIKFMLEALGGSEAELAWFENWIADFEDS LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.59
259	MGSWFAFKHRLAVIKYMLEALGGSEAELAFFEHWIAQFEHD LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	11.985
260	MGSWYEFKHRLAVIKYMLEALGGSEAELAFFENWIAQFEHE LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	3.71
261	MGSWYKFKHKLAVIKYMLEALGGSEAELAWFEEWIAEFEVT LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	4.54
262	MGSWFYFKQKLAFIKWYLEALGGSEAELANFEIYIAEFEVM LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.23
263	MGSWFSFKHHLAVIKWNLEALGGSEAELASFEEQIAEFESV LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.45
264	MGSWGNFKYRLAIIKFHLEALGSSEAELATFEAWIANFESM LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	22.7
265	MGSWSYFKYGLAIIKIRLEALGGSEAELADFERWIAAFEHD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.33
266	MGSWSYFKFGLAHIKLRLEALGGSEAELADFEQWIASFEEQ LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.354
267	MGSWSYFKWGLAHIKLRLEALGGSEAELADFEFWIAEFEGL LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	17.64
268	MGSWIYFKYGLAHIKTRLEALGGSEAELADFEQWIAEFEKM LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	21.12
269	MGSWGYFKYGLATIKHRLEALGGSEAELADFELWIAKFEEQ LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.01

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
270	MGSWEYFKYGLATIKMHLEALGGSEAELADFEHWIAHFEHQ LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.4033
271	MGSWSYFKYGLATIKEKLEALGGSEAELADFETWIAMFEKQ LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.15
272	MGSWHYFKNGLAIIKEKLEALGGSEAELADFEIWIAMFEME LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	19.85
273	MGSWQYFKYGLAIIKIKLEALGGSEAELADFEAWIATFEKQ LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.28
274	MGSWVYFKHGLAVIKMRLEALGGSEAELADFETWIAQFEMT LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	21.45
275	MGSWVYFKYGLAVIKEKLEALGGSEAELADFETWIAEFEFG LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	17.58
276	MGSWYYFKYGLAVIKGKLEALGGSEAELADFETWIAKFENH LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	3.84
277	MGSWTYFKYGLALIKYRLEALGGSEAELADFEEWIAQFEVS LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.21
278	MGSWDYFKYGLALIKIKLEALGGSEAELADFEVWIAQFEMA LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.76
279	MGSWTYFKFGLAHIKDSLEALGGSEAELADFEQWIAMFEQD LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	17.01
280	MGSWGYFKHGLAHIKSSLEALGGSEAELADFEVWIAAFENE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.505
281	MGSWGYFKTGLAIIKAQLEALGGSEAELADFELWIAQFEET LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.75
282	MGSWAYFKYGLAVIKLHLEALGGSEAELADFERYIAEFEYE LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.44
283	MGSWLDFKEGLADIKRSLEALGGSEAELADFEGVIALFEWK LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	3.03
284	MGSWEVFKHELAVIKDYLEALGGSEAELAHFEWGIAWFEGF LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.33
285	MGSWIVFKQSLAWIKEHLEALGGSEAELAEFEFYIANFEHT LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.57
286	MGSWIYFKDSLAYIKKYLEALGGSEAELATFEYYIANFEHE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	3.2
287	MGSWDHFKYNLAWIKKYLEALGGSEAELATFEWYIANFEKR LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.81
288	MGSWFTFKQNLAWIKLHLEALGGSEAELARFEYYIADFENK LQLYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.204
289	MGSWREFKYGLAHIKRVLEALGGSEAELAVFEYYIAKFEQE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	14.7
290	MGSWIQFKYGLAHIKRTLEALGGSEAELAVFEWYIADFEQQ LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	8.35667
291	MGSWVEFKHNLAWIKVTLEALGGSEAELAVFEYYIAQFEEQ LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	15.83
292	MGSWISFKDNLAMIKEFLEALGGSEAELAVFEWYIATFEVE LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.16

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
293	MGSWHIFKDNLATIKAFLEALGGSEAELAVFEWYIAKFEEE LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	3.47
294	MGSWTSFKHGLAGIKRVLEALGGSEAELATFEWYIAQFERH LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	9.765
295	MGSWQSFKHALADIKINLEALGGSEAELAQFEYAIAVFEYR LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	13.7188
296	MGSWHTFKEALAQIKGELEALGGSEAELASFEYAIAVFEYR LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.76
297	MGSWTDFKTSLADIKAELEALGGSEAELAKFEYYIAIFEYR LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	18.76
298	MGSWTNFKEGLAEIKRDLEALGGSEAELARFEYVIAVFEFR LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	12.3267
299	MGSWHTFKDGLAEIKSELEALGGSEAELAMFEYVIAIFEYR LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.65
300	MGSWQFFKEHLASIKFWLEALGGSEAELAFFEDAIADFEYH LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.58
301	MGSWTYFKEHLASIKFWLEALGGSEAELAFFEDAIAEFEKD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	6.59507
302	MGSWIIFKGYLAHIKHHLEALGGSEAELADFEFYIAIFEME LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	5.18
303	MGSWYLFQSHLAHIKHHLEALGGSEAELAWFEFTIAGFEQE LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	7.69
304	MGSWYSFKWTLARIKLELEALGGSEAELAYFENVIAHFEME LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	4.05
305	MGSWTTLKWRLAHIKQHLEALGGSEAELALFEYDIAHFEEL LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	17.82
306	MGSWYGFKWYLATIKKHLEALGGSEAELALFETEIATFELW LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	BCMA	10.65
307	MGSWIEFNMRVLAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRYEACLDPWSSAAYRHN	CD123	3.2
308	MGSWIEFHERLWAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREMAASIRHGLQAYRHN	CD123	3.4
309	MGSWFEFYERLWAIDDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAASIRSSLQAYRHN	CD123	6
310	MGSWFEFWDRLEAIDDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRYNAAEIRKELQAYRHN	CD123	4.9
311	MGSWHEFWSRLDAIDDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRGAAADIRAELQAYRHN	CD123	3.8
312	MGSWYEFWIRLEAIDDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVDILRDFAADIRTELQAYRHN	CD123	10.4
313	MGSWHEFWDRLEAIDDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAYIRELLQAYRHN	CD123	10.6
314	MGSWEEFWDRLFAIDDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRNEAAEIRMALQAYRHN	CD123	3.1
315	MGSWWEFDDRLFAIDTRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREWAATIRMELQAYRHN	CD123	3.5
316	MGSWTEFHDRLEAIDDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREEAAQIRWELQAYRHN	CD123	5.8

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
317	MGSWAEFEDRLWAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREEAAAIRFELQAYRHN	CD123	6.2
318	MGSWVEFWFRLEAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAAAIREDLQAYRHN	CD123	3.2
319	MGSWVEFWQRLEAIESRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAEIRWELQAYRHN	CD123	7.7
320	MGSWSEFWQRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRENAAMIRDELQAYRHN	CD123	4.7
321	MGSWSEFITRLEAIDDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILREEAAEIRQHLQAYRHN	CD123	3.3
322	MGSWYEFETRLEAIYDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRVEAAEIREDLQAYRHN	CD123	3.2
323	MGSWTEFYYRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRVEAANIRDMLQAYRHN	CD123	7.5
324	MGSWYEFVIRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRWYAADIRHELQAYRHN	CD123	6.4
325	MGSWTEFSIRLEAIYDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRTYAANIRHELQAYRHN	CD123	11.9
326	MGSWTEFSIRLEAIYDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRTYAAFIRHELQAYRHN	CD123	10.2
327	MGSWTEFVWRLEAIWDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLREDAAVIRHFLQAYRHN	CD123	3.6
328	MGSWVEFHERLEAIEDRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREDAAFIRQLLQAYRHN	CD123	3.7
329	MGSWVEFHDRLEAIEDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAYIRSILQAYRHN	CD123	4.6
330	MGSWIEFYDRLEAIYDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAFIRSWLQAYRHN	CD123	7.5
331	MGSWVEFDQRLEAIYDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAQIRKWLQAYRHN	CD123	5.1
332	MGSWVEFHDRLEAIEDRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLREYAAGIRWFLQAYRHN	CD123	3.3
333	MGSWEEFAQRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRYVAAQIRYHLQAYRHN	CD123	16.9
334	MGSWDEFAWRLDVIFARLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRKNAAQIRDGLQAYRHN	CD123	4.6
335	MGSWDEFYYRLEAIEMRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHYAAQIRHMLQAYRHN	CD123	7.2
336	MGSWEEFYDRLEAIYNRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLREYAADIREMLQAYRHN	CD123	18.6
337	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRKEAAVIRENLQAYRHN	CD123	
338	MGSWDEFGRRLYAIEWQLYALGGTEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRKEAAVIRENLQAYRHN	CD123	
339	MGSWDEFGRRLYAIETQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
340	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
341	MGSWDEFGRRLYAIKWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
342	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRKIAAVIRENLQAYRHN	CD123	
343	MGSWDEFGRRLYAIEWQLYALGGGEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
344	MGSWDEFGRRLYAIEWQLYALGGTEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
345	MGSWDEFGRRLYAIEWQLYALGGGEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
346	MGSWDEFGRRLYAIEWQLYALGGTEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
347	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
348	MGSWDEFGRRLAAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
349	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEALREIAAVIRENLQAYRHN	CD123	
350	MGSWDEFGRRLYAIEWQLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREEAAVIRENLQAYRHN	CD123	
351	MGSWDEFGRRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGSPEVEKLREIAAVIRSNLQAYRHN	CD123	
352	MGSWDEFGRRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	5.8
353	MGSWDEFGRRLYAIEWRLYALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
354	MGSWDEFGRRLYAIEWQLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
355	MGSWDEFSRRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHN	CD123	
356	MGSWDEFGRRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
357	MGSWDEFGRRLAAIKTQLAALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
358	MGSWDEFGRRLAAIKTQLAALGGTEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRENLQAYRHN	CD123	
359	MGSWDEFGRRLAAIKTQLAALGGEEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRKEAAVIRENLQAYRHN	CD123	
360	MGSWDEFGRRLAAIKTQLAALGGTEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRKEAAVIRENLQAYRHN	CD123	
361	MGSWDEFEQRLIAIEERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAAVIRKYLQAYRHN	CD123	5.9
362	MGSWVEFDQRLGAIWDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRQGAAVIRDDLQAYRHN	CD123	5.3
363	MGSWVEFDMRLSAIWERLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAEIREFLQAYRHN	CD123	3.3
364	MGSWVEFDQRLDAIYERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAEIREHLQAYRHN	CD123	10.5

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
365	MGSWHEFDQRLWAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRLYAALIRHDLQAYRHN	CD123	3.3
366	MGSWVEFWDRLDAIEGRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWLAAEIRADLQAYRHN	CD123	3.5
367	MGSWVEFYSRLDAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRIAAASIREDLQAYRHN	CD123	9.4
368	MGSWYEFYERLDAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDWAAWIREDLQAYRHN	CD123	8.4
369	MGSWFEFDDRLWAIENRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRDNAAWIREILQAYRHN	CD123	4.2
370	MGSWYEFWDRLDALEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRDSAAFIREELQAYRHN	CD123	9.7
371	MGSWMEFVDRLDAIESRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRIEAAFIREELQAYRHN	CD123	5.8
372	MGSWDEFVDRLWAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRIQAAIIREALQAYRHN	CD123	6
373	MGSWFEFNYRLGAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRQIAAEIREFLQAYRHN	CD123	6.9
374	MGSWEEFFTRLDAINERLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRYEAAEIRHMLQAYRHN	CD123	3.9
375	MGSWYEFSNRLDAIGERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILRHQAAEIRWFLQAYRHN	CD123	3.9
376	MGSWYEFWGRLDAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGRGNPEVEMLREDAAEIRGQLQAYRHN	CD123	5.4
377	MGSWVEFWDRLWAIDYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRDEAAWIREELQAYRHN	CD123	3.6
378	MGSWVEFVDRLWAIDERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRTWAAWIREDLQAYRHN	CD123	3.2
379	MGSWFEFWDRLEAIWERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRREAAIIREDLQAYRHN	CD123	10.3
380	MGSWFEFEDRLEAIYQRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAWIRSDLQAYRHN	CD123	5.5
381	MGSWFEFHDRLWAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILREEAADIRLDLQAYRHN	CD123	3.5
382	MGSWYEFEDRLWAIDNRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRVHAADIRDDLQAYRHN	CD123	4.9
383	MGSWFEFQDRLWAIDNRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRDHAAMIRWELQAYRHN	CD123	3.2
384	MGSWDEFEERLFAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRYLAADIREELQAYRHN	CD123	5
385	MGSWEEFWERLDAIDTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRNDAADIREPLQAYRHN	CD123	6.8
386	MGSWMEFWERLEAIDMRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRDDAAVIRDDLQAYRHN	CD123	4.2
387	MGSWLEFMWRLDAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLREMAAAIRDDLQAYRHN	CD123	5.1
388	MGSWTEFYNRLDAIDQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLREYAADIRTDLQAYRHN	CD123	3.3

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
389	MGSWWEFIWRLEAIEQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRSRAADIRTDLQAYRHN	CD123	4
390	MGSWSEFYDRLWAIEERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRYYAAEIREELQAYRHN	CD123	17
391	MGSWSEFEDRLWAIDQRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRAYAADIRWELQAYRHN	CD123	4.2
392	MGSWTEFWERLNAIDERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRLYAAEIRSELQAYRHN	CD123	4
393	MGSWWEFEERLWAIDYRLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRSWAAEIRALLQAYRHN	CD123	4.1
394	MGSWWEFENRLWAIEERLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRNYAAEIRWELQAYRHN	CD123	5.6
395	MGSWVEFEERLWAIDERLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDWAADIRWWLQAYRHN	CD123	4.1
396	MGSWVEFEERLEAIEERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDDAANIRHWLQAYRHN	CD123	3.8
397	MGSWMEFEERLWAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRSEAAWIRMELQAYRHN	CD123	3.2
398	MGSWSEFEHRLEAIESRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRSEAAWIREQLQAYRHN	CD123	7.6
399	MGSWFEFWERLDAIEWRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRSTAADIRRYLQAYRHN	CD123	3.4
400	MGSWFEFWGRLEAIESRLKALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREHAAWIRAYLQAYRHN	CD123	4.9
401	MGSWQEFTMRLDAIYNRLETLGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRQSAANIRSELQAYRHN	CD123	13.7
402	MGSWSEFNMRLDAIYERLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRHSAARIRLELQAYRHN	CD123	13.7
403	MGSWSEFNMRLDAIYERLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRHSAALIRLELQAYRHN	CD123	11.4
404	MGSWIEFNMRLDAIYERLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRKVAANIRLELQAYRHN	CD123	11.4
405	MGSWYEFHHRLDAIYERLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRSSAANIRKELQAYRHN	CD123	11.9
406	MGSWYEFAKRLDAIYERLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRSSAANIREELQAYRHN	CD123	15.3
407	MGSWTEFYVRLDAIYERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRMVAANIRTELQAYRHN	CD123	16
408	MGSWVEFYTRLDAIYGRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRQVAANIRMELQAYRHN	CD123	14.4
409	MGSWVEFHMRLDAIYERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRTAAANIRVELQAYRHN	CD123	9.1
410	MGSWYEFAIRLDAIYERLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRVWAANIRTELQAYRHN	CD123	25.5
411	MGSWNEFVIRLDAIYERLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRMAAANIRMELQAYRHN	CD123	16.6
412	MGSWSEFYVRVDAIYARLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRVWAANIRHELQAYRHN	CD123	14.7

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
413	MGSWSEFHVRLDAIYARLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVERLREWAANIRRELQAYRHN	CD123	14.4
414	MGSWVEFHLRLDAIYGRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVWAANIRNELQAYRHN	CD123	17.5
415	MGSWVEFEMRLDAIVGRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRRWAANIRSELQAYRHN	CD123	25.3
416	MGSWVEFNIRLDAIYERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRHWAASIRRELQAYRHN	CD123	13.4
417	MGSWHEFGVRLDAIYDRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRQAAANIRSELQAYRHN	CD123	15.6
418	MGSWTEFNLRLDAIYDRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRASAAAIRVELQAYRHN	CD123	14.4
419	MGSWTEFNLRLDAIYGRLSALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRAAAANIRVELQAYRHN	CD123	19.3
420	MGSWVEFNWRLDAIYDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRVSAAKIRGELQAYRHN	CD123	9.3
421	MGSWNEFAWRLDAIYSRLAALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRVAAANIRYELQAYRHN	CD123	17.7
422	MGSWTEFAWRLDAIYDRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRHVAANIRRELQAYRHN	CD123	16.1
423	MGSWVEFSIRLDAIYTRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRKGAANIRKELQAYRHN	CD123	15.1
424	MGSWVEFYIRLDAIYVRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRSYAANIRQELQAYRHN	CD123	16.1
425	MGSWYEFSMRLDAIYDRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEQLRGYAANIRNELQAYRHN	CD123	13
426	MGSWVEFIYRLDAIYDRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRRYAANIRNELQAYRHN	CD123	17
427	MGSWIEFEVRLDAIYNRLAALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVERLRRYAANIRHELQAYRHN	CD123	20.8
428	MGSWFEFYDRLDAIYMRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRRYAANIRAELQAYRHN	CD123	13.6
429	MGSWFEFYMRLDAIYDRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVERLRTFAANIRKELQAYRHN	CD123	13.1
430	MGSWYEFDYRLDAIYDRLAALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVERLRKWAANIREELQAYRHN	CD123	24.9
431	MGSWSEFYLRLDAIYDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRKTAANIREELQAYRHN	CD123	15.7
432	MGSWFEFYERLDAINWRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRGEAAAIREDLQAYRHN	CD123	3
433	MGSWNEFEDRLDAIWWRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRVEAAFIRTMLQAYRHN	CD123	5.1
434	MGSWFYFKDDLADINYMLEALGGSEAELAMFEDDIAGFELT LLKYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.7
435	MGSWHFFKDDLAWIKNELEALGGSEAELAMFEDDIAMFETM LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.2
436	MGSWHWFKTDLADIKEELEALGGSEAELAMFEDDIAEFEEF LQMYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.5

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
437	MGSWWLFKDDLAEIKYWLEALGGSEAELAFFEDDIAEFERG LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
438	MGSWYEFKDDLAEIKEWLEALGGSEAELAFFELDIADFEWL LQLYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
439	MGSWQWFKDDLAYIKETLEALGGSEAELALFEDMIADFEFE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.3
440	MGSWILFKDDLAWIKETLEALGGSEAELAFFEDNIADFEEQ LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6
441	MGSWIVFKDDLADIKRWLEALGGSEAELAMFEDEIADFEWQ LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.9
442	MGSWGHFKQDLAWIKDTLEALGGSEAELAFFEDDIAMFEME LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.9
443	MGSWGYFKDDLAWIKGELEALGGSEAELAEFEWFIAVFEED LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.5
444	MGSWYWFKDDLAEIKGLLEALGGSEAELAEFEDEIAVFEQE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	10.4
445	MGSWMFFKEDLADIKWALEALGGSEAELAFFEEEIALFEQH LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.2
446	MGSWTFFKEDLAGIKWELEALGGSEAELAWFEDEIALFEEE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	7
447	MGSWVFFKDDLADIKDELEALGGSEAELAFFEIAIALFEWE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	8.8
448	MGSWTFFKNDLAEIKDWLEALGGSEAELADFEWDIAEFEYS LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.9
449	MGSWTYFKDDLADIKQWLEALGGSEAELAFFEIEIAEFEEE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.6
450	MGSWTVFKYDLADIKWWLEALGGSEAELADFEEEIAEFEEE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.9
451	MGSWYWFKQDLAHIKSMLEALGGSEAELAWFEEDIADFESE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
452	MGSWTFFKWDLADIKANLEALGGSEAELAWFEEDLAGFEAE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.8
453	MGSWSFFKEELANIQVYLEALGGSEAELAWFEEDIADFEED LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
454	MGSWEFFKYELADIKDELEALGGSEAELAWFEEDIATFEEW LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.4
455	MGSWQTFKDELAHIKWELEALGGSEAELAWFEWDIANFEEE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.5
456	MGSWYWFKEELAFIKWELEALGGSEAELALFEEDIAYFEEM LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	9.4
457	MGSWNSFKDELAEIKAELEALGGSEAELAFFEEDIAWFEEH LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
458	MGSWDLFKWELAEIKLGLEALGGSEAELAEFEYDIAWFEED LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.4
459	MGSWIFFKQDLAEIKLNLEALGGSEAELAWFEDDIAWFESH LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
460	MGSWHLFKWTLAEIKYELEALGGSEAELAWFEDDIATFEEE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
461	MGSWVTFKDELADIKDFLEALGGSEAELAFFEVDIAEFEAE LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	7.6
462	MGSWVYFKDELADIKDFLEALGGSEAELAEFEEDIATFEYD LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.6
463	MGSWETFKYELAEIKDYLEALGGSEAELAWFEDDIAEFEFE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.4
464	MGSWNTFKYELAEIKHFLEALGGSEAELAMFEDDIAMFEWE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5
465	MGSWYVFKDELAEIKQFLEALGGSEAELAWFEDDIAEFETQ LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	9.9
466	MGSWIFFKEQLAIIKWELEALGGSEAELAWFEDDIAAFEDD LQFYKGQGNPEVEALRKEAAAIRDELQAYRHN	CD123	15
467	MGSWEFFKEVLAEIKYDLEALGGSEAELAWFETDIAGFEID LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	8.2
468	MGSWVFFKEDLATIKNDLEALGGSEAELAWFEMMIADFEAD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.1
469	MGSWEEFKEDLAEIKVWLEALGGSEAELAWFEMGIADFEDG LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.3
470	MGSWHWFKEDLANIKDWLEALGGSEAELAWFEDNIADFEGD LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
471	MGSWFWFKEDLAFIKEDLEALGGSEAELAWFEDGIAFFEWD LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	13.7
472	MGSWQWFKEDLAEIKHDLEALGGSEAELAWFEDFIAQFEFD LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
473	MGSWHWFKEDLAIIKQDLEALGGSEAELATFEQWIAEFEWD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.5
474	MGSWNWFKEDLAIIKMDLEALGGSEAELAWFEHNIAGFEFE LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.1
475	MGSWSWFKEDLAEIKMELEALGGSEAELAYFEWYIAEFEFQ LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.8
476	MGSWSWFKQDLADIKIQLEALGGSEAELAWFEWDIAEFEFE LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4
477	MGSWSWFKEDLADIKFELEALGGSEAELAWFELDIADFEQA LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.8
478	MGSWSWFKEDLASIKAVLEALGGSEAELAFFESDIAEFEQE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.9
479	MGSWWEFKEDLAEIKWFLEALGGSEAELAWFEHDIAKFEFE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.1
480	MGSWEWFKSDLASIKWELEALGGSEAELAWFEHDIAEFEED LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.7
481	MGSWNEFKDDLAMIKMTLEALGGSEAELAWFEHDIAEFEDD LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.5
482	MGSWTFFKDDLAEIKWMLEALGGSEAELAWFESDIAYFEDE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
483	MGSWSDFKDDLAEIKMILEALGGSEAELAYFENDIAWFEDD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.7
484	MGSWSMFKDDLAEIKASLEALGGSEAELAWFEDDIAWFEDD LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.2

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
485	MGSWQYFKDDLAEIKMVLEALGGSEAELAWFEADIAMFEDD LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.6
486	MGSWSFFKDDLAEIKYFLEALGGSEAELAMFEQTIAEFEYD LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	10.1
487	MGSWMEFKEELAEIKYILEALGGSEAELAWFEQSIADFEYD LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5
488	MGSWAWFKEDLAEIKVFLEALGGSEAELAEFEVSIADFEYE LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.5
489	MGSWYEFKFDLAEIKEQLEALGGSEAELALFEDDIAFFEYD LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.6
490	MGSWYDFKYDLAEIKMDLEALGGSEAELAQFEFDIAFFEEE LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.2
491	MGSWYIFKEDLAEIKEELEALGGSEAELAYFEEEIALFEME LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	11.1
492	MGSWVLFKEELAYIKFELEALGGSEAELALFENVIAIFESN LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.5
493	MGSWQDFKEDLAWIKYELEALGGSEAELAFFEYDIAIFENN LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.2
494	MGSWDHFKNDLAWIKKHLEALGGSEAELAEFEAVIAYFELY LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
495	MGSWYDFKEDLADIKWMLEALGGSEAELAEFENVIAYFEND LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	8
496	MGSWYMFKEELADIKWYLEALGGSEAELAWFEDDIAGFEWD LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	7
497	MGSWYYFKDELADIKWDLEALGGSEAELAWFEMLIAQFELD LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4
498	MGSWMYFKDTLADIKWYLEALGGSEAELAFFEDWIAEFEDD LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.1
499	MGSWYQFKHDLADIKYGLEALGGSEAELAWFEDDIADFELD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.7
500	MGSWYVFKDDLADIKYMLEALGGSEAELAWFEWEIANFEFD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
501	MGSWNFFKYDLADIMAYLEALGGSEAELAFFEDEIANFEHD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.4
502	MGSWHWFKIVLADIKDGLEALGGSEAELAYFETTIADFEMD LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.3
503	MGSWHWFKIVLADIKDGLEALGGSEAELAYFETTIADFEMD LHHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.5
504	MGSWFMFKEELADIKDWLEALGGSEAELASFESYIAWFEQD LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.7
505	MGSWFMFKQELAWIKEDLEALGGSEAELADFEWDIAEFEWD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	7.2
506	MGSWQIFKGELAYIKQYLEALGGSEAELAFFEFDIAEFEED LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.7
507	MGSWDFFKEELAEIKHYLEALGGSEAELAFFEFWIADFEQD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.7
508	MGSWFNFKEELAVIKFQLEALGGSEAELAFFEWVIADFEDD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.1

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
509	MGSWYQFKTELAWIKDDLEALGGSEAELAWFEWVIADFEDD LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.6
510	MGSWFEFKDYLADIKWDLEALGGSEAELAIFEHDIAYFEHN LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
511	MGSWVRFKDFLADIKMDLEALGGSEAELADFEYHIAEFEHN LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.8
512	MGSWWLFKEQLALIKYNLEALGGSEAELADFESWIAEFEHQ LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.1
513	MGSWHVFKTELADIKFYLEALGGSEAELAMFELWIAEFEHE LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.4
514	MGSWIWFKDWLADIKDLLEALGGSEAELAEFEYDIALFEDQ LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	7.3
515	MGSWGWFKHELAFIKADLEALGGSEAELAWFEEEIAEFEYE LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
516	MGSWTWFKDNLAWIKEDLEALGGSEAELAWFELEIASFETA LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.9
517	MGSWTYFKNDLAGIKEDLEALGGSEAELAQFEFEIAEFEWL LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.6
518	MGSWTWFKWDLADIKGDLEALGGSEAELAFFEEEIAEFEWR LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.9
519	MGSWLYFKEYLADIKSDLEALGGSEAELAWFEYEIADFEEQ LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.7
520	MGSWHWFKEELAEIKEDLVALGGSEAELAWFEYDIAMFELS LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.1
521	MGSWNDFKEELAWIKFDLEALGGSEAELAWFEEDIAMFEQQ LQAYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.8
522	MGSWWDFKDWLAEIKHDLEALGGSEAELALFESEIADFEFG LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.2
523	MGSWDEFKEDLAHIKTDLEALGGSEAELALFEDEIADFEMY LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	6.3
524	MGSWDFFKYDLANINEWLEALGGSEAELADFEYGIADFELW LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.5
525	MGSWYQFKDDLAHIKHLLEALGGSEAELAVFEYIIADFESF LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4
526	MGSWAEFKHDLADIKRELEALGGSEAELAWFELSIAFFEDE LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.3
527	MGSWVVFKQDLADINHQLEALGGSEAELAWFEWEIADFEWE LQHYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.6
528	MGSWFQFKEFLAMITHNLEALGGSEAELAEFEHDIALFESE LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	3.1
529	MGSWHWFKEDLAMITDVLEALGGSEAELAAFESEIAVFEAD LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	5.2
530	MGSWSWFQWDLAGIKDHLEALGGSEAELAEFESEIAYFEDE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	12.9
531	MGSWTEFKGELAEIKWILEALGGSEAELAFFEDEIAAFEWD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	8.2
532	MGSWFEFKWTLALIKQELEALGGSEAELADFEQEIAEFEWW LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD123	4.9

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
533	MGSWAEFKQRLAAIKTRLEALGGSEAELAAFMDEIMAFEWE LWAYKGKGNPEVEALMNEAFAIDVELYAYRHN	CD123	3.4
534	MGSWAEFKQRLAAIKTRLEALGGSEAELAAFEWEIVAFFSE LFAYKGKGNPEVEALRDEAIAIETELVAYRHN	CD123	3.6
535	MGSWWEFDHRLTAIDTRLQALGGSEAELAEFESSIAEFEWW LQDYKGKGNPEVEALFAEAEAIYVELDAYRHN	CD123	4.3
536	MGSWWEFQFRLYAIDQRLLALGGSEAELAEFEQDIADFEWM LQDYKGKGNPEVEALMLEADAIEAELKAYRHN	CD123	3.1
537	MGSWYEFDHRLDAIYQRLWALGGSEAELAEFEYGIAEFEEY LQDYKGKGNPEVEALISEAWAIEWELSAYRHN	CD123	4.6
538	MGSWYEFDMRLDAIWERLTALGGSEAELADFEQYIAEFERQ LQDYKGKGNPEVEALFDEAWAIEDELYAYRHN	CD123	13.7
539	MGSWSEFDSRLDAIAYRLFALGGSEAELAQFEWIIADFEED LQMYKGKGNPEVEALFSEAYAIEIELNAYRHN	CD123	4.3
540	MGSWYEFDDRLDAIAYRLNALGGSEAELAWFEWEIAEFELD LQWYKGKGNPEVEALVWEADAIEWELEAYRHN	CD123	4.6
541	MGSWFEFDERLDAIGSRLTALGGSEAELASFEFYIADFEEW LQQYKGKGNPEVEALEWEAFAIDEELGAYRHN	CD123	3.8
542	MGSWEEFDQRLDAIDVRLYALGGSEAELAEFEFDIAAFEEW LQLYKGKGNPEVEALNMEAFAITDELCAYRHN	CD123	3.6
543	MGSWEEFDVRLDAIFNRLWALGGSEAELAEFEFDIAWFEMD LQEYKGKGNPEVEALFDEAEAITNELVAYRHN	CD123	4.7
544	MGSWEEFDKRLDAITRRLMALGGSEAELAEFESTIAWFEWD LQEYKGKGNPEVEALDWEAYAIDYELGAYRHN	CD123	4.5
545	MGSWYEFDHRLEAIYDRLWALGGSEAELAFFEFDIADFEWD LQSYKGKGNPEVEALFDEAAAIGHELLAYRHN	CD123	4.5
546	MGSWNEFDDRLLAIWGRLDALGGSEAELAFFEEQIAGFEDE LQWYKGKGNPEVEALDQEAEAIEKELWAYRHN	CD123	4.1
547	MGSWVEFDDRLDAIWERLDALGGSEAELAWFEEQIAVFEHQ LQDYKGKGNPEVEALNQEAEAIDLELKAYRHN	CD123	5
548	MGSWTEFDDRLFAIYWRLDALGGSEAELAWFEEVIAEFEND LQVYKGKGNPEVEALDDEAHAISIELEAYRHN	CD123	6.4
549	MGSWSEFDQRLEAIWNRLDALGGSEAELADFEREIAYFENQ LQWYKGKGNPEVEALNNEAFAIVDELGAYRHN	CD123	3.4
550	MGSWYEFDERLWAIWERLDALGGSEAELAHFEWVIADFEND LQWYKGKGNPEVEALEFEAEAIVTELHAYRHN	CD123	3.6
551	MGSWMEFDYRLEAIWMRLIALGGSEAELADFESSIADFEHH LQSYKGKGNPEVEALEWEAFAIGVELDAYRHN	CD123	3.1
552	MGSWYEFESRLEAIWWRLEALGGSEAELAQFEQYIADFEQH LQWYKGKGNPEVEALDWEADAIWLELQAYRHN	CD123	4.4
553	MGSWEEFYMRLVAIHMRLRALGGSEAELAVFENYIAEFEEY LQYYKGKGNPEVEALTIEADAIGTELGAYRHN	CD123	4.4
554	MGSWDEFYYRLVAITHRLHALGGSEAELAWFEDDIAGFEWD LQTYKGKGNPEVEALYKEAGAIGMELTAYRHN	CD123	5.4
555	MGSWEEFDTRLLAIFGRLGALGGSEAELALFEMLIAKFEDD LQNYKGKGNPEVEALSEEAFAIDHELGAYRHN	CD123	6.7
556	MGSWREFDQRLWAIDWRLEALGGSEAELAMFEWMIATFEDD LQWYKGKGNPEVEALYREAFAIDWELDAYRHN	CD123	3.4

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
557	MGSWEEFHERLDAIDERLEALGGSEAELAFFEDDIASFEDW LQWYKGKGNPEVEALSREADAINFELEAYRHN	CD123	4.3
558	MGSWNEFYERLEAIDRRLFALGGSEAELALFEWMIADFEDD LQMYKGKGNPEVEALINEAGAIGFELEAYRHN	CD123	5.2
559	MGSWTEFTQRLEAIVDRLFALGGSEAELAEFENSIADFEWD LQWYKGKGNPEVEALNREAVAIDNELWAYRHN	CD123	3.9
560	MGSWVEFIMRLDAIYERLDALGGSEAELAEFEWHIADFEDH LQWYKGKGNPEVEALFEEADAIWEELWAYRHN	CD123	6.4
561	MGSWNEFLLRLDAIEHRLFALGGSEAELAEFEWEIADFEDD LQWYKGKGNPEVEALVEEAEAIDVELVAYRHN	CD123	3.2
562	MGSWYEFNMRLGAIDDRLQALGGSEAELAWFEDMIAIFEDD LQIYKGKGNPEVEALEQEAAAIHQELWAYRHN	CD123	3.8
563	MGSWEEFHWRLGAIDARLEALGGSEAELAWFEDGIADFEAI LQDYKGKGNPEVEALDSEAVAIHHELWAYRHN	CD123	3.3
564	MGSWYEFYERLWAIDDRLWALGGSEAELAEFEDSIATFEPS LQMYKGKGNPEVEALVAEAWAIFDELAAYRHN	CD123	3.6
565	MGSWFEFDQRLDAITFRLWALGGSEAELAEFEDVIALFEYH LQDYKGKGNPEVEALEVEAWAIFHELGAYRHN	CD123	3.2
566	MGSWSEFWFRLDAIEDRLWALGGSEAELAEFEDNIALFEYS LQHYKGKGNPEVEALVKEANAIDDELGAYRHN	CD123	4.5
567	MGSWYEFWDRLTAIEHRLWALGGSEAELAYFEDSIAHFEGS LQVYKGKGNPEVEALYKEAEAIEWELEAYRHN	CD123	4.4
568	MGSWYEFDDRLWAIFDRLFALGGSEAELAFFEDSIAEFEEE LQHYKGKGNPEVEALYLEAWAIENELGAYRHN	CD123	4.7
569	MGSWNEFVERLSAIDHRLWALGGSEAELADFEQQIAEFEIH LQEYKGKGNPEVEALDFEADAIFDELLAYRHN	CD123	3.2
570	MGSWSEFVDRLDAIFDRLWALGGSEAELAWFEDTIAHFEWN LQEYKGKGNPEVEALNGEADAITDELHAYRHN	CD123	5.3
571	MGSWAEFDSRLDAIAQRLFALGGSEAELAHFEDFIAQFEYS LQEYKGKGNPEVEALSNEADAIFNELKAYRHN	CD123	3.6
572	MGSWAEFDSRLIAIFDRLWALGGSEAELAWFEDDIAQFEQH LQAYKGKGNPEVEALRQEADAITFELKAYRHN	CD123	3.6
573	MGSWTEFEERLEAIWDRLYALGGSEAELAAFEWDIAYFEDG LQEYKGKGNPEVEALFMEAEAIIRELKAYRHN	CD123	5.9
574	MGSWYEFEDRLAAIWDRLNALGGSEAELAIFEWDIAWFEEG LQEYKGKGNPEVEALKHEASAIQTELFAYRHN	CD123	6.4
575	MGSWLEFESRLWAIWDRLDALGGSEAELAHFEQDIADFEMS LQEYKGKGNPEVEALIREAEAIETELYAYRHN	CD123	3.4
576	MGSWMEFEDRLIAIWARLDALGGSEAELAWFEADIADFEES LQEYKGKGNPEVEALIFEAIAINKELMAYRHN	CD123	3.7
577	MGSWFEFTIRLEAIQDRLDALGGSEAELAWFEWDIAEFEEG LQFYKGKGNPEVEALHTEADAIMNELVAYRHN	CD123	3.5
578	MGSWYEFVSRLDAIEYRLWALGGSEAELAWFEWDIADFEQG LQFYKGKGNPEVEALAQEANAIGSELTAYRHN	CD123	3.2
579	MGSWEEFDYRLYAIQDRLYALGGSEAELAFFEWEIADFEHM LQMYKGKGNPEVEALFQEADAIDAELHAYRHN	CD123	4.4
580	MGSWIEFFHRLDAIQDRLDALGGSEAELAYFEWAIADFEHM LQLYKGKGNPEVEALQFEAFAIEGELYAYRHN	CD123	3.5

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
581	MGSWYEFSSRLNAIDDRLWALGGSEAELAYFETDIADFESL LQWYKGKGNPEVEALLNEADAIDYELYAYRHN	CD123	3.8
582	MGSWFEFEYRLDAIIDRLFALGGSEAELAEFESMIANFEYS LQEYKGKGNPEVEALYFEADAIVDELTAYRHN	CD123	4
583	MGSWLEFEYRLDAIYDRLFALGGSEAELAAFEQDIADFEKY LQYYKGKGNPEVEALWEEADAIMWELFAYRHN	CD123	3.1
584	MGSWHEFEERLMAIEDRLWALGGSEAELAEFEQWIALFEYD LQEYKGKGNPEVEALGMEAFAINNELSAYRHN	CD123	5.8
585	MGSWYEFEERLDAIEDRLIALGGSEAELAIFEDIIAFFEQD LQYYKGKGNPEVEALEMEAEAISIELDAYRHN	CD123	4.1
586	MGSWHEFEKRLYAIEDRLIALGGSEAELAWFEDSIAWFEWD LQMYKGKGNPEVEALNEEADAIYQELDAYRHN	CD123	3.6
587	MGSWIEFEDRLDAITDRLWALGGSEAELAEFEHQIAFFEED LQWYKGKGNPEVEALHMEAEAIMEELGAYRHN	CD123	9.5
588	MGSWMEFEDRLMAIVDRLWALGGSEAELADFEWNIAMFEEE LQWYKGKGNPEVEALGDEAEAIEWELYAYRHN	CD123	6.8
589	MGSWEEFEDRLFAIDSRLWALGGSEAELAEFENIIASFEEV LQEYKGKGNPEVEALSVEAFAIDRELGAYRHN	CD123	3.7
590	MGSWEEFLFRLEAIQDRLWALGGSEAELAWFEYEIASFEDV LQSYKGKGNPEVEALSTEAKAIDYELFAYRHN	CD123	8.2
591	MGSWVEFDNRLFAIDERLWALGGSEAELAWFEEEIASFEDN LQKYKGKGNPEVEALQLEAFAIMEELDAYRHN	CD123	3.3
592	MGSWFEFDDRLEAIFDRLWALGGSEAELAMFEFAIAEFEDA LQEYKGKGNPEVEALYEEAVAIDEELYAYRHN	CD123	4.1
593	MGSWFEFDARLMAINDRLWALGGSEAELAAFEYHIALFEDQ LQMYKGKGNPEVEALTLEAVAINEELWAYRHN	CD123	4
594	MGSWVEFDSRLAAIDYRLEALGGSEAELAWFEYTIANFEHT LQMYKGKGNPEVEALVYEAHAIATELQAYRHN	CD123	3.4
595	MGSWTEFDERLDAIDWRLEALGGSEAELAWFEGDIALFEQY LQVYKGKGNPEVEALMEEADAIKAELDAYRHN	CD123	4.5
596	MGSWIEFDERLDAIDFRLWALGGSEAELAWFEGWIAEFESD LQLYKGKGNPEVEALNEEANAIFHELSAYRHN	CD123	7
597	MGSWWEFDSRLDAIDFRLWALGGSEAELAWFEVEIADFEDW LQLYKGKGNPEVEALWHEADAIVTELYAYRHN	CD123	3.2
598	MGSWYEFDERLDAIFDRLWALGGSEAELAYFEQVIATFEKT LQRYKGKGNPEVEALDTEAKAISWELDAYRHN	CD123	3
599	MGSWYEFQERLDAIDSRLWALGGSEAELAWFEYTIAEFEKE LQMYKGKGNPEVEALGTEAVAISEELMAYRHN	CD123	5.5
600	MGSWEEFEDRLWAIDGRLYALGGSEAELAWFEQWIATFEED LQDYKGKGNPEVEALEYEASAIFEELEAYRHN	CD123	9.4
601	MGSWFEFGDRLEAIDERLYALGGSEAELAQFEWWIAEFEHH LQDYKGKGNPEVEALEYEADAIWGELHAYRHN	CD123	4.5
602	MGSWFEFNDRLDAISERLSALGGSEAELAYFEWQIAVFEKT LQNYKGKGNPEVEALTLEANAIFEELEAYRHN	CD123	3.9

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
603	MGSWVEFMDRLEAIEERLSALGGSEAELAFFEWEIAEFEEH LQVYKGKGNPEVEALEWEALAITEELAAYRHN	CD123	4
604	MGSWIEFMDRLWAIDQRLWALGGSEAELAWFEEEIAWFEEE LQVYKGKGNPEVEALEWEATAISEELWAYRHN	CD123	6.5
605	MGSWEEFNWRLRAIDERLFALGGSEAELAWFEYDIAEFEEQ LQVYKGKGNPEVEALRVEAAAIAEELYAYRHN	CD123	5.4
606	MGSWWEFEIRLDAIDERLWALGGSEAELAWFEQSIAFFEND LQVYKGKGNPEVEALRWEANAIIEELFAYRHN	CD123	3.2
607	MGSWYEFEWRLDAIDRRLWALGGSEAELADFEEEIADFEWM LQNYKGKGNPEVEALVDEASAIQTELWAYRHN	CD123	10
608	MGSWYEFVYRLRAIDERLDALGGSEAELAMFEFEIAFFEDQ LQRYKGKGNPEVEALVDEAQAIDFELFAYRHN	CD123	4.5
609	MGSWWEFEDRLYAIDDRLWALGGSEAELAQFEREIAQFEIW LQEYKGKGNPEVEALDDEATAINSELFAYRHN	CD123	5.5
610	MGSWDEFEFRLEAIDSRLWALGGSEAELAVFEYEIAQFEFM LQEYKGKGNPEVEALGMEAWAIENELFAYRHN	CD123	3.6
611	MGSWEEFEWRLDAIDERLWALGGSEAELATFEYEIAIFENE LQQYKGKGNPEVEALDSEAYAIERELGAYRHN	CD123	4.3
612	MGSWYEFFDRLDAIDERLWALGGSEAELAWFEAEIAEFEME LQGYKGKGNPEVEALDVEAHAIEMELFAYRHN	CD123	3.7
613	MGSWYEFMGRLEAIDERLQALGGSEAELAWFEHEIAEFEWS LQWYKGKGNPEVEALRFEAGAIPWELWAYRHN	CD123	3.5
614	MGSWVEFSNRLDAIWERLQALGGSEAELAYFEWEIAEFEWE LQSYKGKGNPEVEALNAEADAIEWELEAYRHN	CD123	5.1
615	MGSWEEFHMRLIAIDERLWALGGSEAELAGFEESIAYFESQ LQDYKGKGNPEVEALDYEAHAIWRELYAYRHN	CD123	3.9
616	MGSWWEFKYRLDAICFRLAALGGSEAELASFEDEIAYFEED LQGYKGKGNPEVEALDYEALAIWDELAAYRHN	CD123	3.1
617	MGSWDEFAMRLEAIQARLFALGGSEAELAIFEDEIAFFETM LQDYKGKGNPEVEALEYEAAAIEAELGAYRHN	CD123	3.7
618	MGSWWEFNARLDAIEDRLMALGGSEAELAYFEDIIASFENI LQQYKGKGNPEVEALWYEAYAIEKELNAYRHN	CD123	3.4
619	MGSWIEFWNRLEAIEERLYALGGSEAELAYFEDEIAEFEIY LQQYKGKGNPEVEALKHEAEAINKELMAYRHN	CD123	5.2
620	MGSWNEFVIRLFAIDDRLYALGGSEAELAWFEDEIATFEYE LQRYKGKGNPEVEALEYEAEAIVSELFAYRHN	CD123	3.5
621	MGSWYEFLARLYAIDERLWALGGSEAELATFEHWIADFEEQ LQSYKGKGNPEVEALTDEAVAIGEELSAYRHN	CD123	4.5
622	MGSWLEFETRLHAIDERLWALGGSEAELAEFEEHIAWFEED LQFYKGKGNPEVEALDFEADAIGWELWAYRHN	CD123	4.6

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
623	MGSWFEFETRLEAIDLRLWALGGSEAELATFEDVIAFFEDW LQFYKGKGNPEVEALKMEAWAIGEELHAYRHN	CD123	6.6
624	MGSWHEFWQRLEAIEGRLWALGGSEAELADFESLIADFEEQ LQEYKGKGNPEVEALMAEAEAIDNELRAYRHN	CD123	7
625	MGSWYEFEQRLEAIEWRLGALGGSEAELATFEEDIADFEEW LQEYKGKGNPEVEALQYEAYAIAEELHAYRHN	CD123	4.4
626	MGSWYEFENRLFAIEERLWALGGSEAELAWFEYEIANFEWG LQSYKGKGNPEVEALDNEAEAIDIELAAYRHN	CD123	3.3
627	MGSWYEFEQRLGAIEERLWALGGSEAELAAFEDIIAYFEYQ LQSYKGKGNPEVEALDEEAWAIDDELWAYRHN	CD123	10.6
628	MGSWWEFEQRLDAIETRLWALGGSEAELAYFEHIIADFEDE LQIYKGKGNPEVEALGWEAFAIDGELTAYRHN	CD123	4.7
629	MGSWFEFPYRLEAIEERLYALGGSEAELAQFEQFIAWFEMD LQDYKGKGNPEVEALWFEANAIVEELDAYRHN	CD123	3.1
630	MGSWVEFYDRLEAIEIRLWALGGSEAELADFESFIAHFEDD LQAYKGKGNPEVEALMDEANAIVFELDAYRHN	CD123	4
631	MGSWVEFWDRLDAIEERLWALGGSEAELAEFEFMIAMFEQH LQEYKGKGNPEVEALIPEAGAIDKELTAYRHN	CD123	10
632	MGSWDEFDARLWAIEERLWALGGSEAELAEFEFMIAAFEDV LQEYKGKGNPEVEALMGEANAIVMELDAYRHN	CD123	4.3
633	MGSWYEFWRRLDAIEERLWALGGSEAELAMFETDIAGFEWM LQLYKGKGNPEVEALEHEAWAINSELDAYRHN	CD123	3.6
634	MGSWHEFIWRLDAIEERLWALGGSEAELAWFETEIATFEAQ LQDYKGKGNPEVEALEWEAIAIAWELDAYRHN	CD123	3.3
635	MGSWYEFYWRLEAIEERLWALGGSEAELAEFEKAIATFEDQ LQTYKGKGNPEVEALETEALAIHAELEAYRHN	CD123	3.7
636	MGSWFEFQWRLEAIEDRLWALGGSEAELAEFETIIAGFEEQ LQVYKGKGNPEVEALEEEAMAIQTELHAYRHN	CD123	3.4
637	MGSWWEFEDRLWAIEQRLDALGGSEAELAVFENSIAKFEDM LQVYKGKGNPEVEALHEEADAIIWELYAYRHN	CD123	4.4
638	MGSWWEFEDRLWAIDRRLMALGGSEAELAVFEQMIAHFEQI LQVYKGKGNPEVEALHFEAHAIGMELAAYRHN	CD123	4.6
639	MGSWWEFLDRLEAIEYRLQALGGSEAELAVFEWEIAMFEDH LQGYKGKGNPEVEALHSEAHAIISELSAYRHN	CD123	3.1
640	MGSWAEFEDRLAAIERRLEALGGSEAELADFESSIAWFEPD LQYYKGKGNPEVEALMYEAEAIFSELYAYRHN	CD123	4.2
641	MGSWWEFYDRLTAIEARLWALGGSEAELADFEEGIADFEYD LQDYKGKGNPEVEALFWEAWAIQSELTAYRHN	CD123	3.2
642	MGSWYEFEDRLAAIEARLWALGGSEAELADFEEEIAYFEHG LQWYKGKGNPEVEALESEAMAIIDELHAYRHN	CD123	3.8

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
643	MGSWWEFSWRLEAIETRLDALGGSEAELAFFEMDIAWFEQD LQLYKGKGNPEVEALEEEAYAIYEELEAYRHN	CD123	3.3
644	MGSWEEFFFRLEAIDDRLYALGGSEAELALFEEVIAYFEQD LQWYKGKGNPEVEALYVEAYAIQEELYAYRHN	CD123	3.2
645	MGSWFEFEERLNAISWRLHALGGSEAELAYFEEDIAWFEDD LQFYKGKGNPEVEALENEAYAIWEELDAYRHN	CD123	13
646	MGSWFEFEERLEAIIYRLWALGGSEAELAMFEESIAWFESD LQQYKGKGNPEVEALEYEAMAISKELKAYRHN	CD123	3.7
647	MGSWAEFDDRLEAIEYRLHALGGSEAELAWFEEGIAGFEHA LQSYKGKGNPEVEALETEAGAINEELWAYRHN	CD123	5.8
648	MGSWDEFEERLQAIEYRLWALGGSEAELAWFEEVIAQFEYD LQKYKGKGNPEVEALSTEAQAIQDELWAYRHN	CD123	3.8
649	MGSWWEFTDRLDAIFDRLWALGGSEAELAAFEESIAIFEQD LQYYKGKGNPEVEALEYEANAIQYELEAYRHN	CD123	7.5
650	MGSWWEFTDRLEAIEDRLWALGGSEAELAHFEDSIAQFEQE LQWYKGKGNPEVEALADEADAIESELHAYRHN	CD123	16.6
651	MGSWVEFFWRLDAIEDRLWALGGSEAELANFEFEIADFEAW LQKYKGKGNPEVEALHSEADAIQLELRAYRHN	CD123	4
652	MGSWVEFYNRLDAIENRLWALGGSEAELAFFEELIAQFEFA LQDYKGKGNPEVEALEDEADAIWEELMAYRHN	CD123	6.9
653	MGSWEEFYYRLHAIDNRLWALGGSEAELAYFEWHIADFELE LQDYKGKGNPEVEALSEEATAIFEELWAYRHN	CD123	3
654	MGSWREFHDRLFAIDGRLWALGGSEAELANFEWDIADFEFE LQDYKGKGNPEVEALSWEADAIMQELGAYRHN	CD123	5.6
655	MGSWEEFDERLWAISDRLWALGGSEAELAYFEGEIAYFEQN LQTYKGKGNPEVEALQTEALAIDTELWAYRHN	CD123	6.5
656	MGSWEEFEQRLWAIDDRLWALGGSEAELAFFEYEIAEFEMD LQWYKGKGNPEVEALFYEAHAINEELWAYRHN	CD123	5.7
657	MGSWDEFHQRLAAIGDRLWALGGSEAELAYFEWEIATFEWD LQVYKGKGNPEVEALYFEATAIDEELMAYRHN	CD123	3.7
658	MGSWVEFEYRLDAISDRLWALGGSEAELAFFENEIASFESD LQFYKGKGNPEVEALMFEAEAIDDELHAYRHN	CD123	6.5
659	MGSWDEFDTRLDAIFSRLYALGGSEAELAMFEGEIAEFEGS LQHYKGKGNPEVEALDFEAHAIDEELWAYRHN	CD123	4
660	MGSWHEFDDRLDAIMSRLDALGGSEAELATFEAEIATFEFV LQLYKGKGNPEVEALLAEAYAIDWELEAYRHN	CD123	7.7
661	MGSWYEFFDRLDAIYDRLYALGGSEAELASFEAQIAEFEVE LQSYKGKGNPEVEALEWEAWAIDEELYAYRHN	CD123	4.7
662	MGSWFEFLYRLDAIEDRLWALGGSEAELAEFEQEIAKFESE LQSYKGKGNPEVEALEWEAHAIDMELEAYRHN	CD123	6.6
663	MGSWLEFEDRLVAIDHRLFALGGSEAELAEFEEEIALFESY LQDYKGKGNPEVEALNWEADAIHAELYAYRHN	CD123	3.9
664	MGSWYEFESRLDAIVDRLWALGGSEAELAEFEYEIAKFEWE LQDYKGKGNPEVEALNWEAGAIEFELYAYRHN	CD123	5.1
665	MGSWYEFEDRLDAILYRLLALGGSEAELAWFERDIAFFESE LQWYKGKGNPEVEALEWEAMAIDDELFAYRHN	CD123	4.3

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
666	MGSWGEFMDRLEAIDYRLWALGGSEAELAWFESDIAEFEQE LQMYKGKGNPEVEALWDEAMAIRDELFAYRHN	CD123	4.6
667	MGSWEEFDDRLDAIEHRLWALGGSEAELADFEGSIAAFESW LQVYKGKGNPEVEALEAEAEAIADELWAYRHN	CD123	4
668	MGSWYEFADRLDAIMDRLVALGGSEAELAYFEWEIAAFEEF LQMYKGKGNPEVEALDEEAEAIKDELMAYRHN	CD123	3.3
669	MGSWNEFWERLDAIEWRLFALGGSEAELAFFELDIAWFEEE LQWYKGKGNPEVEALIFEAHAITLELDAYRHN	CD123	3
670	MGSWYEFDARLDAIEERLYALGGSEAELAAFEFEIAGFEEA LQWYKGKGNPEVEALLKEAEAITDELYAYRHN	CD123	8.9
671	MGSWDEFSERLDAIWGRLEALGGSEAELATFEFHIAEFEHE LQYYKGKGNPEVEALQGEAAAIINELYAYRHN	CD123	3.2
672	MGSWDEFWDRLDAIEDRLFALGGSEAELADFERVIAWFEND LQEYKGKGNPEVEALDNEADAIRIELHAYRHN	CD123	3.9
673	MGSWDEFDDRLEAIVDRLFALGGSEAELAMFEFEIAQFEHQ LQYYKGKGNPEVEALRDEADAIWIELDAYRHN	CD123	5.6
674	MGSWEEFTIRLGAIYWRLFALGGSEAELANFEWFIAEFEYE LQPYKGKGNPEVEALVIEANAIDGELQAYRHN	CD123	3.3
675	MGSWFEFEWRLDAIENRLNALGGSEAELAWFEYHIAAFEDS LQHYKGKGNPEVEALEWEAHAIQSELQAYRHN	CD123	3.3
676	MGSWYEFDDRLEAIWDRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRETAADIRAELQAYRHN	CD123	3.3
677	MGSWGEFWARLEAIWIRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAADIRRSLQAYRHN	CD123	15
678	MGSWIEFEVRLDAIWDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRDEAADIRQSLQAYRHN	CD123	4.2
679	MGSWTEFDRRLDAIWDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAADIRDYLQAYRHN	CD123	9.2
680	MGSWTEFDMRLDAIWDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREEAATIRGVLQAYRHN	CD123	3.1
681	MGSWEEFHDRLMAIETRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRYEAADIRDYLQAYRHN	CD123	4.3
682	MGSWVEFRDRLDAIETRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRYEAAEIRMVLQAYRHN	CD123	4.2
683	MGSWMEFIDRLDAIEHRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAEIRMYLQAYRHN	CD123	4.3
684	MGSWTEFVWRLDAIEWRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAEIRDWLQAYRHN	CD123	4.2
685	MGSWVEFYDRLYAIEVRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRQEAAEIRDWLQAYRHN	CD123	5.8
686	MGSWYEFYDRLDAIEWRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAQIRDFLQAYRHN	CD123	6.2
687	MGSWVEFYDRLDAIEHRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAFIRDMLQAYRHN	CD123	3.4
688	MGSWFEFVDRLTAIQVRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREEAALIRYSLQAYRHN	CD123	5.1
689	MGSWFEFLDRLDAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAAVIRDSLQAYRHN	CD123	12.2

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
690	MGSWYEFMVRLDAIEERLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAASIRYHLQAYRHN	CD123	4.1
691	MGSWYEFEDRLDAIQWRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRESAANIRQHLQAYRHN	CD123	6.3
692	MGSWSEFEYRLFAIENRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAMIRQLLQAYRHN	CD123	3.2
693	MGSWVEFEYRLDAITERLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILREEAAFIRQWLQAYRHN	CD123	3.9
694	MGSWWEFLDRLDAIEMRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREEAALIRNMLQAYRHN	CD123	9
695	MGSWWEFEDRLDAIEYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREEAAFIRIFLQAYRHN	CD123	4.9
696	MGSWWEFESRLDAIFMRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLREDAAFIREFLQAYRHN	CD123	3.7
697	MGSWVEFWHRLDAIKARLNALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAADFRLILQAYRHN	CD123	3.5
698	MGSWYEFYNRLSAIYARLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAADIRYMLQAYRHN	CD123	10.6
699	MGSWYEFYDRLSAIYARLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAADIRYMLQAYRHN	CD123	5.3
700	MGSWNEFYDRLSAIYFRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRWYAADIRMILQAYRHN	CD123	10.6
701	MGSWNEFYDRLSAIYFRLQALGGFEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRWYAADIRMILQAYRHN	CD123	9
702	MGSWEEFYDRLGAIFARLHALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAADIRMILQAYRHN	CD123	3.9
703	MGSWVEFYDRLHAIYFRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRWYAADIRLVLQAYRHN	CD123	4.8
704	MGSWKEFDNRLYAIEDRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRWYAADIRMILQAYRHN	CD123	3.9
705	MGSWVEFWDRLWAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRHYAADIRVWLQAYRHN	CD123	4.5
706	MGSWYEFADRLWAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRYYAADIRWVLQAYRHN	CD123	4
707	MGSWYEFEERLYAIEDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRQEAADIRLMLQAYRHN	CD123	11.5
708	MGSWTEFEWRLYAIEDRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRDEAADIRQYLQAYRHN	CD123	4.2
709	MGSWIEFESRLWAIEDRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRLEAADIREDLQAYRHN	CD123	8.7
710	MGSWFEFEDRLDAIWDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRMDAAMIRYILQAYRHN	CD123	5.1
711	MGSWEEFEDRLWAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILRYDAAYIREILQAYRHN	CD123	4.1
712	MGSWIEFEDRLYAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRYEAAEIRYWLQAYRHN	CD123	4
713	MGSWYEFWDRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRYSAAEIRYQLQAYRHN	CD123	4.2

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
714	MGSWVEFESRLAAIEHRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREYAAEIRDWLQAYRHN	CD123	3.7
715	MGSWWEFEHRLFAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRDYAAEIRDYLQAYRHN	CD123	7.6
716	MGSWYEFDSRLMAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRQEAAEIRMILQAYRHN	CD123	3.2
717	MGSWYEFEWRLMAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRHEAAEIRDVLQAYRHN	CD123	3.4
718	MGSWYEFYNRLDAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRQEAADIRGQLQAYRHN	CD123	11.3
719	MGSWWEFHDRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRIEAADIRRQLQAYRHN	CD123	6.4
720	MGSWYEFWDRLEAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRLEAADIRRILQAYRHN	CD123	4.6
721	MGSWYEFEERLWAIEERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRYEAAWIRDFLQAYRHN	CD123	5.4
722	MGSWYEFENRLEAIEERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLREEAAFIRDWLQAYRHN	CD123	6.1
723	MGSWYEFEYRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREEAAWIRVWLQAYRHN	CD123	6.2
724	MGSWYEFENRLGAIGDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAYIRAVLQAYRHN	CD123	4.8
725	MGSWYEFEHRLDAIYDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREEAAWIRLWLQAYRHN	CD123	6.3
726	MGSWYEFEWRLDAIYDRLGALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAEIRALLQAYRHN	CD123	6
727	MGSWVEFENRLEAIENRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREDAAQIRMMLQAYRHN	CD123	6.2
728	MGSWYEFEERLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLREQAAFIRTMLQAYRHN	CD123	6
729	MGSWFEFEWRLEAIFDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLRAEAAEIRLRLQAYRHN	CD123	6.9
730	MGSWWEFEDRLMAIYDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRAEAALIRETLQAYRHN	CD123	15.3
731	MGSWFEFEDRLYAIEDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRWGAATIRDELQAYRHN	CD123	4.7
732	MGSWIEFWDRLEAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRDEAAWIRDSLQAYRHN	CD123	4.5
733	MGSWFEFWDRLDAIEDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRDEAAWIRGTLQAYRHN	CD123	4.9
734	MGSWEEFTDRLWAIEDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAFIRKSLQAYRHN	CD123	8.9
735	MGSWVEFVDRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRDQAAYIRFMLQAYRHN	CD123	4.9
736	MGSWFEFVDRLEAIEMRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRWRAAMIRYDLQAYRHN	CD123	7.1
737	MGSWWEFEMRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRWEAAFIRDILQAYRHN	CD123	4

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
738	MGSWFEFEIRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLRDEAAEIRQVLQAYRHN	CD123	3
739	MGSWYEFYQRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRDEAAEIRVVLQAYRHN	CD123	3
740	MGSWIEFEDRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEWLRQEAAEIRLMLQAYRHN	CD123	21.8
741	MGSWHEFYDRLDAIYFRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRLLAAEIRKELQAYRHN	p26	9.6
742	MGSWHEFITRLEAIDQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFWAAEIRFILQAYRHN	p26	16.91
743	MGSWMEFFDRLVAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRMWAAEIRFLLQAYRHN	p26	18.62
744	MGSWVEFSGRLIAIDNRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRMWAAEIRYILQAYRHN	p26	5.28
745	MGSWVEFHHRLFAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRMVAAEIRYILQAYRHN	p26	21.39
746	MGSWHEFMERLIAIDGRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFVAAFIRDVLQAYRHN	p26	17.85
747	MGSWKEFIQRLDAIHYRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFVAAFIRFELQAYRHN	p26	18.41
748	MGSWSEFIFRLDAIHSRLQALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLRFIAAEIRLKLQAYRHN	p26	28.3
749	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAAIREWLQAYRHN	p26	5.92
750	MGSWLEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAAIREWLQAYRHN	p26	
751	MGSWFEFYHRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAAIREWLQAYRHN	p26	
752	MGSWFEFYDRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAAIREWLQAYRHN	p26	
753	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVHAAAIREWLQAYRHN	p26	
754	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRDHAAAIREWLQAYRHN	p26	
755	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLREHAAAIREWLQAYRHN	p26	
756	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAHIREWLQAYRHN	p26	
757	MGSWLEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRVHAAAIREWLQAYRHN	p26	
758	MGSWLEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAHIREWLQAYRHN	p26	19.23
759	MGSWFEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAHIREWLQAYRHN	p26	
760	MGSWLEFYDRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAHIREWLQAYRHN	p26	
761	MGSWLEFYHRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAHIREWLQAYRHN	p26	

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
762	MGSWLEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRDHAAHIREWLQAYRHN	p26	
763	MGSWLEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVHAAHIREWLQAYRHN	p26	
764	MGSWLEFYHRLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAAIREWLQAYRHN	p26	
765	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDHAAHIREWLQAYRHN	p26	
766	MGSWFEFYERLNAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRAHAASIRTWLQAYRHN	p26	27.1
767	MGSWIEFYWRLEAIDQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRVHAAAIRWWLQAYRHN	p26	9.4
768	MGSWSEFVKRLDAIDQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVHAAAIRAWLQAYRHN	p26	27
769	MGSWEEFYYRLEAIDARLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRVHAAHIRDWLQAYRHN	p26	30.3
770	MGSWVEFHYRLQAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRVHAAHIRKWLQAYRHN	p26	14.8
771	MGSWVEFVGRLNAIDARLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRHHAAEIRNWLQAYRHN	p26	26
772	MGSWNEFMDRLNAIDNRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLRKQAASIRLWLQAYRHN	p26	10
773	MGSWNEFFQRLNAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRQHAANIRWWLQAYRHN	p26	28.7
774	MGSWYEFVVRLFAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREHAAHIRSWLQAYRHN	p26	18.25
775	MGSWYEFYLRLDAIDHRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLREHAAHIRKWLQAYRHN	p26	16
776	MGSWYEFRARLLAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLREHAAHIRNFLQAYRHN	p26	20.9
777	MGSWTEFWHRLEAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREHAAHIRVWLQAYRHN	p26	13.19
778	MGSWTEFQNRLNAIDHRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREHAAKIRVWLQAYRHN	p26	30.5
779	MGSWSEFFKRLEAIDRRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREHAAHIRVWLQAYRHN	p26	30.2
780	MGSWYEFQQRLEAIDTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELREHAAHIRHWLQAYRHN	p26	27.3
781	MGSWTEFEKRLHAIDYRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLREHAAAIRHWLQAYRHN	p26	17.1
782	MGSWTEFHQRLDAIDERLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEFLREHAAKIRMWLQAYRHN	p26	24.4
783	MGSWLEFSQRLTAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVENLREHAAKIRNWLQAYRHN	p26	30.4
784	MGSWTEFVNRLYAIDSRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEGLRTHAAKIRHWLQAYRHN	p26	16.7
785	MGSWMEFVDRLSAIDRRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLREHAANIRQWLQAYRHN	p26	32.1

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
786	MGSWVEFVSRLYAIDFRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALREHAAQIRDWLQAYRHN	p26	29
787	MGSWSEFHTRLDAIDTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRRHAAAIRFWLQAYRHN	p26	23.5
788	MGSWLEFHSRLDAIDTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREHAAAIRHYLQAYRHN	p26	30.8
789	MGSWTEFYQRLDAIDTRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEGLRQQAAQIRAWLQAYRHN	p26	29.7
790	MGSWAEFSDRLNAIDQRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILREHAAEIRKFLQAYRHN	p26	25.3
791	MGSWMEFNHRLQAIDGRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLREHAAAIRAFLQAYRHN	p26	33.4
792	MGSWYEFYKRLEAIDNRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEYLREHAAAIRHWLQAYRHN	p26	30.8
793	MGSWYEFYYRLEAIDNRLIALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEVLREHAAKIREWLQAYRHN	p26	29.6
794	MGSWYEFVSRLEAIDDRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEMLRQHAAAIRHWLQAYRHN	p26	33.1
795	MGSWYEFSHRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEPLREHAAYIRHWLQAYRHN	p26	26
796	MGSWFEFFERLAAIEDRLWALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVHAAAIRAFLQAYRHN	p26	20.3
797	MGSWIEFKYRLDAIEWRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRIHAAAIRTWLQAYRHN	p26	18.3
798	MGSWYEFMYRLDAIEYRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRIHAAMIREWLQAYRHN	p26	19.4
799	MGSWVEFVTRLEAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRAHAAHIRHWLQAYRHN	p26	11.7
800	MGSWYEFVIRLDAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEHLRVHAAHIRVWLQAYRHN	p26	30.1
801	MGSWVEFVERLDAIEFRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRNHAAHIRSWLQAYRHN	p26	23.8
802	MGSWSEFVHRLDAIEVRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRYHAAKIRSWLQAYRHN	p26	16.9
803	MGSWSEFYYRLAAIESRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVERLREHAAHIRRWLQAYRHN	p26	30.8
804	MGSWYEFYLRLSAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVQAAHIRTWLQAYRHN	p26	27.4
805	MGSWYEFYDRLDAIEDRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRDQAAYIRTWLQAYRHN	p26	31.9
806	MGSWHEFWVRLEAIESRLFALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRVQAAHIRSWLQAYRHN	p26	26.9
807	MGSWVEFYHRLEAIEQRLMALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREQAAAIRSWLQAYRHN	p26	28.5
808	MGSWVEFYERLNAIEYRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLREHAAYIRQWLQAYRHN	p26	28.7
809	MGSWVEFYHRLDAIFDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRANAAGIRSWLQAYRHN	p26	20

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
810	MGSWSEFTDRLFAIEDRLLALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEDLRMHAASIRLWLQAYRHN	p26	25.4
811	MGSWHEFYDRLYAIWDRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEGLRNAAAVIRIFLQAYRHN	p26	22.91
812	MGSWFEFSNRLYAIWHRLTALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRTQAAFIRILLQAYRHN	p26	15.25
813	MGSWFEFSDRLYAIWERLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRFQAAFIRYQLQAYRHN	p26	18.99
814	MGSWFEFEDRLFAIWTRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRQSAASIRWLLQAYRHN	p26	10.89
815	MGSWHEFSERLFAIWTRLEALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEALRQSAAFIRVMLQAYRHN	p26	8.21
816	MGSWGEFTVRLYAIDRRLDALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEELRRFAAIIRAFLQAYRHN	p26	8.54
817	MGSWYEFDHRLMAISFRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVETLRRRAANIRHLLQAYRHN	p26	20.1
818	MGSWSIFKYHLADIKLLLEALGGSEAELAYFEFLIADFEFT LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	20.21
819	MGSWHHFKYFLADIKSILEALGGSEAELAIFEVQIAYFEDL LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	8
820	MGSWLYFKYNLAVIKHWLEALGGSEAELAIFEMSIADFEYE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	13.3
821	MGSWFYFKYELAWIKHWLEALGGSEAELASFETHIAFFEHQ LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	13.7
822	MGSWADFKWTLAYIKHRLEALGGSEAELAFFEMEIAYFEQS LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	31.5
823	MGSWAYFKGQLAYIKSGLEALGGSEAELAYFELRIAYFEHW LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	11.4
824	MGSWENFKDTLAWIKEYLEALGGSEAELAGFEHRIAIFEHY LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	19.2
825	MGSWVLFKDYLADIKHYLEALGGSEAELANFEHLIANFEGD LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	13.8
826	MGSWSLFKHRLANIKVYLEALGGSEAELADFETFIAYFEKD LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	19.6
827	MGSWEHFKVELAGIKAYLEALGGSEAELALFEWAIADFESI LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	18.1
828	MGSWIYFKDELAGIKKYLEALGGSEAELAMFEVAIADFEAI LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	15.9
829	MGSWVLFKQELAWIKWLLEALGGSEAELAAFEEQIARFEHD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	29.5
830	MGSWVLFKQELAWIKWYLEALGGSEAELAAFEWEIAAFEQR LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	22.5
831	MGSWFLFKSELAWIKWRLEALGGSEAELAYFEYQIAEFEFW LQSYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	25.8
832	MGSWLLFKSELAWIKWYLEALGGSEAELAEFEWNIAEFEKN LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	25.7
833	MGSWLLFKSDLAWIKWRLEALGGSEAELAEFEESIAMFEHW LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	33.3

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
834	MGSWLYFKSDLAWIKWRLEALGGSEAELADFEEAIAEFEQA LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	21.2
835	MGSWKLFKYELAWIKWRLEALGGSEAELADFEASIAQFEKY LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	23.4
836	MGSWYLFKNELAWIKWRLEALGGSEAELADFEMVIAMFEDH LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	31.1
837	MGSWVYFKAHLAFIKWELEALGGSEAELANFESTIAEFEKY LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	20.8
838	MGSWMYFKSHLAWIKWELEALGGSEAELAFFEDNIAQFEYW LQLYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	19.8
839	MGSWTLFKWDLAFIKWQLEALGGSEAELAWFEYEIAAFEDS LQNYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	12.1
840	MGSWILFKEDLAFIKWQLEALGGSEAELAWFETTIANFESD LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	23.3
841	MGSWYFFKSRLAYIKVYLEALGGSEAELAGFEWEIAHFEEW LQRYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	30.1
842	MGSWYIFKSELAWIKWYLEALGGSEAELANFEVEIATFETW LQGYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	29.6
843	MGSWYIFKQELASIKLSLEALGGSEAELAHFEAEIAWFEWW LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	19.4
844	MGSWVRFKTELAYIKESLEALGGSEAELAMFESEIAIFEHS LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	20.5
845	MGSWYLFKTELAAIKYRLEALGGSEAELASFEYEIAWFEHI LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	20.1
846	MGSWYWFKYELAEIKWHLEALGGSEAELAHFEHSIAVFESQ LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	21.5
847	MGSWWVFKKTLAEIKWTLEALGGSEAELAYFEAEIAFFEFI LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	18.6
848	MGSWVYFKDHLAEIKSQLEALGGSEAELALFEYDIAWFEFI LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	22.1
849	MGSWVYFKHRLAEIKDQLEALGGSEAELAEFETDIAWFEWM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	11.1
850	MGSWIIFKTDLARIKNYLEALGGSEAELATFERDIAWFEFM LQIYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	16.7
851	MGSWMHFKQDLAEIKGYLEALGGSEAELAIFEMDIAWFEYM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	18.9
852	MGSWQIFKQDLAAIKDYLEALGGSEAELAIFEFDIAWFEHM LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	17.4
853	MGSWLAFKEDLAHIKSILEALGGSEAELAEFEHDIAWFEYM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	18.6
854	MGSWFVFKEDLAGIKFILEALGGSEAELAMFETDIAWFEYM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	14.2
855	MGSWTHFKEDLAHIKDRLEALGGSEAELAAFELDIAWFEFM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	30.4
856	MGSWYYFKERLAAIKDRLEALGGSEAELAIFEADIAWFEFM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	31.5
857	MGSWYTFKGSLAEIKNRLEALGGSEAELAMFESDIAWFEFM LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	32.3

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
858	MGSWFTFKDDLAQIKNRLEALGGSEAELANFEMSIAWFEFM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	30.8
859	MGSWVLFKQDLAMIKQRLEALGGSEAELAMFEYDIAWFEHM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	29.7
860	MGSWVEFKRDLANIKQRLEALGGSEAELAQFEMQIAWFEHT LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	30.4
861	MGSWSYFKEDLANIKSSLEALGGSEAELAWFESSIAWFEHT LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	11.6
862	MGSWSIFKQDLADIKDSLEALGGSEAELAMFEMDIAWFEHT LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	16.6
863	MGSWEIFKDDLASIKKVLEALGGSEAELALFESDIAWFELM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	27.9
864	MGSWSIFKDDLAVIKERLEALGGSEAELAHFEQDIAWFEHL LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	25.6
865	MGSWSVFKDDLAQIKDRLEALGGSEAELAQFELDIAWFEYV LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	30.3
866	MGSWAVFKDSLAHIKDVLEALGGSEAELALFEMDIAWFEYV LQDYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	24.1
867	MGSWIAFKDHLAIIKQRLEALGGSEAELARFEFEIAWFEWM LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	29.9
868	MGSWIHFKNDLAVIKDELEALGGSEAELARFEIMIAWFEDA LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	17.9
869	MGSWMVFKQDLAEIKANLEALGGSEAELADFEFAIAWFEYE LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	17.8
870	MGSWKNFKLELALIKSKLEALGGSEAELAQFEADIAFFEWS LQWYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	20.6
871	MGSWHSFKQDLAYIKYLLEALGGSEAELAQFEELIAFFEYY LQTYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	25.6
872	MGSWVVFKSSLAQIKILLEALGGSEAELAIFEVKIAHFEQE LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	8.6
873	MGSWDQFKNSLASIKRVLEALGGSEAELAIFEVKIAHFEHF LQQYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	15.6
874	MGSWNNFKSSLASIKQVLEALGGSEAELAVFELQIAHFERE LQYYKGKGNPEVEALRKEAAAIRDELQAYRHN	p26	24.1
875	MGSWVEFGHRLWAIDQRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLRQRAAFIRFRLQAYRHN	CD137	
876	MGSWAEFKQRLAAIKTRLEALGGSEAELAAFLGEIWAFEME LAAYKGKGNPEVEALGREAAAIRMELQAYRHN	CD137 (BB10)	
877	MGSWYEFDLRLHAIYDRLVALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEILRDNAAYIRQMLQAYRHN	CD47	
878	MGSWHEFHDRLQAIHERLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVESLRIAAAHIRQVLQAYRHN	CTLA4	
879	MGSWNYFKDHLAWIKNSLEALGGSEAELAHFETAIASFERQ LQEYKGKGNPEVEALRKEAAAIRDELQAYRHN	DR5	
880	MGSWLWFKIFLAEIKYFLEALGGSEAELAAFDFEIHAFHVE LFAYKGKGNPEVEVLREVAAEIRWDLQAYRHN	KIR	
881	MGSWTEFQSRLDAIHSRLRALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVELLRDDAAFIRHFLQAYRHN	PDL1	

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
882	MGSWVVFKVDLATIKYILEALGGSEAELAEFEGEIAGFEYS LQFYKGKGNPEVEALRKEAAAIRDELQAYRHN	TIM3	
883	MGSWTIFKEWLAFIKTDLEALGGSEAELAFFEGWIASFEME LQKYKGKGNPEVEALRKEAAAIRDELQAYRHN	PD1	
884	MGSWEEFELRLNAIEERLYALGGSEAELAYFEYVIADFEGN LQRYKGKGNPEVEALYFEADAIFEELVAYRHN	CD19	
885	MGSWVVFKQRLAYIKDLLEALGGSEAELAYFEMSIAFFEED LQVYKGKGNPEVEALRKEAAAIRDELQAYRHN	CD22	
886	MGSWVEFYERLDAIDRRLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRVHAASIRAWLQAYRHN	p26	
887	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLRAHAAAIREWLQAYRHN	p26	
888	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLRVHAAAIREWLQAYRHN	p26	
889	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLRAHAAAIREWLQAYRHN	p26	
890	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLKAHAAAIREWLQAYRHN	p26	
891	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLQAHAAAIREWLQAYRHN	p26	
892	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLRAHAAGIREWLQAYRHN	p26	
893	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLREHAAHIREWLQAYRHN	p26	
894	MGSWFEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLREHAAAIREWLQAYRHN	p26	
895	MGSWSEFYDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLREHAAAIREWLQAYRHN	p26	
896	MGSWVEFEARLSAIYERLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEKLRRHAAGIRSNLQAYRHN	CS1	
897	MGSWVEFFVRLDAIWERLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRFHAAGIRQKLQAYRHN	CS1	
898	MGSWTEFNLRLDAIYERLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEALRWHAAGIRQQLQAYRHN	CS1	
899	MGSWMEFYDRLDAIWVRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEVLRFHAAGIREQLQAYRHN	CS1	
900	MGSWHEFNGRLWAIYARLDALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRRHAAGIRGILQAYRHN	CS1	
901	MGSWYEFVQRLHAINDRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEVLRRHAAGIRYTLQAYRHN	CS1	
902	MGSWAEFYQRLNAIWNRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEVLRRHAAGIRGQLQAYRHN	CS1	
903	MGSWVEFNERLHAIYLRLDALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRRHAAGIRWQLQAYRHN	CS1	
904	MGSWNEFKLELAFIKDWLEALGGSEAELANFEEAIAEFEAGLQGYK GKGNPEVEALRKEAAAIRDELQAYRHN	CS1	
905	MGSWMEFEARLEAIWDRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVESLRFHAAGIRQHLQAYRHN	CS1	
906	MGSWVEFEDRLNAIWWRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEKLRRHAAGIRTQLQAYRHN	CS1	
907	MGSWHHFKMHLAGIKLQLEALGGSEAELAEFEEWIADFEGALQDYK GKGNPEVEALRKEAAAIRDELQAYRHN	CS1	

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
908	MGSWAEFFARLDAIWERLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRFHAAGIRQKLQAYRHN	CS1	
909	MGSWAEFFARLDAIWDRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRFHAAGIRQKLQAYRHN	CS1	
910	MGSWAEFFARLDAIWERLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLKFHAAGIRQKLQAYRHN	CS1	
911	MGSWHEFRWRLFAIWQRLHALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRLDAALIRVMLQAYRHN	HER2	10.02
912	MGSWAEFRWRLHAIWLKLGELGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLREDAEQIKYILQAYRHN	HER2	
913	MGSWAEFRWALHAIWLKLGELGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLREDAEQIKYILQAYRHN	HER2	
914	MGSWAEFRWRLHAIWLKLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
915	MGSWAEFRWRLHAIWLQLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
916	MGSWAEFRWRLHAIWLRLGALGGTEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
917	MGSWAEFRWRLHAIWLRLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
918	MGSWAEFRWKLEAIWLRLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
919	MGSWAEFRWKLGAIWLRLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIKYILQAYRHN	HER2	
920	MGSWYEFRWRLHAIWLRLGALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEWLRQDAAQIRYILQAYRHN	HER2	7.18
921	MGSWHEFLRRLLAIEMRLYALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEHLRVRAASIRQMLQAYRHN	HER2	8.15
922	MGSWWGFKVNLAWIKWKLEALGGSEAELAYFELWIANFEHSLQEYK GKGNPEVEALRKEAAAIRDELQAYRHN	HER2	8.69
923	MGSWVNFKTHLARIKVHLEALGGSEAELALFEHDIANFEQVLQQYK GKGNPEVEALRKEAAAIRDELQAYRHN	HER2	7.91
924	MGSWLVFKDELAGIKNYLEALGGSEAELATFEQDIAWFEQWLQNYK GKGNPEVEALRKEAAAIRDELQAYRHN	HER2	3.28
925	MGSWKTFKIELAGIKLELEALGGSEAELAGFENAIAQFESSLQYYK GKGNPEVEALRKEAAAIRDELQAYRHN	HER2	4.95
926	MGSWWEFKVRLSAIQYRLYALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEALREQAALIRTILQAYRHN	HER2	5.17
927	MGSWWEFHIRLHAINYRLAALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEALRELAAKIRGDLQAYRHN	HER2	11.90
928	MGSWWEFQVRLRAIQYRLNALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEYLRGLAAQIRFDLQAYRHN	HER2	14.39
929	MGSWWEFKIRLYAIEYRLNALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEALRAKAAQIRYNLQAYRHN	HER2	4.49
930	MGSWFEFNIRLHAIEYRLKALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRNYAASIRKLLQAYRHN	HER2	7.86
931	MGSWFEFEIRLRAIEYRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEKLRELAAEIRYALQAYRHN	HER2	7.75
932	MGSWFEFKIRLYAIQYRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRNLAAEIRHSLQAYRHN	HER2	13.08
933	MGSWWEFKVRLRAIEYRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRVLAASIRIHLQAYRHN	HER2	10.09

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SEQ NO:	D-Domain Sequence	Target	ELISA_avg
934	MGSWSEFWFRLHAILYRLQALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVETLRDAAAEIRVALQAYRHN	HER2	14.79
935	MGSWIEFWVRLNAILYRLYALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEALRDSAAEIRRWLQAYRHN	HER2	3.91
936	MGSWVEFWIRLNAIKYRLLALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEKLRQDAADIRELLQAYRHN	HER2	10.62
937	MGSWTEFWWRLSAIVYRLNALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRDMAADIRSLLQAYRHN	HER2	5.76
938	MGSWWEFYLRLRAISYRLQALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEGLRQDAAEIRKLLQAYRHN	HER2	5.10
939	MGSWWEFHVRLRAIEYRLEALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEQLRLIAANIRHLLQAYRHN	HER2	5.48
940	MGSWWEFHVRLKAIEYRLLALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEDLRYIAANIRQLLQAYRHN	HER2	4.56
941	MGSWWEFKVRLKAIEYRLLALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEDLRYIAANIRQLLQAYRHN	HER2	
942	MGSWWEFQVRLAAIEYRLKALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVENLRQLAAHIRSVLQAYRHN	HER2	6.33
943	MGSWWEFQVRLSAIEYRLTALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEELRQKAARIRSLLQAYRHN	HER2	9.61
944	MGSWWEFNIRLHAIDYRLKALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVELLREKAAQIRAQLQAYRHN	HER2	9.75
945	MGSWWEFRVRLEAIDYRLKALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEYLRMKAATIRAILQAYRHN	HER2	6.82
946	MGSWYEFDIRLEAIKYRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEYLRKKAAVIRSMLQAYRHN	HER2	5.35
947	MGSWWEFRIRLEAIWYRLHALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEDLRIFAANIRSKLQAYRHN	HER2	8.04
948	MGSWWEFNVRLQAIKYRLSALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEDLRKTAAHIRWQLQAYRHN	HER2	5.23
949	MGSWWEFNVRLSAIRYRLLALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEDLRASAAQIRAMLQAYRHN	HER2	6.73
950	MGSWWEFNMRLSAIKYRLYALGGSEAELAAFEKEIAAFESELQAYK GKGNPEVEILRRLAADIRERLQAYRHN	HER2	3.08

[0346] In some embodiments, the disclosure provides compositions comprising one or more of the DD sequences disclosed on Table 1. In other embodiments, the disclosure provides compositions comprising one or more DDs comprising a sequence with 60-70%, 70-75%, 75-80%, 80-85%, 85-90%, 95-99% homology (and overlapping ranges therein) with a sequence disclosed in Table 1. In some embodiments, the DD(s) having such homology are functionally similar or identical as compared to the respective reference sequence in Table 1. In some embodiments, the disclosure provides a polypeptide that comprises one or more DD that compete with (wholly or partially) one or more of the DD sequences disclosed in Table 1 (reference sequence) for its respective target. The ability of one polypeptpide to compete with a reference polypeptide for binding to a respective target

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can routinely be determined using a standard competition assay known in the art. In some embodiments, competition does not require that the polypeptide competes for the same epitope as a polypeptide (DD) of Table 1, rather the polypeptide can compete by binding a sterically inhibiting epitope, an overlapping epitope, *etc.*

Affinity Maturation and de-immunization of DD and DDpp

[0347] Affinity maturation strategies can be used to generate high affinity DD and DDpp that can be used in the DDpp fusion proteins described herein. An improved DD and DDpp that specifically binds a desired target (*e.g.,* BCAM, CD123, CS1, HER2, AFP, and AFP p26) can also be prepared based on a known DDpp reference sequence. For example, at least one, two, three, four, five, or more amino acid mutations (*e.g.,* conservative or non-conservative substitutions), deletions or insertions can be introduced into a DD sequence disclosed in Table 1 (*i.e.*, a reference sequence) and the resulting DDpp can be screened for binding to the respective target and biological activity, such as the ability to antagonize the biological activity of the respective target or agonize the biological activity of the respective target.

[0348] The discosed DDpp, particularly those administered to a subject, are preferably not antigenic with respect to the subject (*e.g.,* human). In some embodiments, the sequence of the DDpp does not contain a human HLA-DR binding motif or cleavage sites for proteasomes and immune-proteasomes. In particular embodiments, the DDpp sequence does not contain an antigenic sequence as determined by a computer prediction model version existent on the filing date of this specification. In particular embodiments, the DDpp sequence does not contain an MHC (class I or class II) binding site sequence as predicted by an algorithm selected from ProPred (*see, e.g.,* Singh, Bioinformatics 17(12): 1236-1237 (2001)), ProPred1 (Singh, Bioinformatics 19(8): 1009-14 (2003)), SYFPEITHI (*see, e.g.,* Schuler, Immunoinf. Meth. in Mol. Biol. 409(1): 75-93 (2007)), SMM-align (*see, e.g.,* Nielsen, BMC Bioinformatics 8: 238 (2007)), RANKPEP (*see, e.g.,* Reche, Hum Immunol 63: 701-709. (2004)), or TEPITOPE (*see*, Sturniolo, Nat Biotechnol 17: 555–561 (1999)), wherein the version of the algorithm and the applied database are in existence on the filing date of this application. In some embodiments, the DDpp does not contain a sequence that shares characteristics with a high affinity (binding threshold less than 6%) T cell epitope. (Singh, Bioinformatics 17: 1236-1237 (2001)). In some embodiments, the DDpp does not contain a sequence that shares characteristics with a promiscuous (present in greater than 50% of relevant alleles) T cell epitope (Singh, Bioinformatics

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17: 1236-1237 (2001)). In some embodiments, the DDpp does not contain a sequence that shares characteristics with a high affinity or a promiscuous T cell epitope. In particular embodiments, the DDpp does not contain the sequence LAAIKTRLQ (SEQ ID NO: 2). Techniques for generating, screening, and identifying affinity matured DDpp variants and target-binding DDpp variants containing a sequence alteration that removes a predicted MHC (class I or class II) binding site sequence are known in the art.

Articles of Manufacture

[0349] Articles of manufacture, including, kits, are provided herein. The article of manufacture may comprise a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials or syringes. The containers may be formed from a variety of materials such as glass or plastic. The container holds one or more DDpp, nucleic acids encoding DDpp and/or vectors or host cells of the present disclosure. The label or package insert may include directions for performing affinity based screening and/or detection.

[0350] Also provided are kits containing a DDpp. Such kits have uses including, but not limited to detecting the target of interest to which the DDpp specifically binds (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26)). Such assay kit may be useful in screening for the presence of a target of interest and/or quantitating the concentrations of a target of interest in a fluid, such as, a biological fluid (*e.g.,* blood, serum, or synovial fluid).

[0351] In one embodiment a DDpp assay kit is contemplated which comprises one or more containers of a DDpp that specifically binds a target of interest and, optionally, a detection means for determining the presence or absence of a target/DDpp interaction or the absence thereof. The kit further optionally contains target of interest protein (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) that may be used, for example as a control or standard. The DDpp may be free or expressed on the surface of a host cell or on the surface of a bacteriophage. In a specific embodiment, the DDpp or target of interest provided in the kit is labeled. Any label known in the art can be used. In some embodiments, the label is selected from the group consisting of biotin, a fluorogen, an enzyme, an epitope, a chromogen, or a radionuclide. In some embodiments, the DDpp is immobilized on a solid support. The detection means employed to detect the label will depend on the nature of the label and can be any known in the art, *e.g.,* film to detect a radionuclide; an enzyme substrate that gives rise to or amplifies a detectable signal to detect the presence of a target of interest.

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[0352] Preferably, the kit further comprises a solid support for the DDpp, which may be provided as a separate element or on which a DDpp that specifically binds a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) is immobilized. Hence, the DDpp that specifically binds the target of interest in the kit may be immobilized on a solid support, or they may be immobilized on such support that is included with the kit or provided separately from the kit. Preferably, DDpp is coated on a microtiter plate. In some embodiments, the detection involves a signal amplifying molecule. Where the signal amplifying molecule is an enzyme, the kit optionally further includes substrates and cofactors required by the enzyme, and where the amplifying molecule is a fluorophore. The kit optionally further includes a dye precursor that provides the detectable chromophore.

[0353] The kit may also contain instructions for carrying out the assay as well as other additives such as stabilizers, washing and incubation buffers, and the like. The components of the kit will be provided in predetermined ratios, with the relative amounts of the various reagents suitably varied to provide for concentrations in solution of the reagents that substantially maximize the sensitivity of the assay. Particularly, the reagents can be provided as dry powders, usually lyophilized, including excipients, which on dissolution will provide for a reagent solution having the appropriate concentration for combining with the sample to be tested.

[0354] Various formats and techniques for binding assays that can be used are known in the art and include but are not limited to, immobilization to filters such as nylon or nitrocellulose; two-dimensional arrays, enzyme linked immunosorbent assay (ELISA), radioimmuno-assay (RIA), competitive binding assays, direct and indirect sandwich assays, immunoprecipitation assays, fluorimetric microvolume assay technology (FMATTM), LuminexTM system assays, fluorescent resonance energy transfer (FRET), bioluminescence resonance energy transfer (BRET), electroimmunoassays, AlphaScreenTM, nanoparticle-derived techniques, and surface plasmon resonance (SPR).

[0355] Binding assays can be homogeneous or semi-homogeneous. A homogeneous assay is an assay where all the components are mixed together, incubated, and then analyzed. A semi-homogeneous assay is one where the majority of the reaction takes place as a complex mixture, but a washing step is required prior to the addition of a final reagent and analysis, in contrast to a typical stepwise assembly sandwich assay where each component is added then washed off before the

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next component is added. In some embodiments, the assay is an immunoassay. In certain embodiments, the assay is a semi-homogeneous Enzyme Immuno-Assay (EIA).

Uses

[0356] DDpp, whether alone, as fusion proteins, as chemical conjugates or as other embodiments, described herein, have a variety of applications. In some embodiments, DDpp are used as detection reagents, diagnostic reagents or analytical reagents. Some embodiments, have *in vivo*, in vitro and/or *ex vivo* applications. Methods that employ the DDpp in vitro can be performed in different formats, such as in microtiter plates, in protein arrays, on biosensor surfaces, on tissue sections, and in additional formats that would be apparent to a person skilled in the art. Likewise, methods that employ the DDpp *in vivo* can be used in different formats that include but are not limited to DDpp-Fc fusion proteins, CAR cells, and DDpp multi-specific antibodies. In particular embodiments, DDpp such as DDpp fusion proteins are used as a therapeutic agent.

Analytical and Diagnostic Applications

[0357] Whether alone, as fusion proteins, as chemical conjugates or as other embodiments, described herein, DDpp have a variety of applications. In some embodiments, DDpp are used as detection reagents of targets of interest in a variety of different sample types.

[0358] In one embodiment a DDpp are used to detect targets of interest in solutions involved in manufacturing processes, such as protein expression. Samples may include, but are not limited to, water, buffers, in-process purification samples, bulk drug substance and final drug product. In still additional embodiments, the DDpp can be used to detect contaminants from a sample, such as a water supply source or water (or other fluid) used in manufacturing.

[0359] In another embodiment, DDpp are used to detect targets of interest in diagnostic samples. Samples may include, but are not limited to tissue homogenates, cell extracts, biopsy samples, sera, plasma, lymph, blood, blood fractions, urine, synovial fluid, spinal fluid, saliva, mucous, sputum, pleural fluid, nipple aspirates, fluid of the respiratory, intestinal, and genitourinary tracts, tear fluid, breast milk, fluid from the lymphatic system, semen, cerebrospinal fluid, intra-organ system fluid, ascitic fluid, tumor cyst fluid, aminotic fluid, and media or lysate from cultured cells.

[0360] In one embodiment, the DDpp are useful for detecting the presence of a factor or multiple factors (*e.g.,* antigens or organisms) in a biological sample. The term "detecting" as used herein encompasses quantitative or qualitative detection. In certain embodiments, a biological sample

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comprises a cell, tissue or fluid. In certain embodiments, such tissues include normal and/or cancerous tissues.

[0361] Various formats and techniques for detection are known in the art and include but are not limited to Western Blot analysis, Immunohistochemistry, ELISA, FACS analysis, enzymatic assays, autoradiography and any of the binding assays mentioned herein.

[0362] In one embodiment, a method is provided for detecting a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) in a solution containing the target comprising: (a) contacting the solution with a DDpp that specifically binds the target of interest under conditions suitable for specific binding of the DDpp to the target and (b) detecting binding of the DDpp and target. The DDpp may be either free or immobilized. Sufficient time is allowed to permit binding between the target of interest and the DDpp, and non-binding components in the solution or mixture are removed or washed away. The formation of a binding complex between the DDpp and the target of interest can then be detected, for example, by detecting the signal from a label on the DDpp, which is one component of the binding complex. A label may be any label that generates a signal that can be detected by standard methods, such as a fluorescent label, a radioactive compound, or an enzyme that reacts with a substrate to generate a detectable signal. Examples of suitable labels for such purposes are described herein and/or otherwise known in the art.

[0363] DDpp that bind to a target of interest such as BCMA, CD123, CS1, HER2, AFP, or AFP p26 can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) using methods known in the art, such as described in WO00/70023 and (Harlow and Lane (1989) Antibodies, Cold Spring Harbor Laboratory, pp. 1-726).

[0364] The detectable marker or label can be any which is capable of producing, either directly or indirectly, a measurable signal, such as a radioactive, chromogenic, luminescence, or fluorescent signal, which can be used to quantitate the amount of bound detectable moiety or label in a sample. Detectable labels known in the art include radioisotopes, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, electrochemiluminescent labels (such as Ruthenium (Ru)-based catalyst in conjunction with substrates, *etc.*), luminescent or bioluminescent labels (*e.g.,* Europium, Vanadium), fluorescent or chemiluminescent compounds, such as fluorescein isothiocyanate, rhodamine, or luciferin, enzymes (*e.g.,* enzyme, such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase),

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colorimetric labels such as colloidal gold, colored glass or plastic beads (*e.g.,* polystyrene, polypropylene, latex, *etc.*), paramagnetic atoms or magnetic agents, electron-dense reagents, a nano- or micro-bead containing a fluorescent dye, nanocrystals, a quantum dot, a quantum bead, a nanotag, dendrimers with a fluorescent label, a micro-transponder, an electron donor molecule or molecular structure, or a light reflecting particle, the microparticles may be nanocrystals or quantum dots. Nanocrystals are substances that absorb photons of light, then re-emit photons at a different wavelength (fluorophores). In addition, additional fluorescent labels, or secondary antibodies may be conjugated to the nanocrystals. Nanocrystals are commercially available from sources such as Invitrogen and Evident Technologies (Troy, N.Y.). Other labels include E)-5-[2-(methoxycarbonyl) ethenyl]cytidine, which is a nonfluorescent molecule that when subjected to ultraviolet (UV) irradiation yields a product, 3 beta-D-ribofuranosyl-2,7-dioxopyrido[2,3-d]pyrimidine, which displays a strong fluorescence signal.

[0365] Competitive inhibition can be determined by any method known in the art, for example, competition ELISA assays. A DDpp, such as a DDpp fusion protein (*e.g.,* a DDpp-Fc, DDpp-CAR, a DDpp-scFv), or other molecule is said to "competitively inhibit" binding of a reference molecule to a given epitope if it binds to that epitope to the extent that it blocks, to some degree, binding of the reference molecule to the epitope. As used herein, a DDpp (*e.g.,* a DDpp fusion protein), or other molecule can be said to competitively inhibit binding of the reference molecule to a given epitope, for example, by at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, by at least 40%, at least 30%, or at least 20%. The terms "compete," "ability to compete" and "competes with" are relative terms used to describe a DDpp, such as a DDpp fusion protein, that produce at least 20%, at least 30%, at least 40%, or at least 50% inhibition of binding of a reference molecule to a target by a DDpp such as a DDpp fusion protein (*e.g.,* a DDpp-Fc, DDpp CAR, a DDpp-scFv, and an antibody-comprising a DDpp) as determined in a standard competition assay as described herein or otherwise known in the art, including, but not limited to, competitive assay systems using techniques such as radioimmunoassays (RIA), enzyme immunoassays (EIA), preferably the enzyme linked immunosorbent assay (ELISA), "sandwich" immunoassays, immunoradiometric assays, fluorescent immunoassays, luminescent, electrochemical luminescent, and immunoelectrophoresis assays. Methods for determining binding and affinity of candidate binding molecules are known in the art and

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include, but are not limited to, affinity chromatography, size exclusion chromatography, equilibrium dialysis, fluorescent probe displacement, and plasma resonance.

Therapeutics

[0366] The DD described herein are useful in a variety of applications including, but not limited to, therapeutic treatment methods, which may be in vitro, *ex vivo*, or *in vivo* methods.

[0367] The application as a therapeutic entity is an attribute of the target binding specificity of the DDpp. The incorporation of DDpp within various molecular compositions, (*e.g.,* a DD-antibody fusions, DD-drug conjugates and DD-chimeric receptors) affords application in a variety of therapeutic indications and modalities, which include, but not limited to soluble and cell-associated compositions.

[0368] In one embodiment, the DDpp is a soluble fusion protein made up of an optional epitope tag 10 and a targeting domain that binds to a target that is associated with a disease or disorder of the metabolic, cardiovascular, musculoskeletal, neurological, or skeletal system. In other embodiments, the DDpp is a soluble fusion protein that binds to a target that is associated with yeast, fungal, viral or bacterial infection or disease. In some embodiments, the DDpp is a soluble fusion protein that binds to a target that is associated with a disease or disorder of the immune system.

[0369] Also provided are therapeutic compositions useful for practicing therapeutic methods described herein. In one embodiment, therapeutic compositions provided herein contain a physiologically tolerable carrier together with at least one species of DDpp fusion as described herein, dissolved or dispersed therein as an active ingredient. In another embodiment, therapeutic compositions provided herein contain a physiologically tolerable carrier together with at least one species of a DDpp as described herein, dissolved or dispersed therein as an active ingredient. In a preferred embodiment, therapeutic composition is not immunogenic when administered to a human patient for therapeutic purposes.

[0370] The preparation of a pharmacological composition that contains active ingredients dissolved or dispersed therein is well understood in the art. Typically such compositions are prepared as sterile injectables either as liquid solutions or suspensions, aqueous or non-aqueous. However, solid forms suitable for solution, or suspensions, in liquid prior to use can also be prepared. The preparation

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can also be emulsified. Thus, a DDpp-containing composition can take the form of solutions, suspensions, tablets, capsules, sustained release formulations or powders, or other compositional forms. In some embodiments, the DDpp compositions (*e.g.,* a DDpp fusion proteins) are formulated to ensure or optimize distribution *in vivo*, For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds and if so desired, the compositions are prepared so as to increase transfer across the BBB, by for example, formulation in liposomes. For methods of manufacturing liposomes, *see, e.g.,* U.S. Pat. Nos. 4,522,811, 5,374,548, and 5,399,331. The liposomes can comprise one or more moieties that are selectively transported into specific cells or organs, thus enhance targeted drug delivery (*see, e.g.,* Ranade, Clin. Pharmacol. 29: 685 (1989)).

[0371] The DDpp (*e.g.* DDpp fusion protein) can be mixed other active ingredients and/or excipients that are pharmaceutically acceptable and compatible with the active ingredient and in amounts suitable for use in therapeutic methods described herein. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents and the like which enhance the effectiveness of the active ingredient.

[0372] Therapeutic DDpp can include pharmaceutically acceptable salts of the components therein. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide) that are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, tartaric, mandelic and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and such organic bases as isopropylamine, trimethylarnine, 2-ethylamino ethanol, histidine, procaine and the like.

[0373] Physiologically tolerable carriers are known in the art. Exemplary of liquid carriers are sterile aqueous solutions that contain no materials in addition to the active ingredients and water, or contain a buffer such as sodium phosphate at physiological pH value, physiological saline or both, such as phosphate-buffered saline. Still further, aqueous carriers can contain more than one buffer salt, as well as salts such as sodium and potassium chlorides, dextrose, propylene glycol, polyethylene glycol, and other solutes.

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[0374] Liquid compositions can also contain liquid phases in addition to, and to the exclusion of water. Exemplary of such additional liquid phases are glycerin, vegetable oils such as cottonseed oil, organic esters such as ethyl oleate, and water-oil emulsions.

[0375] In one embodiment, a therapeutic composition contains a DDpp fusion protein, typically in an amount of at least 0.1 weight percent of DDpp fusion protein per weight of total therapeutic composition. A weight percent is a ratio by weight of DDpp fusion per total composition. Thus, for example, 0.1 weight percent is 0.1 grams of DDpp per 100 grams of total composition.

[0376] A DDpp fusion protein-containing therapeutic composition typically contains about 10 micrograms (μg) per milliliter (ml) to about 100 milligrams (mg) per ml of DDpp fusion protein as active ingredient per volume of composition, and more preferably contains about 1 mg/ml to about 10 mg/ml (*i.e.*, about 0.1 to 1 weight percent).

[0377] The dosage ranges for the administration of the DDpp (*e.g.,* a DDpp fusion protein) are those large enough to produce the desired effect in which the disease symptoms mediated by the target molecule are ameliorated. The dosage should not be so large as to cause adverse side effects, such as hyperviscosity syndromes, pulmonary edema, congestive heart failure, and the like. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by one of skill in the art. The dosage can be adjusted by the individual physician in the event of any complication.

[0378] The DDpp (*e.g.,* a DDpp fusion protein) can be administered parenterally by injection or by gradual infusion over time. Although the target molecule can typically be accessed in the body by systemic administration and therefore most often treated by intravenous administration of therapeutic compositions, other tissues and delivery means are contemplated where there is a likelihood that the tissue targeted contains the target molecule. Thus, DDpp can be administered intravenously, intraperitoneally, intramuscularly, subcutaneously, intracavity, transdermally, and can be delivered by peristaltic means. DDpp fusion proteins can also be delivered by aerosol to airways and lungs.

[0379] Therapeutic compositions containing a DDpp can be conventionally administered intravenously, as by injection of a unit dose, for example. The term "unit dose" when used in reference to a therapeutic composition provided herein refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to

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produce the desired therapeutic effect in association with the required diluent; *e.g.,* carrier, or vehicle. In some embodiments, therapeutic compositions containing a DDpp are administered subcutaneously.

[0380] The DDpp (*e.g.,* a DDpp fusion protein) are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered depends on the subject to be treated, capacity of the subject's system to utilize the active ingredient of the administered composition, and degree of therapeutic effect desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. However, suitable dosage ranges for systemic application are disclosed herein and depend on the route of administration. Suitable regimes for administration are also variable, but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other administration. Alternatively, continuous intravenous infusion sufficient to maintain concentrations in the blood in the ranges specified for *in vivo* therapies are contemplated.

[0381] The DDpp compositions are formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The dosage ranges for the administration of the DDpp are those large enough to produce the desired effect in which the disease symptoms mediated by the target molecule are ameliorated. The dosage should not be so large as to cause adverse side effects, such as, hyperviscosity syndromes, pulmonary edema, congestive heart failure, and the like. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by one of skill in the art. The dosage can be adjusted by the individual physician in the event of any complication.

[0382] The dosage schedule and amounts effective for therapeutic and prophylactic uses, *i.e.*, the "dosing regimen," will depend upon a variety of factors, including the cause, stage and severity of the disease or disorder, the health, physical status, age of the mammal being treated, and the site and mode of the delivery of the DD. Therapeutic efficacy and toxicity of the complex and formation can be determined by standard pharmaceutical, pharmacological, and toxicological procedures in cell cultures or experimental animals. Data obtained from these procedures can likewise be used in formulating a range of dosages for human use. Moreover, therapeutic index (*i.e.*, the dose

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therapeutically effective in 50 percent of the population divided by the dose lethal to 50 percent of the population (ED50/LD50)) can readily be determined using known procedures. The dosage is preferably within a range of concentrations that includes the ED50 with little toxicity or none dose limiting toxicity, and may vary within this range depending on the dosage form employed, sensitivity of the patient, and the route of administration.

[0383] The dosage regimen also takes into consideration pharmacokinetics parameters known in the art, such as, drug absorption rate, bioavailability, metabolism and clearance (*see, e.g.,* Hidalgo-Aragones, J. Steroid Biochem. Mol. Biol. 58: 611-617 (1996); Groning *et al.*, Pharmazie 51: 337-341 (1996); Fotherby, Contraception 54: 59-69 (1996); and Johnson *et al.*, J. Pharm. Sci. 84: 1144-1146 (1995)). It is well within the state and level of skill of the clinician to determine the dosage regimen for each subject being treated. Moreover, single or multiple administrations of DDpp compositions can be administered depending on the dosage and frequency as required and tolerated by the subject. The duration of prophylactic and therapeutic treatment will vary depending on the particular disease or condition being treated. Some diseases are amenable to acute treatment whereas others require long-term, chronic therapy. DDpp can be administered serially, or simultaneously with the additional therapeutic agent.

[0384] In some embodiments, the DDpp is administered at about 1 mg/kg to about 50 mg/kg, about 1 mg/kg to about 25 mg/kg, about 1 mg/kg to about 20 mg/kg, about 1 mg/kg to about 15 mg/kg, about 1 mg/kg to about 10 mg/kg, or about 1 mg/kg to about 5 mg/kg.

[0385] In another embodiment, the DDpp is administered in combination with one or more additional therapeutics.

[0386] A therapeutically effective amount of the DDpp (*e.g.,* a DDpp fusion protein) can be an amount such that when administered in a physiologically tolerable composition is sufficient to achieve a plasma concentration of from about 0.1 microgram (μg) per milliliter (ml) to about 100 μg/ml, preferably from about 1 μg/ml to about 5 μg/ml, and usually about 5 μg/ml. Stated differently, the dosage can vary from about 0.1 mg/kg to about 300 mg/kg, preferably from about 0.2 mg/kg to about 200 mg/kg, most preferably from about 0.5 mg/kg to about 20 mg/kg, in one or more dose administrations daily, for one or several days.

[0387] In some embodiments, the DDpp described herein are useful for treating a disease or disorder of the immune system, such as inflammation or an autoimmune disease.

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[0388] In some embodiments, the DDpp described herein are useful for treating cancer. Thus, in some embodiments, the disclosure provides a method of treating cancer that comprises administering a therapeutically effective amount of a DDpp (*e.g.* a DDpp fusion) to a patient.

[0389] In additional embodiments, the disclosure provides a chimeric antigen receptor (CAR), wherein the CAR includes a targeting domain, a transmembrane domain, and an intracellular signaling domain. In some embodiments, the targeting domain is made up of, at least in part, a target-binding DDpp disclosed herein.

[0390] The disclosure also provides cells comprising a nucleic acid sequence encoding a CAR, wherein the CAR comprises an antigen binding domain made up of, at least in part, a disclosed polypeptide that binds a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, and AFP p26), a transmembrane domain, and a signaling domain. In some embodiments, the CAR binds specifically to a tumor antigen (and thus functions to deliver the cell expressing the CAR to the tumor. In some embodiments, the tumor antigen is associated with a hematologic malignancy. In some embodiments, the tumor antigen is BCMA. In some embodiments, the tumor antigen is CD123. In some embodiments, the tumor antigen is CS1. In additional embodiments, tumor antigen is associated with a solid tumor. In some embodiments, the tumor antigen is HER2. In some embodiments, both solid and hematologic tumors are targeted. In some embodiments, the cell expressing the CAR is a T cell, a natural killer (NK) cell or other immune cell type. In some embodiments, the cell expressing the CAR (whether T cell, NK cell or other cell type) exhibits an anti-tumor immunity when the polypeptide binds to its corresponding tumor antigen.

[0391] In some embodiments, the disclosure provides a method of treating a subject having cancer, comprising administering to the subject a therapeutically effective amount of a CAR immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises a target binding domain that comprises a DD that specifically binds BCMA (e.g., comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306), a transmembrane domain, and an intracellular domain (comprising a signaling domain). In some embodiments, the administered CAR immune cell is a T cell. In some embodiments, the administered CAR immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject.

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[0392] In some embodiments, the target binding domain of the administered CAR immune cell specifically binds BCMA expressed by a cancer cell of the subject, and induces the CAR immune cell to generate a cytotoxic signal that results in cytotoxic effects on the cancer cell, thereby treating the cancer.

[0393] In some embodiments, the disclosure provides a method of treating a subject having cancer, comprising administering to the subject a therapeutically effective amount of a CAR immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises a target binding domain that comprises a DD that specifically binds CD123 (e.g., comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 307-739, and 740), a transmembrane domain, and an intracellular domain (comprising a signaling domain). In some embodiments, the administered CAR immune cell is a T cell. In some embodiments, the administered CAR immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject. In some embodiments, the target binding domain of the administered CAR immune cell specifically binds CD123 expressed by a cancer cell of the subject, and induces the CAR immune cell to generate a cytotoxic signal that results in cytotoxic effects on the cancer cell, thereby treating the cancer.

[0394] In some embodiments, the disclosure provides a method of treating a subject having cancer, comprising administering to the subject a therapeutically effective amount of a CAR immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises a target binding domain that comprises a DD that specifically binds CS1 (e.g., comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 896-909, and 910), a transmembrane domain, and an intracellular domain (comprising a signaling domain). In some embodiments, the administered CAR immune cell is a T cell. In some embodiments, the administered CAR immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject. In some embodiments, the target binding domain of the administered CAR immune cell specifically binds CS1 expressed by a cancer cell of the subject, and induces the CAR immune cell to generate a cytotoxic signal that results in cytotoxic effects on the cancer cell, thereby treating the cancer.

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[0395] In some embodiments, the disclosure provides a method of treating a subject having cancer, comprising administering to the subject a therapeutically effective amount of a CAR immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises a target binding domain that comprises a DD that specifically binds HER2 (e.g., comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 911-949, and 950), a transmembrane domain, and an intracellular domain (comprising a signaling domain). In some embodiments, the administered CAR immune cell is a T cell. In some embodiments, the administered CAR immune cell is a NK cell. In some embodiments, the administered CAR immune cell is not a T cell or an NK cell. In further embodiments, a combination of different CAR immune cell types (*e.g.,* NK cells and T cells) is administered to the subject. In some embodiments, the target binding domain of the administered CAR immune cell specifically binds HER2 expressed by a cancer cell of the subject, and induces the CAR immune cell to generate a cytotoxic signal that results in cytotoxic effects on the cancer cell, thereby treating the cancer.

[0396] Additionally provided are methods for treating or preventing cancer comprising administering a DDpp-CAR T lymphocyte to a patient predisposed to or having a cancer that expresses a tumor antigen on the surface of target cells, and wherein the DDpp specifically binds the antigen.

[0397] In some embodiments, wherein CAR T cells are administered to the subject having cancer, the binding of the target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) stimulates the CAR T cell to initiate intracellular signaling. In further embodiments, the binding of the CAR T cell to the target of interest stimulates the T cell to initiate intracellular signaling and produce cytokines. In further embodiments, the binding of the CAR T cell to the target of interest stimulates the T cell to initiate intracellular signaling, produce cytokines, and degranulate, leading to the cytotoxic effects on the cancer cell. In some embodiments, the CAR T cell proliferates in response to binding the target of interest. Advantageously, in some embodiments, the activity of the CAR T cell does not result in the T cell exhibiting a phenotype associated with T cell exhaustion. In some embodiments, the transmembrane domain of the CAR T cell comprises 41BB or CD28, and the cytoplasmic domain comprises an alpha, beta, or zeta chain of the T cell receptor.

[0398] In some embodiments, the administered CAR further comprises 2, 3, 4, 5, or more than 5, DD and/or other binding domains (*e.g.,* scFv) that specifically bind the target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) expressed by the cancer cell. In additional

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embodiments, the administered CAR further comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically binds a different target of interest expressed by the cancer cell. In additional embodiments, the administered CAR further comprises 2, 3, 4, 5, or more than 5, DD or other binding domains (*e.g.,* scFv) that specifically binds a different target of interest expressed by a different cancer cell or a vascular endothelial cell.

[0399] In some embodiments, the administered immune cell further comprises a second CAR polypeptide having a DD or other binding domain (*e.g.,* scFv) that specifically binds a second target of interest expressed by the cancer cell. In some embodiments, the administerd immune cell further comprises a second CAR polypeptide having a DD or other binding domain (*e.g.,* scFv) that specifically binds a second target of interest expressed by a different cancer cell or a vascular endothelial cell.

[0400] In some embodiments, the administration of the immune cells with a CAR is intravenous. In other embodiments, the immune cells with a CAR is administered through an intra-arterial, intramuscular, local, or other acceptable route for the given treatment scenario.

[0401] In some embodiments, the disclosure also provides methods of treating a subject having cancer, comprising, administering to the subject an immune cell comprising a chimeric antigen receptor (CAR), wherein the CAR comprises a target binding domain, wherein the target binding domain comprises a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306; SEQ ID NO: 307-739, and 740; SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950; wherein the polypeptide specifically binds a target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) expressed by a cancer cell.

[0402] In additional embodiments, the disclosure provides a method of treating a subject having cancer, the method comprising intravenously administering to the subject an immune cell comprising a chimeric antigen receptor (CAR) expressed on a T cell, wherein the CAR comprises a target binding domain comprising a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306; SEQ ID NO: 307-739, and 740; SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950; a transmembrane domain selected from 41BB and CD28, and an intracellular domain, wherein the intracellular domain comprises a signaling domain selected from an alpha, beta, or zeta chain of the T cell receptor,

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wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) expressed by a cancer cell, and wherein the binding of the target of interest induces the CAR T cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell. In some embodiments, the cytotoxic effects result from degranulation of the CAR T cells. Advantageously, in some embodiments, the activation and cytotoxic activity of the CAR T cells is not associated with the CAR T cells exhibiting a phenotype associated with T cell exhaustion. In some embodiments, the CAR optionally further comprises a second target binding domain comprising a second polypeptide having a different target than the target binding domain. In still further embodiments, additional targeting domains can optionally be included to enhance binding capacity to a marker, or impart binding specificity to other markers.

[0403] In some embodiments, the disclosure provides for the use of an immune cell comprising a chimeric antigen receptor (CAR) for the treatment of cancer, wherein the CAR comprises a target binding domain comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 11-305, and 306; SEQ ID NO: 307-739, and 740; SEQ ID NO: 741-874 and 886-895; SEQ ID NO: 896-909 and 910; or SEQ ID NO: 911-949, and 950; a transmembrane domain selected from 41BB and CD28, and an intracellular domain, wherein the intracellular domain comprises a signaling domain selected from an alpha, beta, or zeta chain of the T cell receptor, wherein, upon administration to a subject having cancer, the target binding domain specifically binds to the target of interest (*e.g.,* BCMA, CD123, CS1, HER2, AFP, or AFP p26) expressed by a cancer cell, and wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell. In different embodiments, the immune cells can be a T cell or a natural killer (NK) cell.

[0404] Cancers that can be treated include tumors that are not vascularized, or not yet substantially vascularized, as well as vascularized tumors. The cancers can comprise non-solid tumors (such as hematological tumors, for example, leukemias and lymphomas) or can comprise solid tumors. Types of cancers to be treated with the DDpp include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies *e.g.,* sarcomas, carcinomas, and melanomas. Adult tumors/cancers and pediatric tumors/cancers are also included.

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[0405] In some embodiments, the DDpp described herein are useful for treating a patient having hematological cancers. Examples of hematological (or hematogenous) cancers include leukemias, including acute leukemias (such as acute lymphocytic leukemia, acute myelocytic leukemia, acute myelogenous leukemia and myeloblasts, promyeiocytic, myelomonocytic, monocytic and erythroleukemia), chronic leukemias (such as chronic myelocytic (granulocytic) leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia), polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma (indolent and high grade forms), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia and myelodysplasia. In some embodiments, the hematological cancer is multiple myeloma.

[0406] Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteosarcoma, and other sarcomas, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, melanoma, and CNS tumors (such as a glioma (such as brainstem glioma and mixed gliomas), glioblastoma (also known as glioblastoma multiforme) astrocytoma, CNS lymphoma, germinoma, medulloblastoma, Schwannoma craniopharyogioma, ependymoma, pineaioma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, neuroblastoma, retinoblastoma and brain metastases). In some embodiemnts, the cancer is breast cancer or ovarian cancer.

[0407] In additional embodiments, the DDpp fusion protein binds (1) a target on a cell or tissue of interest (*e.g.,* a tumor antigen on a tumor cell) and (2) a target on an effector cell, such as, a T cell receptor molecule. According to one embodiment, the binding of one or more targets by the DDpp fusion protein is used to direct an immune response to an infectious agent, cell, tissue, or other location of interest in a patient. For example, in some embodiments, the DDpp fusion protein specifically binds a target on the surface of an effector cell. Thus, in some embodiments, the DDpp fusion protein specifically binds a target on the surface of a T cell. In specific embodiments, the DDpp fusion protein

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specifically binds CD3. In other embodiments, the DDpp fusion protein specifically binds CD2. In a further embodiment, the DDpp fusion protein specifically binds the T cell receptor (TCR). According to additional embodiments, the DDpp fusion protein specifically binds a target on the surface of a Natural Killer Cell. Thus, in some embodiments, the DDpp fusion protein specifically binds a NKG2D (Natural Killer Group 2D) receptor. In additional embodiments, the DDpp fusion protein specifically binds CD16 (*i.e.*, Fc gamma RIII) CD64 (*i.e.*, Fc gamma RI), or CD32 (*i.e.*, Fc gamma RII).

[0408] In one embodiment, a DDpp fusion protein binds a target on a leukocyte and a tumor antigen on a tumor cell. In some embodiments, the DDpp fusion protein binds NKG2D. In a further embodiment, a DDpp fusion protein binds NKG2D and a target selected from ErbB2, EGFR, IGF1R, CD19, CD20, CD80 and EPCAM. In one embodiment, a DDpp fusion protein binds CD3. In particular embodiments, the DDpp specifically binds CD3 epsilon. In one embodiment, a DDpp fusion protein binds CD4.

DDpp Drug Conjugates

[0409] In a further embodiment a DDpp fusion protein may be linked to other organic or inorganic molecules or substrates through the use of chemically conjugation. In one embodiment, DDpp-drug conjugates are intended to facilitate the local delivery of cytotoxic agents through the targeting specificity of the DDpp. This combination of targeting specificity and cytotoxic agent, allows targeted delivery of the drug to tumors, and intracellular accumulation therein, where systemic administration of these unconjugated drug agents may result in unacceptable levels of toxicity to normal cells as well as the tumor cells sought to be eliminated (Baldwin *et al.*, Lancet pages 603-605 (1986); Thorpe, "Antibody Carriers Of Cytotoxic agents In Cancer Therapy: A Review," in Monoclonal Antibodies '84: Biological And Clinical Applications, A. Pinchera *et al.*, (ed.s), pp. 475-506 (1985)).

[0410] Cytotoxic agents include chemotherapeutic agents, growth inhibitory agents, toxins (*e.g.,* an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), radioactive isotopes (*i.e.*, a radioconjugate), *etc.* Chemotherapeutic agents useful in the generation of such immunoconjugates include, for example, methotrexate, adriamicin, doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents. Chemotherapeutic agents useful in the generation of such immunoconjugates also include antitubulin drugs, such as auristatins, including monomethyl auristatin E (MMAE) and monomethyl auristatin F (MMAF). Enzymatically

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active toxins and fragments thereof that can be used according to the disclosed methods include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain, ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

[0411] In one embodiment, a DDpp (*e.g.,* a DDpp fusion protein) is conjugated to a radioisotope. In a further embodiment, a DDpp is conjugated to an isotope selected from ^{90}Y, ^{125}I, ^{131}I, ^{123}I, ^{111}In, ^{105}Rh, ^{153}Sm, ^{67}Cu, ^{67}Ga, ^{166}Ho, ^{177}Lu, ^{186}Re and ^{188}Re using anyone of a number of known chelators or direct labeling. In other embodiments, the DDpp is coupled to drugs, prodrugs or lymphokines such as interferon. Conjugates of the DDpp and cytotoxin can routinely be made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyidithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis(p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazo-niumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). In a specific embodiment, the toxin is conjugated to a DDpp fusion protein through an enzyme-cleavable linker system (*e.g.,* such as that present in SGN-35). Conjugates of a DDpp and one or more small molecule toxins, such as a calicheamicin, maytansinoids, a trichothene, and CC1065, and the derivatives of these toxins that have toxin activity, can also be used.

[0412] In some embodiments, the cytotoxic agent is covalently attached to a DDpp by a linker. In some embodiments, the linker attaching the DDpp and the cytotoxic agent is cleavable by a protease.

Therapeutic Use as Cell Associated Receptor

[0413] In one embodiment, the disclosed DDpp-CARs are used for the purpose of redirecting transduced T cells to a tumor target defined by the binding specificity of the DDpp-CAR. In one embodiment, primary T cells are transduced with a lentiviral vector encoding a CAR that combines a DD target binding domain with a transmembrane domain and an intracellular domain of CD3-zeta, CD28, 41BB. The resultant population of transduced T cells may therefore elicit a DDpp-CAR-mediated T cell response. In some embodiments, T cells are genetically modified to express DDpp-

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CAR and the DDpp-CAR T cell is infused to a recipient in need thereof. In further embodiments, the infused cell is able to kill tumor cells in the recipient. Particularly advantageous properties of DDpp-CARs include one, several or all of the following benefits: (i) target-binding specificity, (ii) enhanced therapeutic efficacy, (iii) reduced off-target side effects, (iv) customizability for markers of a particular patient or patient population, (v) enhanced stability during production and processing, and (vi) ability to target one, two, or more specific targets to enhance target-directed therapy.

[0414] "Genetically modified cells", "redirected cells", "genetically engineered cells" or "modified cells" as used herein refer to cells that express a DDpp provided herein. In a particular embodiment, the genetically modified cells express a DDpp fusion protein such as a DDpp-CAR. In a further embodiment, the genetically modified cells express and display a DDpp-CAR on the cell surface.

[0415] "Disease targeted by genetically modified cells" as used herein encompasses the targeting of any cell involved in any manner in any disease by the genetically modified cells, irrespective of whether the genetically modified cells target diseased cells or healthy cells to effectuate a therapeutically beneficial result. The genetically modified cells include but are not limited to genetically modified T cells, NK cells, hematopoietic stem cells, pluripotent embryonic stem cells or embryonic stem cells. The genetically modified cells express the DDpp-CAR, which can target any of the antigens expressed on the surface of target cells.

[0416] In one embodiment, the DDpp portion of the DDpp-CAR is designed to treat a particular cancer. Cancers that can be treated include tumors that are not vascularized, or not yet substantially vascularized, as well as vascularized tumors. The cancers can comprise non-solid tumors (such as hematological tumors, for example, leukemias and lymphomas) or can comprise solid tumors. Types of cancers to be treated with the DDpp-CARs include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies *e.g.,* sarcomas, carcinomas, and melanomas. Adult tumors/cancers and pediatric tumors/cancers are also included.

[0417] Examples of hematological (or hematogenous) cancers include leukemias, including acute leukemias (such as acute lymphocytic leukemia, acute myelocytic leukemia, acute myelogenous leukemia and myeloblasts, promyelocytic, myelomonocytic, monocytic and erythroleukemia), chronic leukemias (such as chronic myelocytic (granulocytic) leukemia, chronic myelogenous leukemia, and

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chronic lymphocytic leukemia), polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma (indolent and high grade forms), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia and myelodysplasia.

[0418] Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteosarcoma, and other sarcomas, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, melanoma, and CNS tumors (such as a glioma (such as brainstem glioma and mixed gliomas), glioblastoma (also known as glioblastoma multiforme) astrocytoma, CNS lymphoma, germinoma, medulloblastoma, Schwannoma craniopharyogioma, ependymoma, pineaioma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, neuroblastoma, retinoblastoma and brain metastases).

[0419] In one embodiment, cancers and disorders can be treated using cell expressing DDpp-CAR that target BCMA, CD123, CS1, HER2, AFP, or AFP p26. In one specific embodiment, the DD-CAR can be designed to target CD22 to treat B cell lymphoma. In another embodiment the cell expressing DDpp-CAR contain a DDpp designed to target CD19 can be used to treat cancers and disorders including but are not limited to pre-B ALL (pediatric indication), adult ALL, mantle cell lymphoma, diffuse large B- cell lymphoma, salvage post allogenic bone marrow transplantation, and the like. In another embodiment the cell expressing DDpp-CAR contain a DDpp designed to target CS1 can be used to treat multiple myeloma. In another embodiment the cell expressing DDpp-CAR contain a DDpp designed to target BCMA can be used to treat multiple myeloma. In another embodiment the cell expressing DDpp-CAR contain a DDpp designed to target CS1 and a DDpp designed to target BCMA can be used to treat multiple myeloma. In another embodiment the cell expressing DDpp-CAR contain a DDpp designed to target HER2 can be used to treat breast cancer or ovarian cancer.

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[0420] "B cell associated diseases" as used herein include B cell immunodeficiencies, autoimmune diseases and/or excessive/uncontrolled cell proliferation associated with B cells (including lymphomas and/or leukemias). Examples of such diseases, wherein DDpp-CAR may be used for therapeutic approaches include but are not limited to systemic lupus erythematosus (SLE), diabetes, rheumatoid arthritis (RA), reactive arthritis, multiple sclerosis (MS), pemphigus vulgaris, celiac disease, Crohn's disease, inflammatory bowel disease, ulcerative colitis, autoimmune thyroid disease, X-linked agammaglobulinaemis, pre-B acute lymphoblastic leukemia, systemic lupus erythematosus, common variable immunodeficiency, chronic lymphocytic leukemia, diseases associated with selective IgA deficiency and/or IgG subclass deficiency, B lineage lymphomas (Hodgkin's lymphoma and/or non-Hodgkin's lymphoma), immunodeficiency with thymoma, transient hypogammaglobulinemia and/or hyper IgM syndrome, as well as virally-mediated B cell diseases such as EBV mediated lymphoproliferative disease, and chronic infections in which B cells participate in the pathophysiology.

[0421] In a preferred embodiment, the DDpp-CAR is expressed in a T cell and provides a method for treating or preventing cancer, comprising the administration of host cells expressing DDpp-CAR to a cancer patient in which the cancer cell expresses a tumor antigen on its surface, and wherein the DDpp specifically binds the target antigen. Exemplary target antigens that the DDpp and DDpp-CAR bind include, but are not limited to, BCMA, CS1, HER2, and CD123.

[0422] The DDpp-CAR-modified T cells can also serve as a type of vaccine for *ex vivo* immunization and/or *in vivo* therapy in a mammal. Preferably, the mammal is a human.

[0423] The DDpp-CAR-modified T cells provided herein can be administered either alone, or as a pharmaceutical composition in combination with diluents and/or with other components such as chemotherapeutics, antibodies, cytokines or cell populations. Compositions provided herein are preferably formulated for intravenous administration that can be administered one or more times.

[0424] "Antigen loss escape variants" as used herein refer to cells which exhibit reduced or loss of expression of the target antigen, which antigens are targeted by a CAR provided herein.

[0425] Various embodiments, of the disclosure will now be illustrated through the description of experiments conducted in accordance therewith. The examples that follow are provided to facilitate the practice of the disclosed embodiments, and are not to be construed as limiting in any way the remainder of the disclosure. In the examples, reference is made to the appended figures.

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EXAMPLES

Example 1. Isolation and Characterization of DDpp that bind exemplary targets of interest

[0426] A DDpp library prepared as described in Intl. Appl. Publ. Nos. WO2016164305 and WO 2016164369, was screened for phage the bind BCMA, CD123, AFP, or AFP p26 through multiple rounds of selection. The contents of each of Intl. Appl. Publ. Nos. WO2016164305 and WO 2016164369, is herein incorporated by reference in its entirety).

[0427] Individual colonies containing phagemid from BCMA panning output were picked and phage were rescued in 96-well format using VCSM13 helper phage following standard protocols. To assay target binding by ELISA, 96-well plates were coated with 1.3 microg/ml goat anti-human IgG1-Fc antibody followed by incubation with 5 nM of recombinant human target (BCMA-Fc, CD123-Fc, AFP, or AFP123) or IgG1-Fc. 50 microl of rescued phage diluted 5x in ELISA blocking buffer was then added to each well. Binding was detected using an HRP-conjugated anti-M13 antibody and the ELISA ratio for each sequence is reported as the absorbance at 450 nm for target (*i.e.*, BCMA-Fc, CD123-Fc, AFP, or AFP123) divided by that for IgG1-Fc averaged across all screened wells containing that clone.

Example 2. DDpp Fusion Proteins

[0428] To assess the modular nature of DDpp as a binding element, the DDpp CD137-binder, bb10 (SEQ ID NO: 876), was reformatted as a fusion to either the N or C terminus of the heavy chain of an antibody derived from the sequence of the RSV-specific monoclonal antibody palivizumab (SYNAGIS®). Bi-specific antibodies, SYN-bb10 and bb10-SYN exhibit binding to both CD137 and RSV (FIGS. 1A-1B; closed squares are bb10-SYN, closed circles are SYN-bb10)), demonstrating that a novel binding activity was imparted to the parental D domain sequence and the functionality of DDpp is retained as both N and C-terminal fusion. In contrast, fusions between a target-less alpha-helical protein scaffold (SEQ ID NO: 1) and SYN (DD-SYN for N-terminal fusion, open circles; SYN-DD for C-terminal fusion, open squares) showed binding only to RSV, but no binding to CD137.

[0429] Binding of DDpp, bb10 to CD137 directly bound to plastic was demonstrated using ELISA (FIGS. 1A-1B). Binding of DDpp bb10 to CD137 as part of a cell membrane was also observed *in situ*, using FACS (data not shown)

Example 3. DDpp-CARs Expressed in Human T Cells Produce Cytokines on Target Binding

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[0430] The ability of target: DDpp-CAR-expressing T cell engagement to result induce cytokine secretion was assessed by 293T cells were transiently transfecting 293T cells with 3rd generation lentiviral packaging vectors (pRSV-REV, pMDLg/pRRE, and pMD2.G) with pELNS vectors encoding DDpp-CARs using LIPOFECTAMINE® 3000. Six hours post-transfection the media was changed, then lentivirus containing media was collected at 30 and 54 hours post-transfection, pooled, then centrifuged to remove cell debris. Lentivirus was then aliquoted and stored at -80°C until used for viral transduction. Transduction of human T cells with CAR lentivirus was performed using total human PBMCs, activated with αCD3/CD28 T cell activation beads in culture media supplemented with 40U/ml of IL2. After 24 hours, 2 x 10^6 PBMCs were plated per well in a 6-well tissue culture plate with 1ml of culture media and 3ml of lentivirus containing media supplemented with 40U/ml of IL2 and protamine sulfate. Plates were then centrifuged for 2 hours at 1000×g at 32°C and then incubated overnight 37°C. The following day the lentivirus transduction procedure was repeated with fresh culture media and lentivirus-containing media. 72 hours after the initial cell activation, T cell activation beads were removed, then T cells were cultured for expansion at ~0.25-0.5×10^6 T cells/ml in fresh media supplemented with 100U/ml of IL2. Every 2-3 days T cells were supplemented with additional T cell media and IL2, until they were used for the cytokine assays (described below) 7-10 days after the initial activation.

[0431] Cytokine production in response to target antigen expression (CD123) was assessed by culturing 25,000 transduced T cells (7 days post-activation) with 25,000 non-target (K562, $CD123^-$) or target (BDCM, $CD123^+$) tumor cells per well in 96-well plates. After 24 hours culture supernatants were collected and cytokine production was assessed by ELISA. Culture supernatants were diluted 1: 5 prior to ELISA. Similarly, cytokine production in response to PDL1 target antigen expression was assessed by culturing 25,000 transduced T cells (7-days post activation) with 25,000 non-target (K562, $PDL1^-$) or target (SUDHL1, $PDL1^+$) tumor cells per well in 96-well plates. After 24 hours culture supernatants were collected and cytokine production was assessed by ELISA. Culture supernatants were diluted 1: 5 prior to ELISA.

[0432] FIG. 2A and FIG. 2B demonstrate that T cells expressing CD123 binding DDpp-CARs produce interferon gamma (IFNγ) following stimulation with $CD123^+$ BDCM cells, but not the $CD123^-$ cell line K562. FIG. 2C and FIG. 2D demonstrates that T cells expressing CD123 binding DDpp-CARs produce interleukin 2 (IL2) following stimulation with $CD123^+$ BDCM cells, but not the

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$CD123^-$ cell line K562. Similarly, FIG. 2E and 2F demonstrate that T cells expressing PDL1 binding DDpp-CARs produce interferon gamma (IFNγ) and IL2 respectively following stimulation with $PDL1^+$ SUDHL1 cells but not the $PDL1^-$ cell line K562.

Example 4. DDpp-CAR Transduced T Cells Do Not Display Phenotypes Associated with T Cell Exhaustion

[0433] To assess potential antigen-independent exhaustion in T cells expressing DDpp-CARs, transduced T cells (day 10 post-activation) were stained with antibodies against CD3 and markers of T cell exhaustion (LAG3, PD1, and TIM3). FIG. 3A summarizes data from individual experiments across several T cell donors. The data demonstrate that expression of the exhaustion markers was not enhanced in CD123-binding DDpp-CAR T cells over that observed with the anti-CD123 CAR comprising the scFv (32176). FIG. 3B shows representative flow cytometry data of LAG3, PD1, and TIM3 expression in T cells transduced with either a scFv-containing CAR (top row) or a DDpp-CAR (in this particular experiment CD123 targeting cg06) 10 days after the initial activation of the T cells. The similarity of these data again demonstrate that DDpp-CAR T cells do not upregulate expression of exhaustion markers, which lends further support to their efficacy in cancer immunotherapy.

Example 5. DDpp-CAR Expressing T Cells Exhibit Target-specific Degranulation and Tumor Cytotoxicity

[0434] To assess degranulation of T cells expressing DDpp-CARs, 1×10^5 transduced T cells (day 9 post-activation) were cultured in T cell media for 4 hours in the presence of monensin and PE-conjugated CD107a/LAMP1. T cells were cultured alone (FIG. 4A) or in the presence of 2×10^5 non-target tumor cells (K562, which are $CD123^-$, FIG. 4B or target-expressing tumor cells (BDCM, $CD123^+$, FIG. 4C), then washed and stained for CD3 expression. T cell degranulation was then assessed by flow cytometry, first gating on the CD3+SSC-low cells (non-tumor), then the CD3+CD107a+ cells. Symbols represent samples from individual experiments using multiple donors.

[0435] The production of CD107a (a marker of degranulation of the DDpp-CAR T cells) was equivalent to negative controls when CD123-targeting DDpp-CAR T cells were cultured alone. Limited CD107a expression when DDpp-CAR T cells were co-cultured with CD123 negative K562 tumor cells and significant CD107a expression was observed when CD123-targeting DDpp-CAR T cells were co-cultured with CD123 positive BDCM cells (data not shown). These data indicate that the T cells are activated, undergoing signaling, undergoing degranulation, and will result in tumor

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eradication. These data also provide further support for the target-dependent activation of DDpp-CAR expressing T cells.

[0436] The cytolytic activity of DDpp-CAR T cells was assessed using T cells prepared from two independent donors. Donor #1 (FIG. 5A-5B) DDpp-CAR T cells effectively kill the CD123 expressing tumor, BDCM, but show very little cytolytic activity on the CD123 negative tumor, K562. Similar results were observed with Donor #2 (FIG. 5C and 5D).

Example 6. Bi-specific DDpp

[0437] As discussed above, DDpp can be monovalent or multivalent and/or multispecific. To evaluate the ability of multispecific DDppCAR T cells to elicit an immune response, bi-specific DDpp-CARs were expressed on Jurkat cells and intracellular signaling in response to tumor cells expressing one or both targets was measured. Two bi-specific DDppCARs were constructed that differed in the fusion order of the binding domains. CG06-pb04 has the pb04 domain fused to the CD8a transmembrane region while the pb04-cg06 has the cgo6 domain fused to the CD8a transmembrane region. Both constructs utilized a GS linker between the target-binding domains.

[0438] FIG. 6A demonstrates that DDpp-CARs comprising cg06 only, , pb04 only (FIG. 6B),cg06-pb04, (FIG. 5C), and pb04-cg06 (FIG. 5D) can be transduced and expressed in the Jurkat NFAT reporter cell line as assessed by anti-FLAG mAb binding to the CARs. The ability of the mono-specific and bi-specific CARs to activate the NFAT pathway was assessed by co-culturing the various CARs with tumor cells with different level of CD123 and/or PDL1 expression. Cells were co-cultured with target cells for 6 hours. NFAT mediated signaling was measured through the addition to the cells of luciferase assay reagent (Promega) and quantitation of relative luminescence units (RLU) as a measure of induced intracellular signaling.

[0439] FIG. 6E depicts the results of this experiment. The leftmost group of bars and the histogram show the relative kill effect of the cg06 DDpp against various cell types. Signaling response after co-culture with highly CD123+ BDCM was the greatest with this DDpp-CAR. The next group to the right depicts data showing intracellular signaling after co-culture of the pb04 DDpp against the same cell types. Signaling was highest in BDCM, followed by SUHDL1, and H460 (these are the highest expressing cell lines for CD123 and PDL1 (data not shown)). The next group to the right depicts data showing intracellular signaling of a bi-specific cg06-pb04 DDpp (cg06 more distal to the T cell membrane as compared to pb04). Finally, the rightmost group shows intracellular signaling

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from a second bi-specific DBPpp (pb04-cg06 DDpp, where pb04 is more distal to the T cell membrane as compared to cg06). These two groups indicate that bi-specific DDpp-CARs do function to promote intracellular signaling. In accordance with embodiments, bi-specific DDpp-CARs show enhanced activity (the magnitude of intracellular signaling in the pb04-cg06 group with BDCM cells is greater than can be accounted for by just the pb04 DDpp alone). Thus in some embodiments, DDpp-CARs comprising two DDpps can cooperate to enhance T cell function. In some embodiments, there is a synergy between the various DDpp used in a bispecific (or other multimeric) DDpp-CAR.

Example 7. Use of dual binding domain Adapters to enhance CAR signalling

[0440] 50,000 reporter cells previously transduced with an AFP (p26 domain)-binding CAR (af03) (SEQ ID NO: 961) were cultured for 5 hours in the presence of the CD123-specific Cg06-adaptor (Cg06-p26, SEQ ID NO: 953) or the Cg06-dual adaptor protein (Cg06-p26-Cg06, SEQ ID NO: 956)in the presence of 50,000 $CD123^+$ MOLM13 or CD123-deficient MOLM13 cells, then assessed for luciferase activity. CD123 deficient cells were generated using CRISPR/Cas9 genetic engineering technology (FIG. 7A). Similarly, 50,000 reporter cells previously transduced with an AFP (p26 domain)-binding CAR (af03) (SEQ ID NO: 961) were cultured for 5 hours in the presence of the BCMA-specific Bc40-adaptor (Bc40-p26, SEQ ID NO: 954) or the Bc40-dual adaptor protein (Bc40-p26-Bc40, SEQ ID NO: 957) in the presence or absence of 50,000 $BCMA^+$ U266 cells, then assessed for luciferase activity (FIG. 7B).

[0441] FIGS. 7A and 7B show that dual-binding (bi-valent) domain adaptor proteins drive enhanced signaling by CAR-expressing Jurkat cells over single-binding domain adaptor proteins.

Example 8. DDpp-mediated Tumor Immunotherapy in vivo

[0442] To assess the *in vivo* anti-tumor activity of a DDpp CAR, T cells were transduced with bc40 DDpp CAR (BCMA targeting CAR). Bc40 is SEQ ID NO: 164. Transduced cells (5X10E6) were administered intravenously to NSG mice 34 days after mice received 10E7 cells of the BCMA expressing, luciferase/gfp labeled U226 tumor cells. As shown in FIG. 8, four mice received the U226 tumor on Day 0 which progressive grew through Day32. On Day 34, mouse #1, #2, and #4 received bc40-DDpp CAR T cells. Mouse #3 received no T cells. On Day 45, the U226 tumor was cleared in mice receiving CAR T cells while the mouse that did not receive T cells died of tumor burden.

[0443] All publications, patents, patent applications, internet sites, and accession numbers/database sequences (including both polynucleotide and polypeptide sequences) cited are

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herein incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, internet site, or accession number/database sequence were specifically and individually indicated to be so incorporated by reference.

[0444] It is contemplated that various combinations or subcombinations of the specific features and aspects disclosed above may be made and still fall within the embodiments, encompassed by the disclosure. Further, the disclosure of any particular feature, aspect, method, property, characteristic, quality, attribute, element, or the like in connection with an embodiment can be used in all other embodiments, set forth herein. Accordingly, it should be understood that various features and aspects of the disclosed embodiments, can be combined with or substituted for one another in order to form varying modes of the disclosed embodiments. Thus, it is intended that the scope of the embodiments, encompassed by the present disclosure should not be limited by the particular disclosed embodiments, described herein. Moreover, while the encompassed embodiments, are susceptible to various modifications, and alternative forms, specific examples thereof have been shown in the drawings and are herein described in detail. It should be understood, however, that the scope of the disclosure is not to be limited to the particular forms or methods disclosed, but to the contrary, the disclosure is to cover all modifications, equivalents, and alternatives falling within the spirit and scope of the various embodiments, described and the appended claims. Any methods disclosed herein need not be performed in the order recited. The methods disclosed herein include certain actions taken by a practitioner; however, they can also include any third-party instruction of those actions, either expressly or by implication. For example, actions such as "administering a T cell comprising a DDpp-CAR" include "instructing the administration of a T cell comprising a DDpp-CAR." In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[0445] The ranges disclosed herein also encompass any and all overlap, sub-ranges, and combinations thereof. Language such as "up to," "at least," "greater than," "less than," "between," and the like includes the number recited. Numbers preceded by a term such as "about" or "approximately" include the recited numbers. For example, "about 10 nanometers" includes "10 nanometers."

TABLE 2: Additional sequence disclosure:

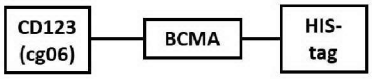
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SEQ ID:	Target	Sequence
1	D Domain (target-less)	MGSWAEFKQRLAAIKTRLQALGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEALRKEAAAIRDEL QAYRHN
2	MHC Epitope	LAAIKTRLQ
3	CD19	LEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSEL MAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEK CCQGQEQEVCFAEEGQKLISKTRAALGV
4	GlySer	GGGGTGGGGS
5	GlySer	GGGGDGGGGS
6	a3D(Q19E) Targetless	MGSWAEFKQRLAAIKTRLEALGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEALRKEAAAIRDEL QAYRHN
7	BCMA ECD	MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA
8	CD123 ECD	TKEDPNPPITNLRMKAKAQQLTWDLNRNVTDIECVKDADYSMPAVNNSYCQFGAISLCEVTNYTVRV ANPPFSTWILFPENSGKPWAGAENLTCWIHDVDFLSCSWAVGPGAPADVQYDLYLNVANRRQQYECL HYKTDAQGTRIGCRFDDISRLSSGSQSSHILVRGRSAAFGIPCTDKFVVFSQIEILTPPNMTAKCNK THSFMHWKMRSHFNRKFRYELQIQKRMQPVITEQVRDRTSFQLLNPGTYTVQIRARERVYEFLSAWS TPQRFECDQEEGANTRAWR
9	AFP	RTLHRNEYGIASILDSYQCTAEISLADLATIFFAQFVQEATYKEVSKMVKDALTAIEKPTGDEQSSG CLENQLPAFLEELCHEKEILEKYGHSDCCSQSEEGRHNCFLAHKKPTPASIPLFQVPEPVTSCEAYE EDRETFMNKFIYEIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVECFQTKAATVTKELRESSLL NQHACAVMKNFGTRTFQAITVTKLSQKFTKVNFTEIQKLVLDVAHVHEHCCRGDVLDCLQDGEKIMS YICSQQDTLSNKITECCKLTTLERGQCIIHAENDEKPEGLSPNLNRFLGDRDFNQFSSGEKNIFLAS FVHEYSRRHPQLAVSVILRVAKGYQELLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQ KLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIR HEMTPVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLI NLVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLISKTRAALGV
10	AFP p26	LEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSEL MAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEK CCQGQEQEVCFAEEGQKLISKTRAALGV
968	P26Q217P	LEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAP QLTSSELMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQC CTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQK PQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGPKLISKTRAALGV
969	P26(Q26-V229)	QESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLS EDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPA FSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEKCCQG QEQEVCFAEEGQKLISKTRAALGV
970	P26(Q26-V229) Q217P	QESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLS EDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPA FSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEKCCQG QEQEVCFAEEGPKLISKTRAALGV
971	p26(K23-V229)	KYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCC QLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLVVDETYV PPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEKC CQGQEQEVCFAEEGQKLISKTRAALGV
972	p26(K23-V229) Q217P	KYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCC QLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLVVDETYV PPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEKC CQGQEQEVCFAEEGPKLISKTRAALGV

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973	p26(G17-V229)	GEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAA TAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLV VDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFS GLLEKCCQGQEQEVCFAEEGQKLISKTRAALGV
974	p26(G17-V229) Q217P	GEEELQKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAA TAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRRPCFSSLV VDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFS GLLEKCCQGQEQEVCFAEEGPKLISKTRAALGV
963	CD22 mature ECD	DSSKWVFEHPETLYAWEGACVWIPCTYRALDGDLESFILFHNPEYNKNTSKFDGTRLYESTKDGKVP SEQKRVQFLGDKNKNCTLSIHPVHLNDSGQLGLRMESKTEKWMERIHLNVSERPFPPHIQLPPEIQE SQEVTLTCLLNFSCYGYPIQLQWLLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKIVTCQ LQDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTTVSWLKDGTSLK KQNTFTLNLREVTKDQSGKYCCQVSNDVGPGRSEEVFLQVQYAPEPSTVQILHSPAVEGSQVEFLCM SLANPLPTNYTWYHNGKEMQGRTEEKVHIPKILPWHAGTYSCVAENILGTGQRGPGAELDVQYPPKK VTTVIQNPMPIREGDTVTLSCNYNSSNPSVTRYEWKPHGAWEEPSLGVLKIQNVGWDNTTIACAACN SWCSWASPVALNVQYAPRDVRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEKNGRLLGKESQ LNFDSISPEDAGSYSCWVNNSIGQTASKAWTLEVLYAPRRLRVSMSPGDQVMEGKSATLTCESDANP PVSHYTWFDWNNQSLPYHSQKLRLEPVKVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETIGRR
965	CS1 mature ECD	SGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIVTQNRNRERVDFPDGGYS LKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHG EEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPD SSM
967	HER2 mature ECD	TQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHN QVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQ RNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGG CARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT FGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVT SANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSV FQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQ ALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNAR HCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQP CPINCTHSCVDLDDKGCPAEQRASPLT

TABLE: 3 Exemplary Adapters

SEQ ID NO:	Adapter Design	Adapter Sequence
951		DEMGSWDEFGRRLYAIEWRLYALGGSEAELAAFEKEIAAFESE LQAYKGKGNPEVEKLREIAAVIRSNLQAYRHNGGGGSGGGGSG GGGSGMLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ RYCNASVTNSVKGTNAGGGGSGGGGSGGGGSHHHHHHHHHH
952		DEGGGGSMGSWAEFKQRLAAIKTRLQALGGSEAELAAFEKEIAAF ESELQAYKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGS GGGGSGMLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQR YCNASVTNSVKGTNAGGGGSGGGGSGGGGSHHHHHHHHHH

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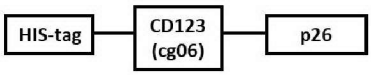
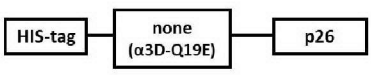
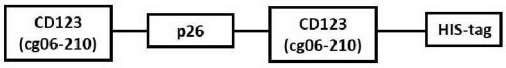
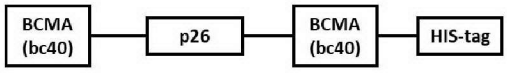
953		DEHHHHHHHHHHKLENLYFQGGGGGSMGSWDEFGRRLYAIEWRLY ALGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEKLREIAAVIR SNLQAYRHNGGGGSGGGGSGGGGSLEKCFQTENPLECQDKGEEEL QKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSE LMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMT PVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKD LCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEK CCQGQEQEVCFAEEGQKLISKTRAALGV
954		DEHHHHHHHHHHKLENLYFQGGGGGSMGSWSEFWVRLGAIRERLD ALGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEKLRYTAATIR RFLQAYRHNGGGGSGGGGSGGGGSLEKCFQTENPLECQDKGEEEL QKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSE LMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMT PVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKD LCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEK CCQGQEQEVCFAEEGQKLISKTRAALGV
955		DEHHHHHHHHHHKLENLYFQGGGGGSMGSWAEFKQRLAAIKTRLE ALGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEALRKEAAAIR DELQAYRHNGGGGSGGGGSGGGGSLEKCFQTENPLECQDKGEEEL QKYIQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSE LMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEMT PVNPGVGQCCTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKD LCQAQGVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGLLEK CCQGQEQEVCFAEEGQKLISKTRAALGV
956		DEGGGGSMGSWDEFGRRLYAIEWQLYALGGTEAELAAFEKEIAAF ESELQAYKGKGNPEVEKLREIAAVIRENLQAYRHNGGGGSGGGGS GGGGSGLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLF QKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQL SEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRR PCFSSLVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLI NLVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKL ISKTRAALGVGGGGSGGGGSGGGGSMGSWDEFGRRLYAIEWQLYA LGGTEAELAAFEKEIAAFESELQAYKGKGNPEVEKLREIAAVIRE NLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH
957		DEGGGGSMGSWSEFWVRLGAIRERLDALGGSEAELAAFEKEIAAF ESELQAYKGKGNPEVEKLRYTAATIRRFLQAYRHNGGGGSGGGGS GGGGSGLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLF QKLGEYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQL SEDKLLACGEGAADIIIGHLCIRHEMTPVNPGVGQCCTSSYANRR PCFSSLVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLI NLVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKL ISKTRAALGVGGGGSGGGGSGGGGSMGSWSEFWVRLGAIRERLDA LGGSEAELAAFEKEIAAFESELQAYKGKGNPEVEKLRYTAATIRR FLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH

TABLE: 4 Exemplary ADBD CAR Sequences

SEQ ID NO:	CAR Design	CAR Sequence
958	CTsp-Flag- GSlinker-α3D(Q19E)-GSlinker-CD8H-TM-41BB-CD3ζ	MAFLWLLSCWALLGTTFGDYKDDDDKGGGGSGGGGSMGSWAEF KQRLAAIKTRLEALGGSEAELAAFEKEIAAFESELQAYKGKGN PEVEALRKEAAAIRDELQAYRHNGQAGSGTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCG VLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIG MKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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959	CTsp-Flag- GSlinker-cg06-GSlinker-CD8H-TM-41BB-CD3ζ	MAFLWLLSCWALLGTTFGDYKDDDDKGGGGSGGGGSMGSWDEF GRRLYAIEWRLYALGGSEAELAAFEKEIAAFESELQAYKGKGN PEVEKLREIAAVIRSNLQAYRHNGGGGSGGGGSGTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
960	CTsp-Flag- GSlinker-bc40-GSlinker-CD8H-TM-41BB-CD3ζ	MAFLWLLSCWALLGTTFGDYKDDDDKGGGGSGGGGSMGSWSEF WVRLGAIRERLDALGGSEAELAAFEKEIAAFESELQAYKGKGN PEVEKLRYTAATIRRFLQAYRHNGGGGSGGGGSGTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
961	CTsp-Flag- GSlinker-af03-GSlinker-CD8H-TM-41BB-CD3ζ	MAFLWLLSCWALLGTTFGDYKDDDDKGGGGSGGGGSMGSWFEF YDRLNAIDARLWALGGSEAELAAFEKEIAAFESELQAYKGKGN PEVENLRVHAAAIREWLQAYRHNGGGGSGGGGSGTTTPAPRPP TPAPTIASMGSWAEFKQRLAAIKTRLEALGGSEAELAAFEKEI AAFESELQAYKGKGNPEVEALRKEAAAIRDELQAYRHNQPLSL RPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
962	CTsp-Flag- GSlinker-af05-GSlinker-CD8H-TM-41BB-CD3ζ	MAFLWLLSCWALLGTTFGDYKDDDDKGGGGSGGGGSMGSWLEF YHRLNAIDSRLWALGGSEAELAAFEKEIAAFESELQAYKGKGN PEVESLRDHAAHIREWLQAYRHNGGGGSGGGGSGTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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CLAIMS:

1. A protein comprising a D Domain (DD) target binding domain wherein the DD specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168.

2. The protein of claim 1, wherein the DD target binding domain comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 168.

3. The protein of claim 2, wherein the DD target binding domain comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 168.

4. The protein of claim 1, wherein the DD target binding domain comprises the amino acid sequence of any one of SEQ ID NOS: 47, 54, 56, 66, 78, 100, 107, 144, 149-175, 177-179, 186-188, and 190.

5. The protein of claim 1, wherein the DD target binding domain comprises the amino acid sequence of SEQ ID NO: 168.

6. The protein of any one of claims 1 to 5 wherein the DD is fused to a heterologous polypeptide.

7. The protein of claim 6, wherein the heterologous polypeptide comprises
   (a) a full-length antibody or an antibody fragment;
   (b) an Fc region;
   (c) the extracellular domain, or a fragment of an extracellular domain, of a receptor selected from the group consisting of: BCMA, CD123, CS1, and CD19;
   (d) a transmembrane domain;
   (e) a membrane associating domain;
   (f) human serum albumin or a fragment thereof;

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(g) AFP or a fragment thereof;

(h) AFP p26 or a fragment thereof; and/or

(i) the extracellular domain of a receptor or a fragment thereof.

8. The protein of claim 7, wherein the heterologous polypeptide comprises AFP p26, and wherein the AFP p26 consists of the amino acid sequence of SEQ ID NO: 10, 968, 969, 970, 971, 972, 973, or 974.

9. The protein according to claim 8, wherein the AFP p26 consists of the amino acid sequence of SEQ ID NO: 969.

10. The protein of any one of claims 7-9, wherein the DD is fused to AFP p26 through a linker.

11. The protein according to any one of claims 1-10, which is labeled and/or conjugated to a therapeutic or cytotoxic agent, wherein optionally the label is selected from the group consisting of an enzymatic label, a fluorescent label, a luminescent label, a bioluminescent label and a biotin moiety.

12. A chimeric antigen receptor (CAR) which comprises a target binding domain comprising the protein according to any one of claims 1-10.

13. The CAR of claim 12, which comprises, a target binding domain, a transmembrane domain, and an intracellular signaling domain, and optionally wherein

(a) the transmembrane domain comprises a CD8, 41BB or CD28 transmembrane domain;

(b) the intracellular signaling domain is selected from the group consisting of a domain of a human T cell receptor alpha, beta, or zeta chain; a human 41BB domain; a human CD28 domain; and any combination thereof; and/or

(c) the intracellular signaling domain comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4lBB,

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OX40, CD30, CD40, PD1, lymphocyte function-associated antigen- 1 (LFA-1), CD2, CD7, LIGHT, NKG2C, NKG2D, B7-H3, a ligand that specifically binds with CD83, and any combination thereof.

14. The protein according to any one of claims 1-11 or the CAR according to claim 12 or claim 13, which further comprises a second target binding domain having the same or a different target than the DD target binding domain.

15. An isolated nucleic acid encoding the protein according to any one of claims 1-11 and 14 or the CAR according to any one of claims 12-14.

16. A vector comprising the nucleic acid of claim 15, wherein optionally the nucleic acid is operably linked with a nucleotide sequence which regulates the expression of the protein encoded by the nucleic acid, wherein optionally the vector is a lentiviral vector.

17. A host cell comprising the nucleic acid according to claim 15 or the vector according to claim 16, wherein optionally the cell is a T cell or a natural killer (NK) cell.

18. A pharmaceutical composition comprising the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, or the cell according to claim 17.

19. A kit comprising the protein according to any one of claims 1-11 and 14 or the CAR according to any one of claims 12-14.

20. Use of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18 in the manufacture of a medicament for the treatment of cancer.

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21. A method of treating cancer in a subject comprising administering a therapeutically effective amount of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18.

22. The use of claim 20 or the method of claim 21, wherein
    (a) the cancer is a B cell malignancy selected from the group consisting of: a lymphoma (*e.g.,* a Hodgkin's lymphoma and non-Hodgkin's lymphoma (NHL), a leukemia, a plasmacytoma and a myeloma);
    (b) the cancer is a B cell malignancy is selected from the group consisting of: chronic lymphocytic leukaemia, follicular lymphoma, mantle cell lymphoma, and diffuse large B-cell lymphoma, plasmacytoma and multiple myeloma; and/or
    (c) the cancer is a myeloid malignancy selected from the group consisting of: chronic myeloid leukemia, acute myeloid leukemia, leukemia, plasmacytoma and myeloma.

23. Use of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18 in the manufacture of a medicament for the treatment of a B cell associated disorder (*e.g.,* monoclonal gammopathy of undetermined significance (MGUS)).

24. A method of treating a subject having a B cell associated disorder (*e.g.,* monoclonal gammopathy of undetermined significance (MGUS)), comprising administering to the subject a therapeutically effective amount of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18.

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25. Use of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18 or the method of claim 21, in the manufacture of a medicament for the treatment of a disorder of the immune system.

26. A method of treating a subject having a disorder of the immune system, comprising administering to the subject a therapeutically effective amount of the protein according to any one of claims 1-11 and 14, the CAR according to any one of claims 12-14, the nucleic acid of claim 15, the vector of claim 16, the cell according to claim 17, or the pharmaceutical composition according to claim 18.

27. The use of claim 25 or the method of claim 26, wherein the disorder of the immune system is an autoimmune disease, wherein the autoimmune disease is optionally rheumatoid arthritis.

28. Use of an immune cell comprising a chimeric antigen receptor (CAR) in the manufacture of a medicament for the treatment of cancer, wherein the CAR comprises:

a) a target binding domain comprising a DD that specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168;

b) a transmembrane domain and an intracellular domain; wherein the intracellular domain comprises a signaling domain, and

wherein, upon administration to a subject, the target binding domain specifically binds to the target of interest expressed by a cancer cell, and

wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell.

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29. A method of treating cancer in a subject comprising administering an immune cell comprising a chimeric antigen receptor (CAR) to the subject, wherein the CAR comprises:

a) a target binding domain comprising a DD that specifically binds BCMA and comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 168;

b) a transmembrane domain and an intracellular domain; wherein the intracellular domain comprises a signaling domain, and

wherein, upon administration to a subject, the target binding domain specifically binds to the target of interest expressed by a cancer cell, and

wherein the binding of the target of interest induces the immune cell to generate cytotoxic signals that result in cytotoxic effects on the cancer cell.

30. The use of claim 29 or the method of claim 30, wherein the immune cell is a T cell or an NK cell.

31. The use of any one of claims 20, 22, 23, 25, 27, or 28, wherein the medicament is formulated for intravenous administration.

32. The use of any one of claims 20, 22, 23, 25, 27, or 28, wherein the medicament is formulated for subcutaneous administration.

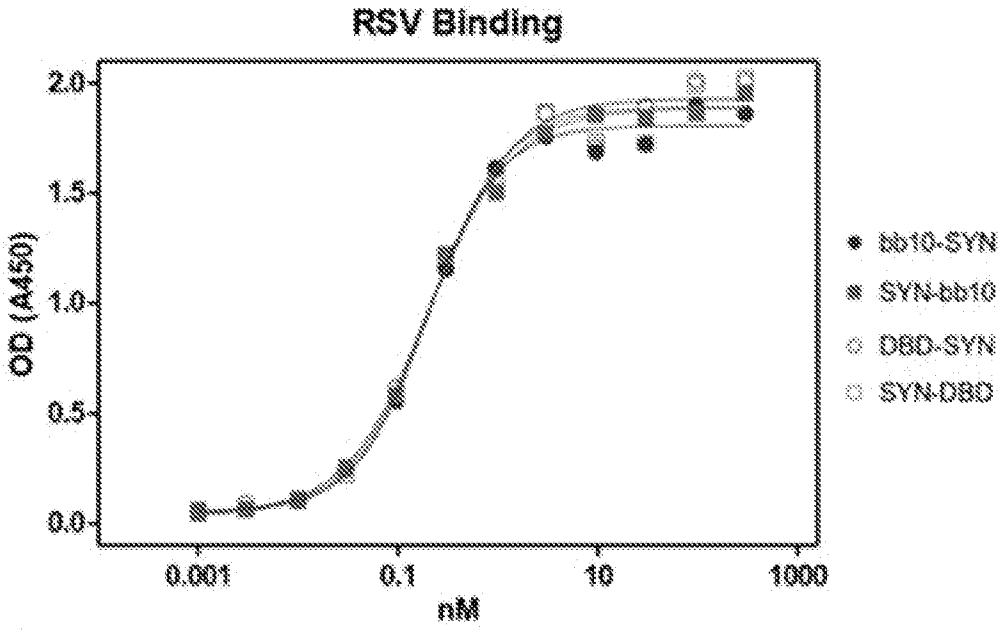

RSV Binding
OD (A450)
2.0
1.5
1.0
0.5
0.0
0.001
0.1
10
1000
nM
bb10-SYN
SYN-bb10
DBD-SYN
SYN-DBD

FIG. 1A

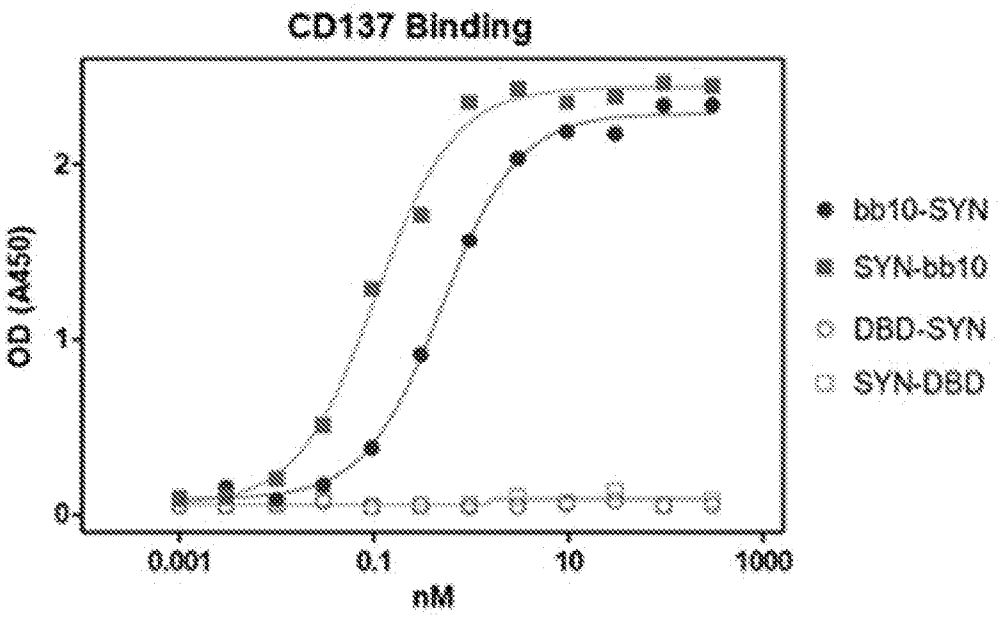

CD137 Binding
OD (A450)
2
1
0
0.001
0.1
10
1000
nM
bb10-SYN
SYN-bb10
DBD-SYN
SYN-DBD

FIG. 1B

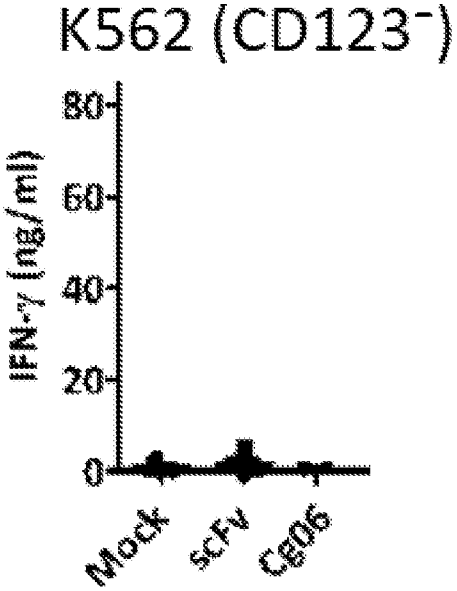


FIG. 2A

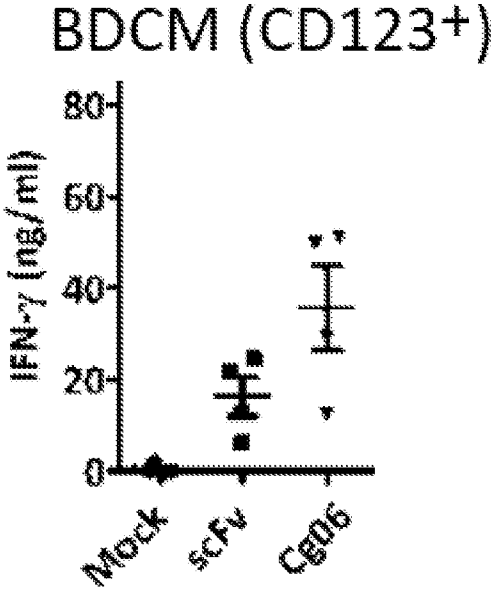


FIG. 2B

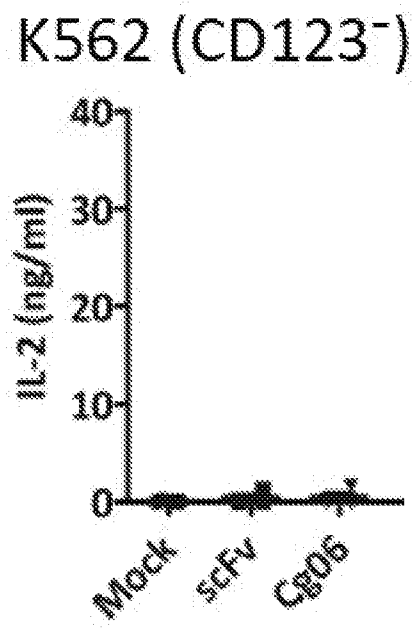


FIG. 2C

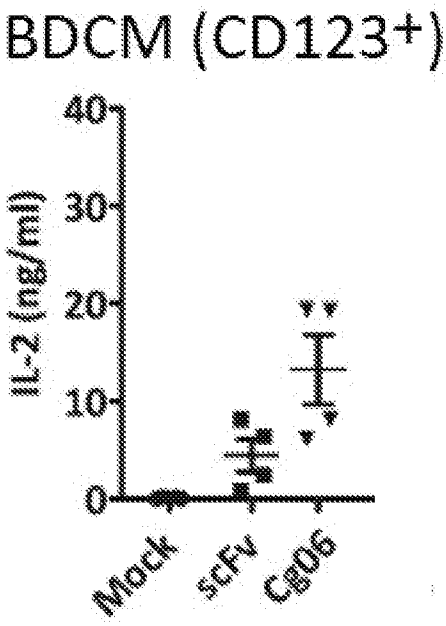


FIG. 2D

FIG. 2E

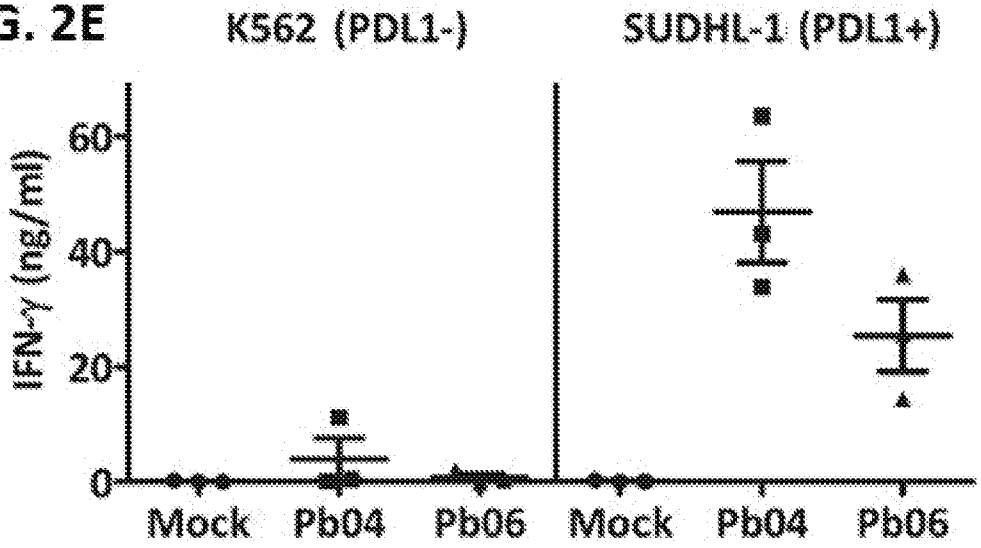

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SUDHL-1 (PDL1+)
IFN-γ (ng/ml)
60
40
20
0
Mock
Pb04
Pb06
Mock
Pb04
Pb06

FIG. 2F

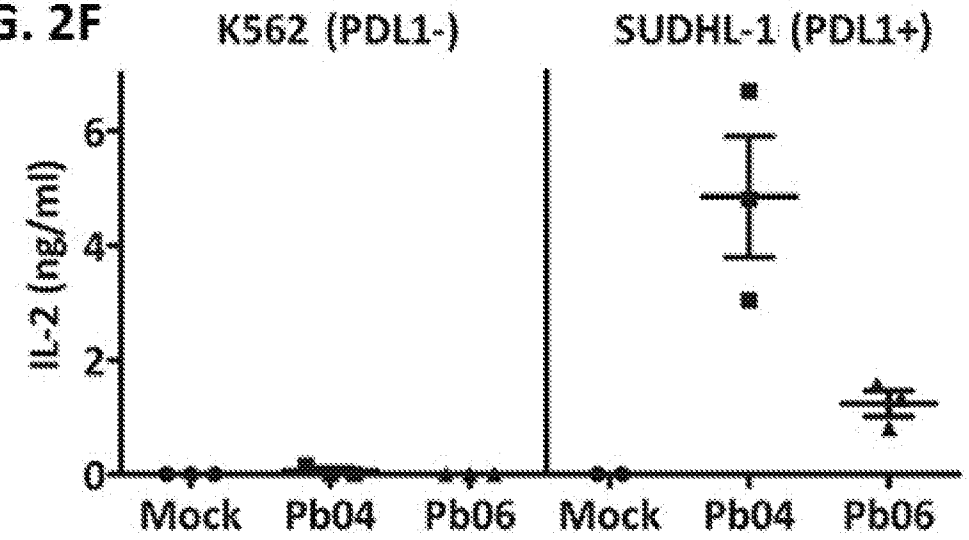

K562 (PDL1-)
SUDHL-1 (PDL1+)
IL-2 (ng/ml)
6
4
2
0
Mock
Pb04
Pb06
Mock
Pb04
Pb06

FIG. 3A

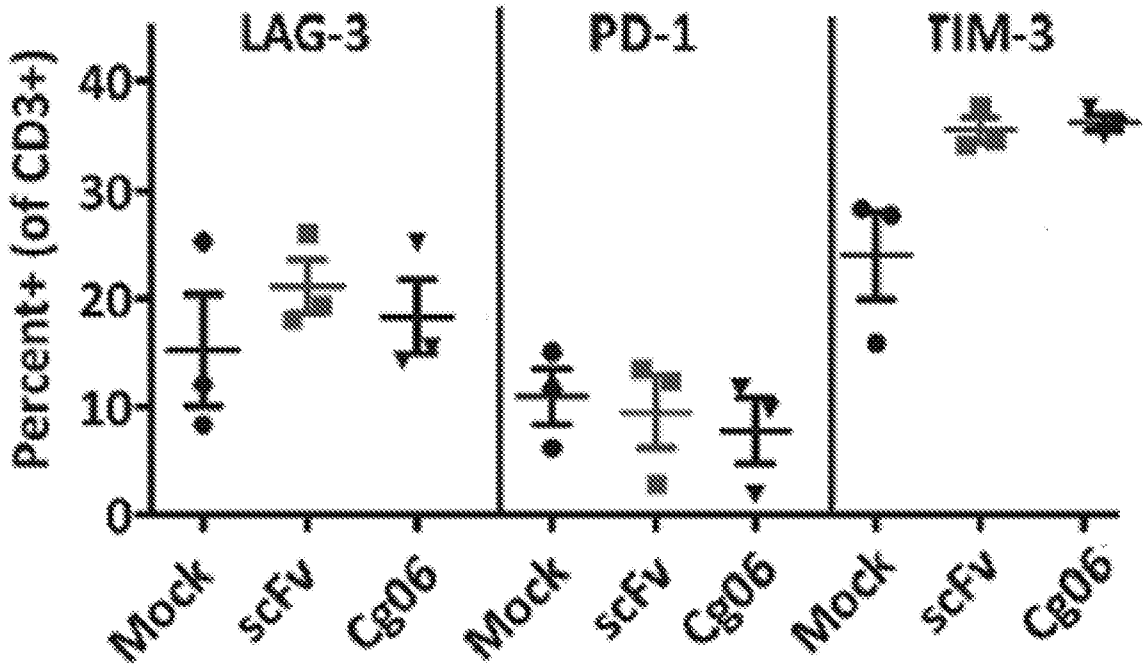

LAG-3
PD-1
TIM-3
Percent+ (of CD3+)
0
10
20
30
40
Mock
scFv
Cg06
Mock
scFv
Cg06
Mock
scFv
Cg06

FIG. 3B

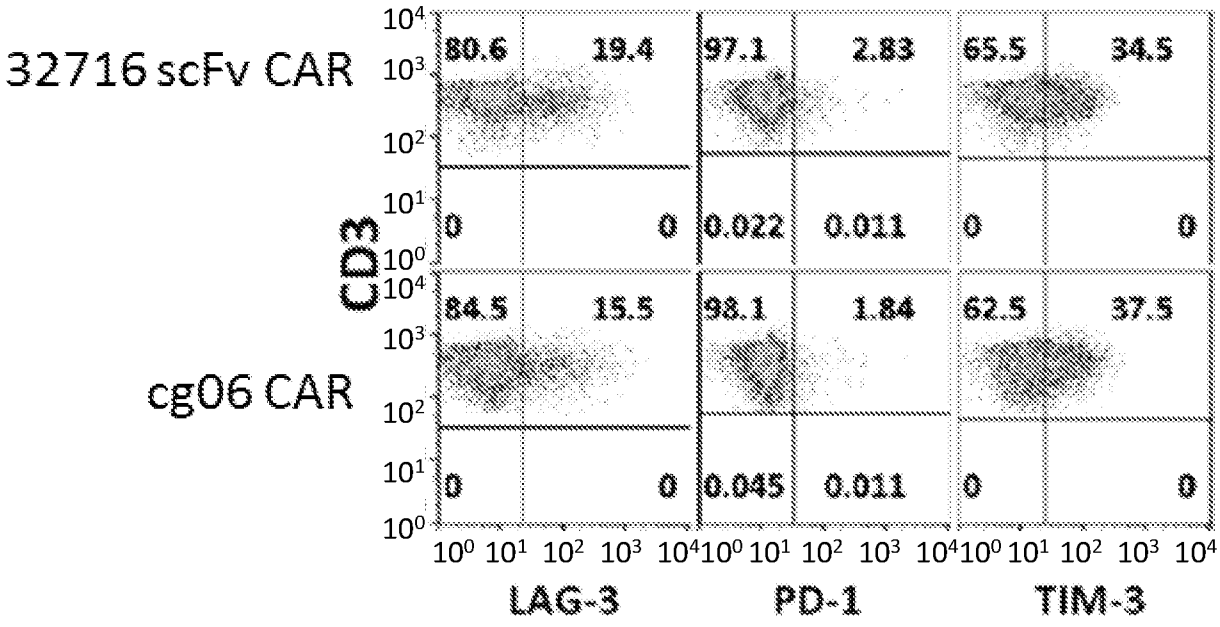

32716 scFv CAR
cg06 CAR
CD3
80.6
19.4
97.1
2.83
65.5
34.5
0
0
0.022
0.011
0
0
84.5
15.5
98.1
1.84
62.5
37.5
0
0
0.045
0.011
0
0
LAG-3
PD-1
TIM-3

FIG. 4A T Cells Only

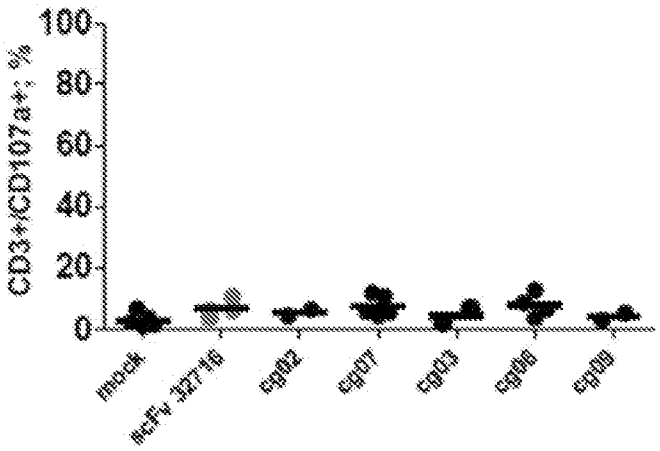


FIG. 4B T Cells + CD123^{-} K562

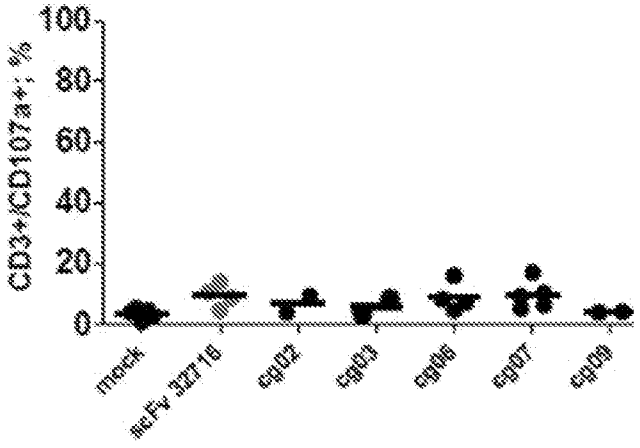


FIG. 4C T Cells + CD123^{+} BDCM

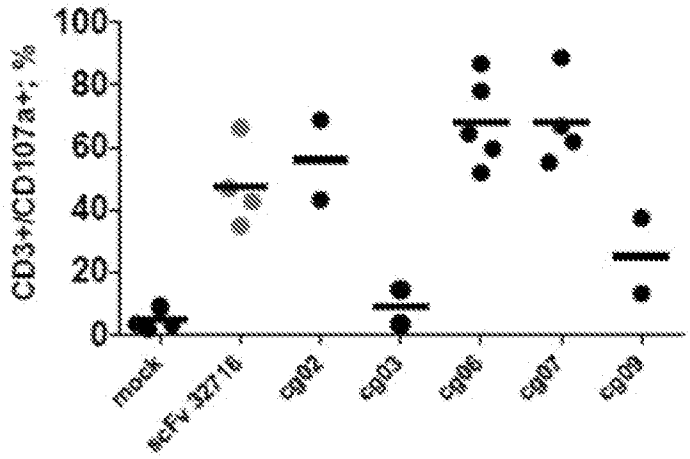


FIG. 5A

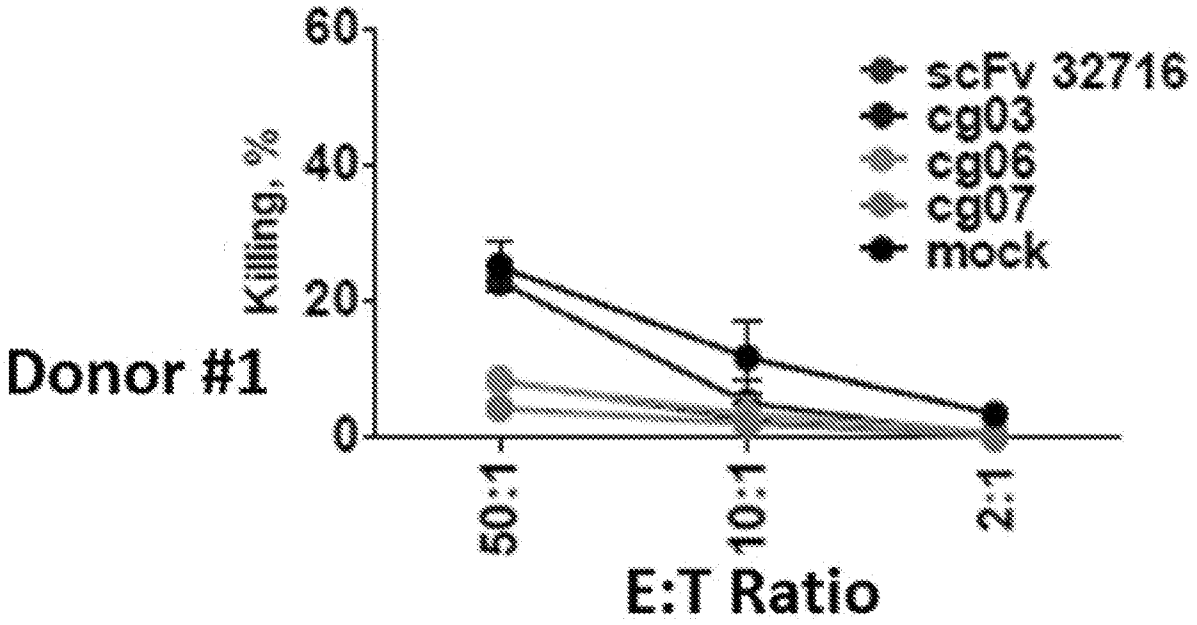

K562 CD123(-)
Killing, %
60
40
20
0
Donor #1
scFv 32716
cg03
cg06
cg07
mock
50:1
10:1
2:1
E:T Ratio

FIG. 5B

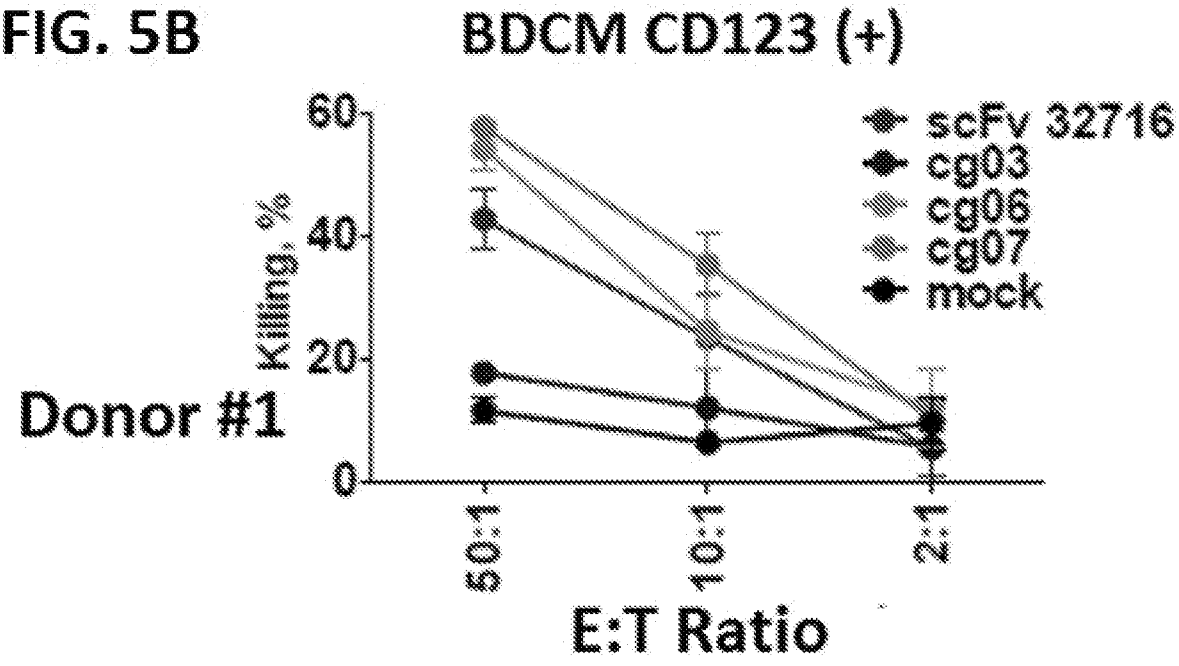

BDCM CD123 (+)
Killing, %
60
40
20
0
Donor #1
scFv 32716
cg03
cg06
cg07
mock
50:1
10:1
2:1
E:T Ratio

FIG. 5C

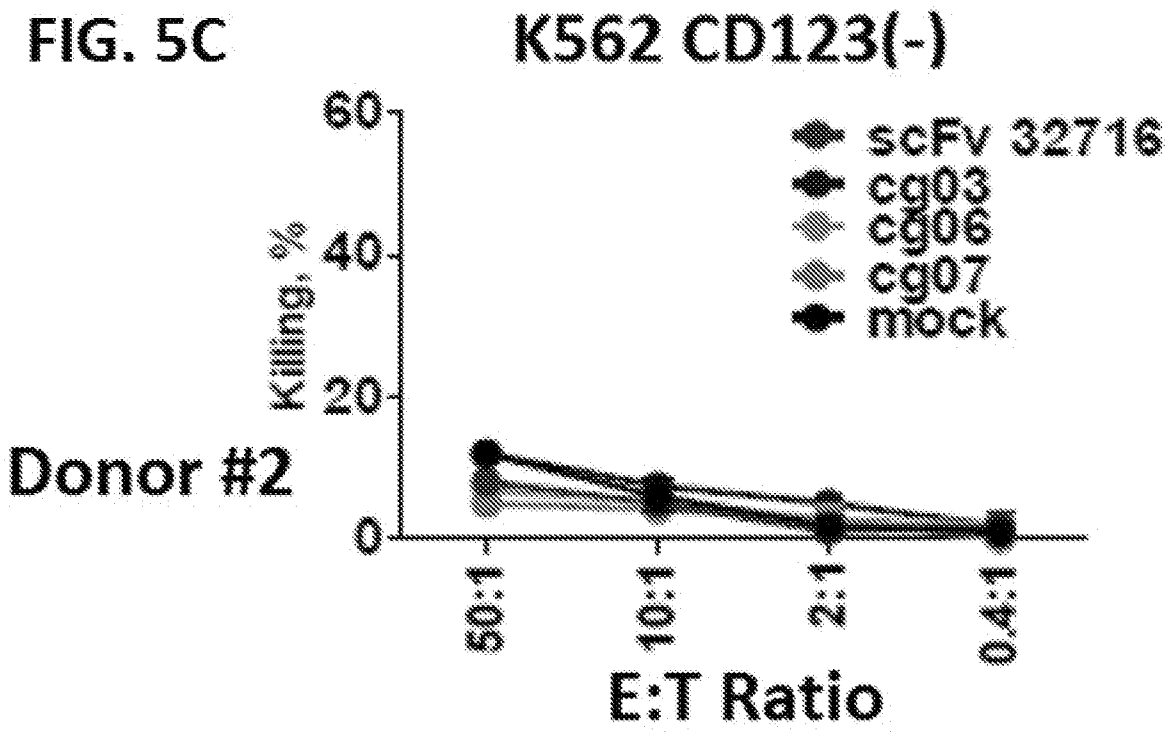

K562 CD123(-)
scFv 32716
cg03
cg06
cg07
mock
Killing, %
60
40
20
0
Donor #2
50:1
10:1
2:1
0.4:1
E:T Ratio

FIG. 5D

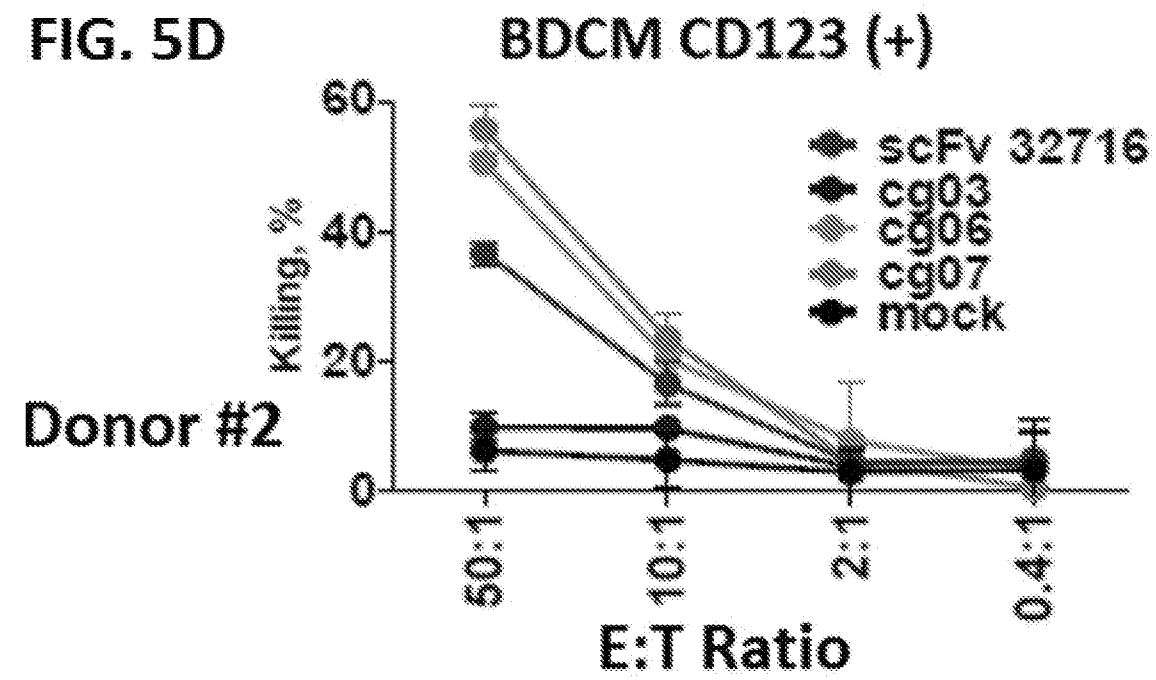

BDCM CD123 (+)
scFv 32716
cg03
cg06
cg07
mock
Killing, %
60
40
20
0
Donor #2
50:1
10:1
2:1
0.4:1
E:T Ratio

FIG. 6A FIG. 6B FIG. 6C FIG. 6D

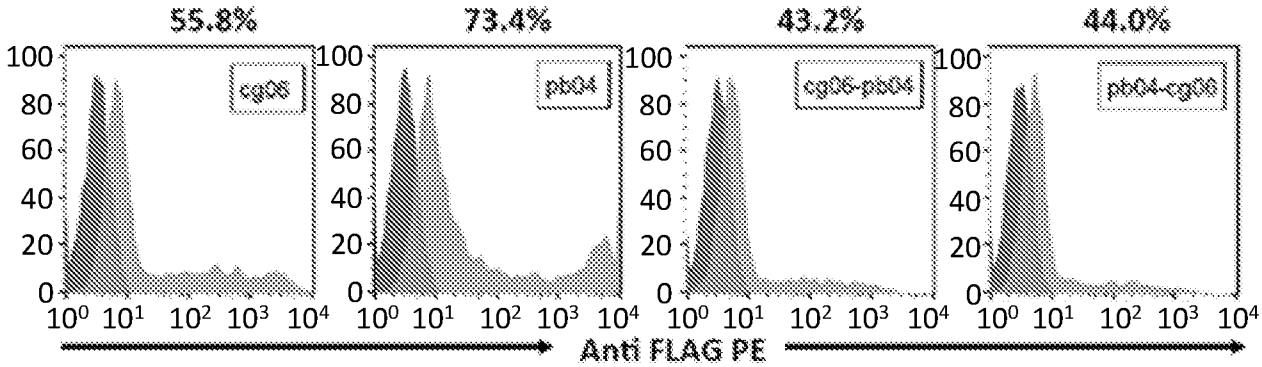


FIG. 6E

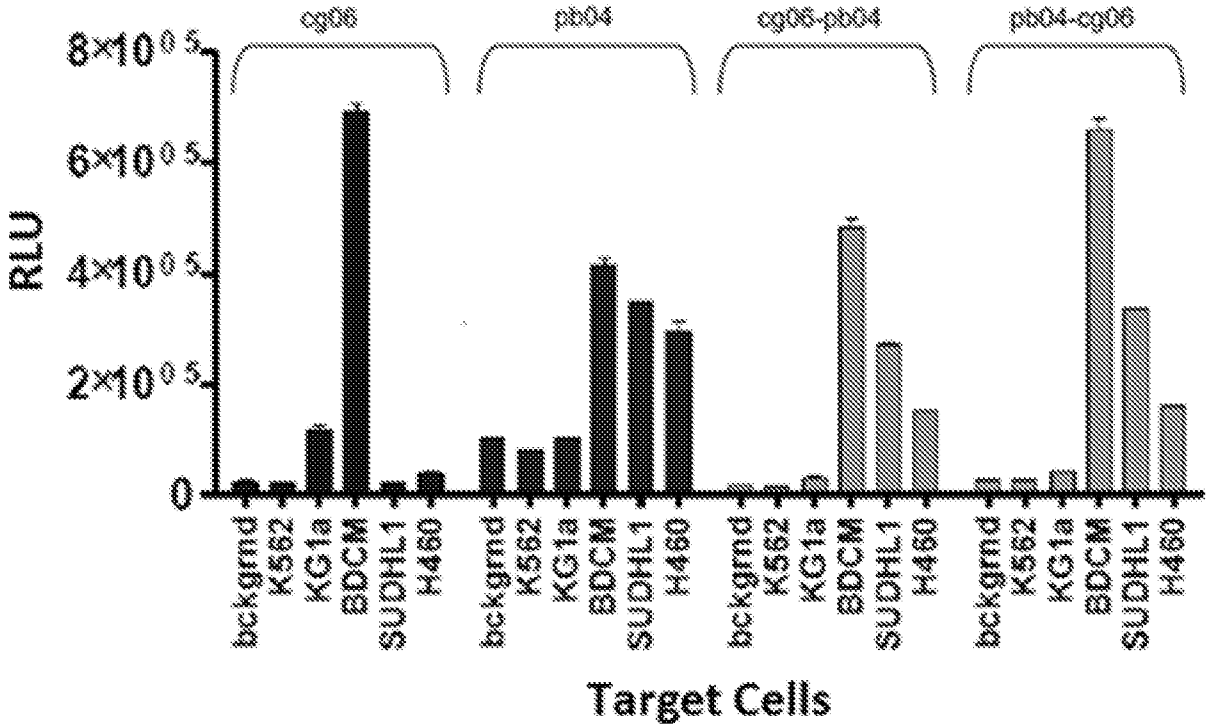


FIG. 7A

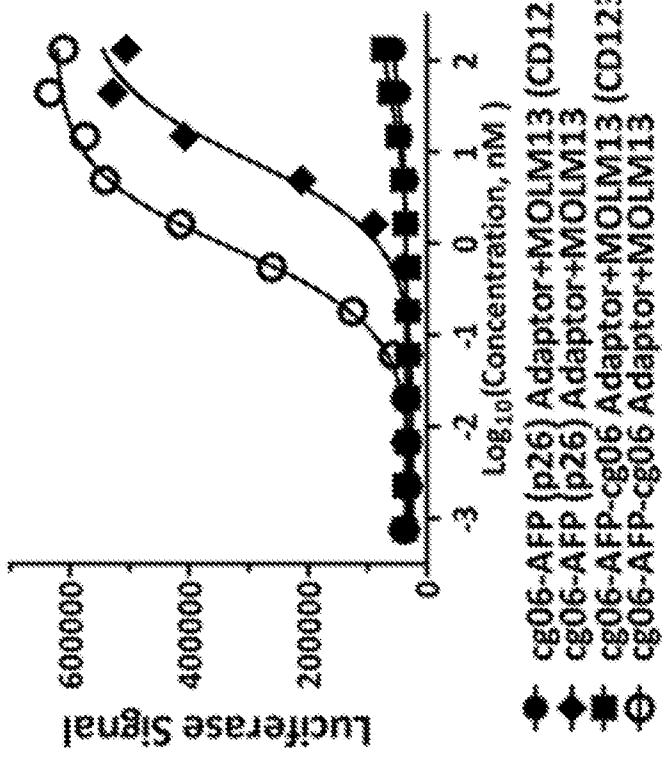

Luciferase Signal
600000
400000
200000
0
-3
-2
-1
0
1
2
Log10(Concentration, nM)
cg06-AFP (p26) Adaptor+MOLM13 (CD123 -/-)
cg06-AFP (p26) Adaptor+MOLM13
cg06-AFP-cg06 Adaptor+MOLM13 (CD123 -/-)
cg06-AFP-cg06 Adaptor+MOLM13
Adapter
Binding Domain Specificity
Antigenic Determinant
Binding Domain Specificity
HIS-tag
CD123 (cg06)
AFP
CD123 (cg06)
HIS-tag
CD123 (cg06)
AFP
CD123 (cg06)

FIG. 7B

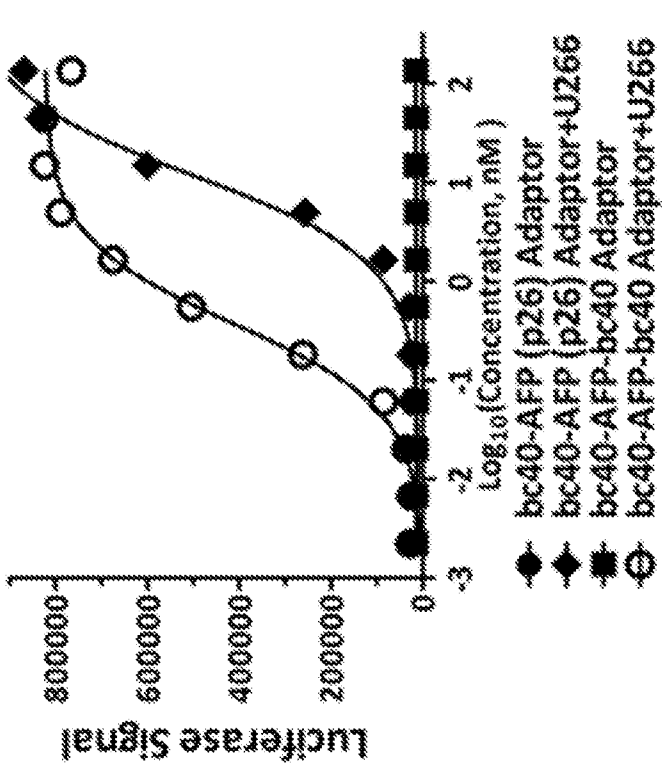
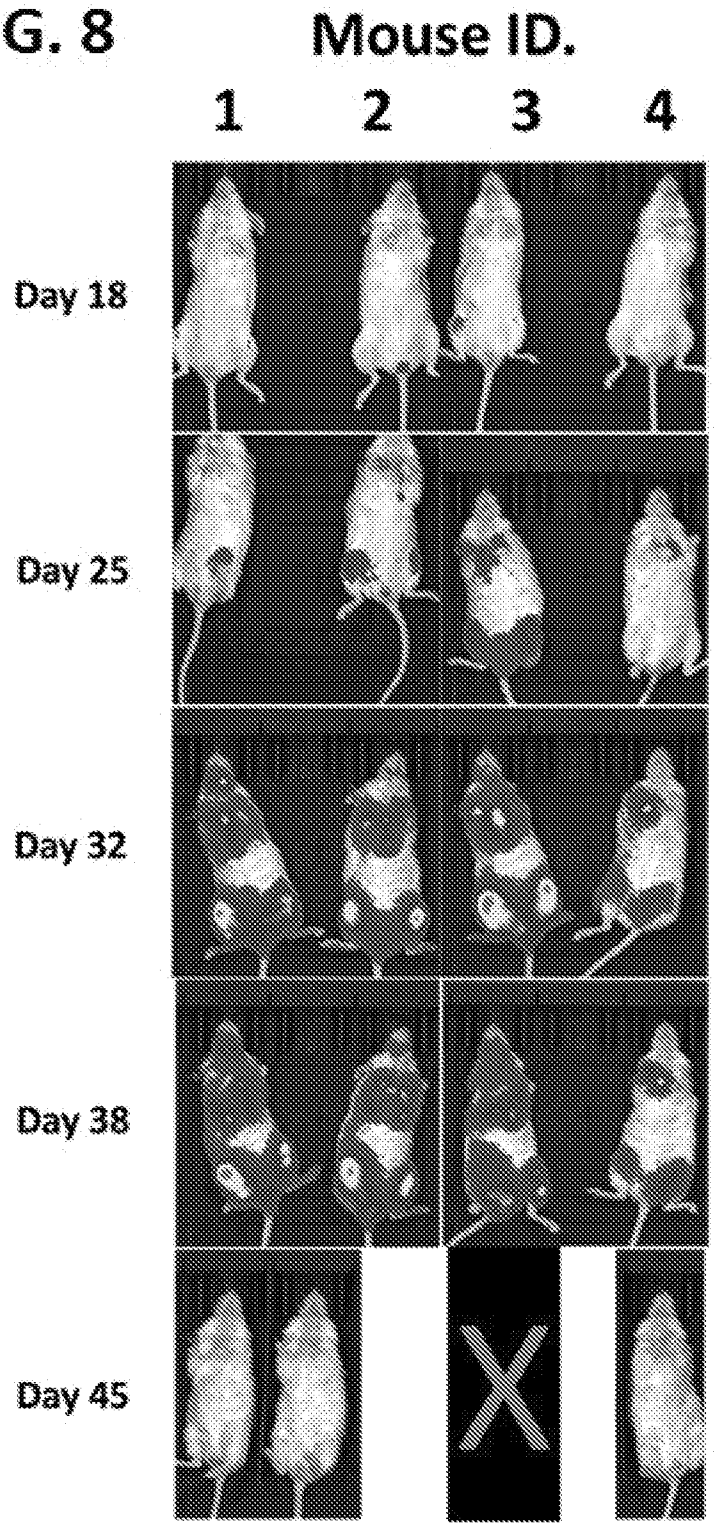

Luciferase Signal
800000
600000
400000
200000
0
-3
-2
-1
0
1
2
Log10(Concentration, nM)
bc40-AFP (p26) Adaptor
bc40-AFP (p26) Adaptor+U266
bc40-AFP-bc40 Adaptor
bc40-AFP-bc40 Adaptor+U266
Adapter
Binding Domain Specificity
Antigenic Determinant
Binding Domain Specificity
HIS-tag
BCMA (bc40)
AFP
BCMA (bc40)
HIS-tag
BCMA (bc40)
AFP
BCMA (bc40)

FIG. 8



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SEQUENCE LISTING

<110> Arcellx, Inc.
HILBERT, David M.
SWERS, Jeffrey S.

<120> D-DOMAIN CONTAINING POLYPEPTIDES AND USES THEREOF

<130> 6666.0200

<140> PCT/US18/060887
<141> 2018-11-14

<150> US 62/585,780
<151> 2017-11-14

<160> 976

<170> PatentIn version 3.5

<210> 1
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 1

Met Gly Ser Trp Ala Glu Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 2
<211> 9
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<220>
<223> synthetic construct

<400> 2

Leu Ala Ala Ile Lys Thr Arg Leu Gln
1 5

<210> 3
<211> 229
<212> PRT
<213> Homo sapiens

<400> 3

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
1 5 10 15

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
20 25 30

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
35 40 45

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

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
65 70 75 80

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
85 90 95

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
100 105 110

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
115 120 125

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
130 135 140

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala

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145 150 155 160

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
165 170 175

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
180 185 190

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
195 200 205

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg
210 215 220

Ala Ala Leu Gly Val
225

<210> 4
<211> 10
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<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 4

Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser
1 5 10

<210> 5
<211> 10
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 5

Gly Gly Gly Gly Asp Gly Gly Gly Gly Ser
1 5 10

<210> 6
<211> 73
<212> PRT

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<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 6

```
Met Gly Ser Trp Ala Glu Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr
1               5                  10                  15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
```

<210> 7
<211> 54
<212> PRT
<213> Homo sapiens

<400> 7

```
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1               5                  10                  15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            20                  25                  30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        35                  40                  45

Val Lys Gly Thr Asn Ala
    50
```

<210> 8
<211> 287
<212> PRT
<213> Homo sapiens

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<400> 8

```
Thr Lys Glu Asp Pro Asn Pro Pro Ile Thr Asn Leu Arg Met Lys Ala
1               5                  10                  15

Lys Ala Gln Gln Leu Thr Trp Asp Leu Asn Arg Asn Val Thr Asp Ile
            20                  25                  30

Glu Cys Val Lys Asp Ala Asp Tyr Ser Met Pro Ala Val Asn Asn Ser
        35                  40                  45

Tyr Cys Gln Phe Gly Ala Ile Ser Leu Cys Glu Val Thr Asn Tyr Thr
    50                  55                  60

Val Arg Val Ala Asn Pro Pro Phe Ser Thr Trp Ile Leu Phe Pro Glu
65                  70                  75                  80

Asn Ser Gly Lys Pro Trp Ala Gly Ala Glu Asn Leu Thr Cys Trp Ile
                85                  90                  95

His Asp Val Asp Phe Leu Ser Cys Ser Trp Ala Val Gly Pro Gly Ala
            100                 105                 110

Pro Ala Asp Val Gln Tyr Asp Leu Tyr Leu Asn Val Ala Asn Arg Arg
        115                 120                 125

Gln Gln Tyr Glu Cys Leu His Tyr Lys Thr Asp Ala Gln Gly Thr Arg
    130                 135                 140

Ile Gly Cys Arg Phe Asp Asp Ile Ser Arg Leu Ser Ser Gly Ser Gln
145                 150                 155                 160

Ser Ser His Ile Leu Val Arg Gly Arg Ser Ala Ala Phe Gly Ile Pro
                165                 170                 175

Cys Thr Asp Lys Phe Val Val Phe Ser Gln Ile Glu Ile Leu Thr Pro
            180                 185                 190

Pro Asn Met Thr Ala Lys Cys Asn Lys Thr His Ser Phe Met His Trp
        195                 200                 205
```

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```
Lys Met Arg Ser His Phe Asn Arg Lys Phe Arg Tyr Glu Leu Gln Ile
    210                 215                 220

Gln Lys Arg Met Gln Pro Val Ile Thr Glu Gln Val Arg Asp Arg Thr
225                 230                 235                 240

Ser Phe Gln Leu Leu Asn Pro Gly Thr Tyr Thr Val Gln Ile Arg Ala
                245                 250                 255

Arg Glu Arg Val Tyr Glu Phe Leu Ser Ala Trp Ser Thr Pro Gln Arg
            260                 265                 270

Phe Glu Cys Asp Gln Glu Glu Gly Ala Asn Thr Arg Ala Trp Arg
        275                 280                 285
```

<210> 9
<211> 591
<212> PRT
<213> Homo sapiens

<400> 9

```
Arg Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser
1               5                   10                  15

Tyr Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe
            20                  25                  30

Phe Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met
        35                  40                  45

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

Ser Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu
65                  70                  75                  80

Cys His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys
                85                  90                  95

Ser Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys
            100                 105                 110
```

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```
Pro Thr Pro Ala Ser Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr
        115                 120                 125

Ser Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe
    130                 135                 140

Ile Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile
145                 150                 155                 160

Leu Leu Trp Ala Ala Arg Tyr Asp Lys Ile Ile Pro Ser Cys Cys Lys
                165                 170                 175

Ala Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr
            180                 185                 190

Lys Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Ala Val
        195                 200                 205

Met Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys
    210                 215                 220

Leu Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu
225                 230                 235                 240

Val Leu Asp Val Ala His Val His Glu His Cys Cys Arg Gly Asp Val
                245                 250                 255

Leu Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser
            260                 265                 270

Gln Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr
        275                 280                 285

Thr Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys
    290                 295                 300

Pro Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp
305                 310                 315                 320
```

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```
Phe Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe
                325                 330                 335

Val His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile
            340                 345                 350

Leu Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln
        355                 360                 365

Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln
    370                 375                 380

Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu
385                 390                 395                 400

Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln Asn Ala Phe Leu Val Ala
                405                 410                 415

Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile
            420                 425                 430

Thr Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu
        435                 440                 445

Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly
    450                 455                 460

His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly
465                 470                 475                 480

Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser
                485                 490                 495

Leu Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys
            500                 505                 510

Phe Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln
        515                 520                 525

Thr Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln
    530                 535                 540
```

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Ile Thr Glu Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser Gly Leu
545 550 555 560

Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu
565 570 575

Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly Val
580 585 590

<210> 10
<211> 229
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 10

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
1 5 10 15

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
20 25 30

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
35 40 45

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

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
65 70 75 80

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
85 90 95

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
100 105 110

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
115 120 125

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Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
130 135 140

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
145 150 155 160

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
165 170 175

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
180 185 190

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
195 200 205

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg
210 215 220

Ala Ala Leu Gly Val
225

<210> 11
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 11

Met Gly Ser Trp Tyr Glu Phe Ser Trp Arg Leu Gln Ala Ile His Gln
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ala Tyr Ala Ala Gly Ile Arg
50 55 60

Gly Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 12
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 12

Met Gly Ser Trp His Glu Phe Thr Trp Arg Leu Ile Ala Ile Gln Gln
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ala Tyr Ala Ala Gly Ile Arg
50 55 60

His His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 13
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 13

Met Gly Ser Trp Arg Glu Phe Ala Trp Arg Leu Val Ala Ile Asn Ser
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His Tyr Ala Ala Ser Ile Arg
50 55 60

Asp Gly Leu Gln Ala Tyr Arg His Asn
65 70

<210> 14
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 14

Met Gly Ser Trp His Glu Phe Ala Trp Arg Leu Gln Ala Ile Asn Gln
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His Tyr Ala Ala His Ile Arg
50 55 60

Asn Gly Leu Gln Ala Tyr Arg His Asn
65 70

<210> 15
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 15

Met Gly Ser Trp Asn Glu Phe Ala Trp Arg Leu Thr Ala Ile Glu Gln
1 5 10 15

24 Oct 2022
2018369639

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His Tyr Ala Ala Gly Ile Arg
50 55 60

Asp Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 16
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 16

Met Gly Ser Trp Thr Glu Phe Ala Trp Arg Leu Gln Ala Ile His Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val Tyr Ala Ala Lys Ile Arg
50 55 60

Ile Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 17
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 17

Met Gly Ser Trp Ile Glu Phe Ala Trp Arg Leu Gln Ala Ile His Gln
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Glu Tyr Ala Ala Asn Ile Arg
50 55 60

Asp Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 18
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 18

Met Gly Ser Trp His Glu Phe Thr Trp Arg Leu Val Ala Ile Gln Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Lys Phe Ala Ala Lys Ile Arg
50 55 60

Tyr Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
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<400> 19

Met Gly Ser Trp His Glu Phe Thr Trp Arg Leu Ile Ala Ile Arg Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu Tyr Ala Ala Ser Ile Arg
50 55 60

Asn Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 20
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<212> PRT
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<400> 20

Met Gly Ser Trp Ile Glu Phe Ser Trp Arg Leu Glu Ala Ile Arg Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ser Tyr Ala Ala Arg Ile Arg
50 55 60

Gln Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 21

Met Gly Ser Trp Val Glu Phe Ser Trp Arg Leu Glu Ala Ile Arg Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ser Tyr Ala Ala Arg Ile Arg
50 55 60

Gln Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 22
<211> 73
<212> PRT
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<220>
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<400> 22

Met Gly Ser Trp Val Glu Phe Ser Trp Arg Leu Glu Ala Ile Arg Gln
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Lys Tyr Ala Ala Arg Ile Arg
50 55 60

Gly Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 23
<211> 73
<212> PRT
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<400> 23

Met Gly Ser Trp Val Glu Phe Ala Trp Arg Leu Thr Ala Ile Asp Gln
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Phe Tyr Ala Ala Lys Ile Arg
50 55 60

Ser His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 24
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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 24

Met Gly Ser Trp Val Glu Phe Ala Trp Arg Leu Glu Ala Ile Lys Gln
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Leu Tyr Ala Ala Lys Ile Arg
50 55 60

Arg Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 25
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 25

Met Gly Ser Trp Val Glu Phe Ala Trp Arg Leu Thr Ala Ile His Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Lys Tyr Ala Ala Lys Ile Arg
50 55 60

Lys Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 26
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<212> PRT
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<223> synthetic construct

<400> 26

Met Gly Ser Trp Thr Glu Phe Ala Trp Arg Leu Glu Ala Ile Asn Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Lys Pro Glu Val Glu Ala Leu Arg Ala Tyr Ala Ala Lys Ile Arg
50 55 60

Thr Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 27
<211> 73
<212> PRT
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<400> 27

Met Gly Ser Trp Ser Glu Phe Ala Trp Arg Leu Glu Ala Ile His Gln
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Leu Phe Ala Ala Gln Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 28
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 28

Met Gly Ser Trp Asn Glu Phe Ala Trp Arg Leu Ile Ala Ile Asn Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg His Phe Ala Ala Asn Ile Arg
50 55 60

Asn Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 29
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 29

Met Gly Ser Trp Thr Glu Phe Ala Trp Arg Leu Ile Ala Ile Asp Gln
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Glu Leu Ala Ala Glu Ile Arg
50 55 60

Phe His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 30
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 30

Met Gly Ser Trp Ser Glu Phe Met Asn Arg Leu Asp Ala Ile Thr Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg His Tyr Ala Ala Gln Ile Arg
50 55 60

Asp Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 31
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 31

Met Gly Ser Trp Thr Glu Phe Met Glu Arg Leu Asp Ala Ile Ser Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Asp Tyr Ala Ala Ile Ile Arg
50 55 60

Asn Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 32
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 32

Met Gly Ser Trp Ala Glu Phe Met Asp Arg Leu Asp Ala Ile Thr Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Gly Tyr Ala Ala Ile Ile Arg
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 33
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 33

Met Gly Ser Trp Ile Glu Phe Gln Glu Arg Leu Asp Ala Ile Phe Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Asp Ala Ala Ala Thr Ile Arg
50 55 60

Arg Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 34
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 34

Met Gly Ser Trp Ile Glu Phe Gln Gln Arg Leu Asp Ala Ile Phe Tyr
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Asp Met Ala Ala Ile Ile Arg
50 55 60

Lys Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 35
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<212> PRT
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<223> synthetic construct

<400> 35

Met Gly Ser Trp Tyr Glu Phe Gln Ser Arg Leu Asp Ala Ile Phe Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ala Ala Ala Ser Ile Arg
50 55 60

Thr Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 36
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 36

Met Gly Ser Trp Ser Glu Phe Ile Asp Arg Leu Asp Ala Ile Thr Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Trp Tyr Ala Gly Val Ile Arg
50 55 60

Glu Gln Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 37
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 37

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Tyr Ala Ile Asn Gln
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Phe Ile Arg
50 55 60

Ala Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 38
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 38

Met Gly Ser Trp Tyr Glu Phe Tyr Asp Arg Leu Asp Ala Ile Val His
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Trp Tyr Ala Ala Met Ile Arg
50 55 60

Val Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 39
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 39

Met Gly Ser Trp Val Glu Phe Gln Asp Arg Leu Glu Ala Ile Thr Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Met Ile Arg
50 55 60

Val Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 40
<211> 73
<212> PRT
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<400> 40

Met Gly Ser Trp Val Glu Phe Gln Glu Arg Leu Met Ala Ile Ser Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Gln Ala Ala Met Ile Arg
50 55 60

Tyr Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 41
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 41

Met Gly Ser Trp Phe Glu Phe Gln His Arg Leu Glu Ala Ile Ser Met
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Gln Ala Ala Tyr Ile Arg
50 55 60

Val Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 42
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 42

Met Gly Ser Trp Val Glu Phe Gln Ser Arg Leu Glu Ala Ile Ala Thr
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Gln Ala Ala Trp Ile Arg
50 55 60

Met Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 43
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 43

Met Gly Ser Trp Glu Glu Phe Gln Tyr Arg Leu Gly Ala Ile Ala Ala
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Gln Ala Ala Met Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 44
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<223> synthetic construct

<400> 44

Met Gly Ser Trp Tyr Glu Phe Gln Val Arg Leu Gln Ala Ile Ser Trp
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn His Glu Val Glu Glu Leu Arg Ile Gln Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 45
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 45

Met Gly Ser Trp Val Glu Phe Arg Ser Arg Leu Glu Ala Ile Ser Asn
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Thr Thr Ala Ala Leu Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 46
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 46

Met Gly Ser Trp Val Glu Phe Lys Ala Arg Leu Glu Ala Ile Ser Ser
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 47
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 47

Met Gly Ser Trp Ser Glu Phe Tyr Thr Arg Leu Glu Ala Ile Asn Asn
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Thr Ala Ala Leu Ile Arg
50 55 60

Ile Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 48
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 48

Met Gly Ser Trp Ala Glu Phe Tyr His Arg Leu Asp Ala Ile Ser Ser
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Thr Ala Ala Leu Ile Arg
50 55 60

Ile Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 49
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 49

Met Gly Ser Trp Thr Glu Phe Ala Ser Arg Leu Val Ala Ile Arg Gln
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Ile Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 50
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 50

Met Gly Ser Trp Ser Glu Phe Asp Gln Arg Leu Ala Ala Ile Tyr Gln
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 51
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 51

Met Gly Ser Trp Val Glu Phe His Asn Arg Leu Ser Ala Ile Ser Asp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 52
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 52

Met Gly Ser Trp Asn Glu Phe Glu Asp Arg Leu Ser Ala Ile Ser Ala
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 53
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 53

Met Gly Ser Trp Val Glu Phe Glu Tyr Arg Leu Val Ala Ile Phe Asp
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Gln Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 54
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 54

Met Gly Ser Trp Val Glu Phe Gln Gly Arg Leu Gly Ala Ile His Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Val Phe Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 55
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 55

Met Gly Ser Trp Tyr Glu Phe Ser Met Arg Leu Ser Ala Ile Trp Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Gln Ala Ala Leu Ile Arg
50 55 60

Phe Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 56
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 56

Met Gly Ser Trp Thr Glu Phe Ser Gln Arg Leu Gly Ala Ile Ser Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 57
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 57

Met Gly Ser Trp Thr Glu Phe His Asp Arg Leu Glu Ala Ile Thr His
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Leu Arg
50 55 60

Val Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 58
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 58

Met Gly Ser Trp Thr Glu Phe Glu His Arg Leu Glu Ala Ile Ala Gly
1 5 10 15

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

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Leu Ile Arg
50 55 60

Phe Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 59
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 59

Met Gly Ser Trp Thr Glu Phe Ala Asn Arg Leu Glu Ala Ile Asn Ala
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Ser Ala Ala Leu Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 60
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 60

Met Gly Ser Trp Glu Glu Phe Asp Arg Arg Leu Tyr Ala Ile Ala Arg
1 5 10 15

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Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Gln Ala Ala Leu Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 61
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 61

Met Gly Ser Trp Ile Glu Phe His Gln Arg Leu Glu Ala Ile Val Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Gln Ala Ala Leu Ile Arg
50 55 60

Val Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 62
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 62

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Lys Ala Ile Ala Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Thr Glu Ala Ala Ile Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 63
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<400> 63

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Ser Ala Ile Met Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Arg Ala Ala Ile Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
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<400> 64

Met Gly Ser Trp Val Glu Phe Glu Glu Arg Leu Ala Ala Ile Ala Thr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Arg Ala Ala Ile Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 65
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<212> PRT
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<400> 65

Met Gly Ser Trp Ser Glu Phe Arg Gly Arg Leu Gln Ala Ile His Ser
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ser Ala Ala Ile Ile Arg
50 55 60

Ile Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 66
<211> 73
<212> PRT
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<400> 66

Met Gly Ser Trp Thr Glu Phe Arg Asp Arg Leu Gly Ala Ile Tyr His
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Gln Ala Ala Ile Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 67
<211> 73
<212> PRT
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<400> 67

Met Gly Ser Trp Val Glu Phe Tyr His Arg Leu Glu Ala Ile Arg Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Val Ala Ala Val Ile Arg
50 55 60

Tyr Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 68
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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 68

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu Glu Ala Ile Arg Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Ile Ala Ala Val Ile Arg
50 55 60

Tyr Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 69
<211> 73
<212> PRT
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<400> 69

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu Ala Ala Ile Arg Lys
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Arg Ala Ala Leu Ile Arg
50 55 60

Ile Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
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<400> 70

Met Gly Ser Trp Glu Glu Phe Ser Glu Arg Leu Glu Ala Ile Ser Ile
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val Ser Ala Ala Ile Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 71
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<223> synthetic construct

<400> 71

Met Gly Ser Trp Ser Glu Phe Ser Asp Arg Leu His Ala Ile Ser Asp
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ile Gln Ala Ala Ile Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 72
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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 72

Met Gly Ser Trp Ile Glu Phe Ser His Arg Leu Glu Ala Ile Val Asp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asn Thr Ala Ala Ile Ile Arg
50 55 60

Val Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 73
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<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 73

Met Gly Ser Trp Glu Glu Phe Ser Asp Arg Leu Glu Ala Ile Leu Arg
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Phe Ala Ala Ala Ile Ile Arg
50 55 60

Val Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 74
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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 74

Met Gly Ser Trp Met Glu Phe Ser His Arg Leu Asp Ala Ile His Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Phe Ala Ala Ala Ile Ile Arg
50 55 60

Val Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 75
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 75

Met Gly Ser Trp Ser Glu Phe Gln Gln Arg Leu His Ala Ile Arg Thr
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Glu Ala Ala Ile Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 76
<211> 73
<212> PRT
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<220>
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<400> 76

Met Gly Ser Trp Tyr Glu Phe Gln Asn Arg Leu Gly Ala Ile Asn Arg
1 5 10 15

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

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Glu Ala Ala Ile Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 77
<211> 73
<212> PRT
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<400> 77

Met Gly Ser Trp Gln Glu Phe Thr Gly Arg Leu His Ala Ile Arg His
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Glu Ala Ala Tyr Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 78
<211> 73
<212> PRT
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<220>
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<400> 78

Met Gly Ser Trp Thr Glu Phe Asp His Arg Leu Gly Ala Ile Trp Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe His Ala Ala Ile Ile Arg
50 55 60

Ile Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 79
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 79

Met Gly Ser Trp Thr Glu Phe His Val Arg Leu Ser Ala Ile Trp Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe His Ala Ala Ile Ile Arg
50 55 60

Ile Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 80
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<223> synthetic construct

<400> 80

Met Gly Ser Trp Asn Glu Phe Asp Asn Arg Leu Gln Ala Ile Trp Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe His Ala Ala Met Ile Arg
50 55 60

Ile Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 81
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 81

Met Gly Ser Trp Thr Glu Phe His Glu Arg Leu Gln Ala Ile Trp Phe
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Arg Ala Ala Ile Ile Arg
50 55 60

Leu Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 82
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 82

Met Gly Ser Trp Asn Glu Phe Ser Gly Arg Leu Thr Ala Ile Lys Asp
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Phe Arg Ala Ala Val Ile Arg
50 55 60

Leu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 83
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 83

Met Gly Ser Trp Val Glu Phe Asp Glu Arg Leu Val Ala Ile Trp Phe
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Ala Arg Ala Ala Tyr Ile Arg
50 55 60

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Ile Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 84
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 84

Met Gly Ser Trp Ser Glu Phe Gly Gln Arg Leu Ser Ala Ile Trp Glu
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Ala Asp Ala Ala Phe Ile Arg
50 55 60

Ile Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 85
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 85

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Val Ala Ile Trp Ile
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr Asn Ala Ala Phe Ile Arg
50 55 60

Gly Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 86
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 86

Met Gly Ser Trp Tyr Glu Phe Gly Asp Arg Leu Ser Ala Ile Trp Glu
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Thr His Ala Ala Glu Ile Arg
50 55 60

Thr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 87
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 87

Met Gly Ser Trp His Glu Phe Tyr Tyr Arg Leu Glu Ala Ile Glu Gln
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Phe Asp Ala Ala Leu Ile Arg
50 55 60

Ile Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 88
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 88

Met Gly Ser Trp Ser Glu Phe Glu Glu Arg Leu Ala Ala Ile Gly Ser
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Phe Asp Ala Ala Leu Ile Arg
50 55 60

Ile Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 89
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 89

Met Gly Ser Trp Leu Glu Phe His Tyr Arg Leu His Ala Ile Gln Phe
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg His Ile Ala Ala Leu Ile Arg
50 55 60

Asn Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 90
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 90

Met Gly Ser Trp Gln Glu Phe Tyr Asn Arg Leu Glu Ala Ile His Met
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gly Leu Arg Ser Asp Ala Ala Pro Ile Arg
50 55 60

Asp Val Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 91
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 91

Met Gly Ser Trp Asn Glu Phe His His Arg Leu Trp Ala Ile Phe Asp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Lys Met Ala Ala Gly Ile Arg
50 55 60

Gly Gly Leu Gln Ala Tyr Arg His Asn
65 70

<210> 92
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 92

Met Gly Ser Trp Tyr Glu Phe His Tyr Arg Leu Lys Ala Ile Asn Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Tyr Ser Ala Ala Met Ile Arg
50 55 60

His Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 93
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 93

Met Gly Ser Trp Thr Glu Phe His Gln Arg Leu Gly Ala Ile His Ala
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Ser Ala Ala Phe Ile Arg
50 55 60

Leu Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 94
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 94

Met Gly Ser Trp Phe Glu Phe Gln Tyr Arg Leu Glu Ala Ile Phe Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Lys Pro Glu Val Glu Glu Leu Arg Val Arg Ala Ala Leu Ile Arg
50 55 60

His Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 95
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 95

Met Gly Ser Trp Val Glu Phe His Ala Arg Leu Asp Ala Ile Tyr Thr
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Val Leu Ala Ala His Ile Arg
50 55 60

Ile Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 96
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 96

Met Gly Ser Trp Val Glu Phe Gly Thr Arg Leu Ser Ala Ile Tyr Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Phe Glu Ala Ala Ile Ile Arg
50 55 60

Ile Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 97
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 97

Met Gly Ser Trp Val Glu Phe Thr His Arg Leu Asp Ala Ile Tyr Ile
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His Glu Ala Ala Val Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 98
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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2018369639 24 Oct 2022

<223> synthetic construct

<400> 98

Met Gly Ser Trp Val Glu Phe His Gly Arg Leu Ala Ala Ile Tyr Val
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Tyr His Ala Ala Met Ile Arg
50 55 60

Arg Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 99
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 99

Met Gly Ser Trp Val Glu Phe Asp Arg Arg Leu Val Ala Ile Tyr Ile
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Asp Asp Ala Ala Leu Ile Arg
50 55 60

Leu Leu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 100
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 100

Met Gly Ser Trp Val Glu Phe Asp Arg Arg Leu Val Ala Ile Tyr Ile
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Glu Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 101
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 101

Met Gly Ser Trp Leu Glu Phe Asp Arg Arg Leu Thr Ala Ile Tyr Leu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Glu Asp Ala Ala Met Ile Arg
50 55 60

Asp Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 102
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 102

Met Gly Ser Trp Ile Glu Phe Asp Arg Arg Leu Leu Ala Ile His Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Met Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 103
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 103

Met Gly Ser Trp Ile Glu Phe Asp Arg Arg Leu Ile Ala Ile Trp Ile
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ser Asp Ala Ala Asp Ile Arg
50 55 60

Gln Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 104
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 104

Met Gly Ser Trp Val Glu Phe Asp Arg Arg Leu Ile Ala Ile Trp Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Ser Asp Ala Ala Met Ile Arg
50 55 60

Glu His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 105
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 105

Met Gly Ser Trp Tyr Glu Phe His Thr Arg Leu Ile Ala Ile Tyr Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gly Asp Ala Ala Lys Ile Arg
50 55 60

Gly Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 106
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 106

Met Gly Ser Trp Ser Glu Phe Ser Thr Arg Leu Ser Ala Ile Tyr Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asn Lys Ala Ala Ser Ile Arg
50 55 60

Lys Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 107
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 107

Met Gly Ser Trp Val Glu Phe Arg Tyr Arg Leu Gly Ala Ile Tyr His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Asp Arg Ala Ala Thr Ile Arg
50 55 60

Arg Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 108
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 108

Met Gly Ser Trp Asn Glu Phe Arg Asn Arg Leu Gly Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Ala His Ala Ala Ile Ile Arg
50 55 60

Ser Val Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 109
<211> 73
<212> PRT
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<223> synthetic construct

<400> 109

Met Gly Ser Trp His Glu Phe Arg Asn Arg Leu Gly Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Ala Arg Ala Ala Met Ile Arg
50 55 60

Ser Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 110
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 110

Met Gly Ser Trp Thr Glu Phe Tyr Gln Arg Leu Glu Ala Ile Asn Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 111
<211> 73
<212> PRT
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<400> 111

Met Gly Ser Trp Asn Glu Phe Tyr Asn Arg Leu His Ala Ile Asn Leu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu His Ala Ala Ile Ile Arg
50 55 60

Gln Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 112
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 112

Met Gly Ser Trp Glu Glu Phe Tyr Gly Arg Leu Ser Ala Ile Gln Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Met His Ala Ala Val Ile Arg
50 55 60

Arg Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 113
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 113

Met Gly Ser Trp Gly Glu Phe Asn Leu Arg Leu Val Ala Ile His Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Ser Gln Ala Ala Asn Ile Arg
50 55 60

Ala Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 114
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 114

Met Gly Ser Trp Gly Glu Phe Ser Asp Arg Leu Glu Ala Ile Asn Glu
1 5 10 15

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Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Glu Leu Arg Trp Gln Ala Ala Phe Ile Arg
    50                  55                  60

Ala Asn Leu Gln Ala Tyr Arg His Asn
65                  70
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<211> 73
<212> PRT
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<220>
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<400> 115

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Met Gly Ser Trp Met Glu Phe Gln Gly Arg Leu Pro Ala Ile Leu Ala
1               5                   10                  15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Lys Ala Ala Tyr Ile Arg
    50                  55                  60

Trp Met Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 116
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 116

Met Gly Ser Trp Met Glu Phe Glu Gly Arg Leu Pro Ala Ile Leu Ala
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Trp Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 117
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 117

Met Gly Ser Trp Phe Glu Phe Gln Asn Arg Leu Gln Ala Ile Leu Phe
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 118
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 118

Met Gly Ser Trp Val Glu Phe Asp Met Arg Leu Gln Ala Ile Leu Glu
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Ser Ala Ala Tyr Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 119
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 119

Met Gly Ser Trp Val Glu Phe Asn Ala Arg Leu Asp Ala Ile Leu Phe
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 120
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 120

Met Gly Ser Trp Met Glu Phe Asn Val Arg Leu Arg Ala Ile Leu Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 121
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 121

Met Gly Ser Trp Ile Glu Phe Asp Thr Arg Leu Ala Ala Ile Val His
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 122
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 122

Met Gly Ser Trp Ile Glu Phe Asp Tyr Arg Leu Lys Ala Ile Leu His
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gly Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Phe Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 123
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 123

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Leu Ala Ile Lys Val
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 124
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 124

Met Gly Ser Trp Tyr Glu Phe Gln Asp Arg Leu Ser Ala Ile Thr Thr
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 125
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 125

Met Gly Ser Trp Glu Glu Phe Asp Asp Arg Leu Asn Ala Ile Val Tyr
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 126
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 126

Met Gly Ser Trp Val Glu Phe Glu Gln Arg Leu His Ala Ile Val Val
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Gly
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 127
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 127

Met Gly Ser Trp Val Glu Phe Glu Trp Arg Leu Glu Ala Ile Val Val
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 128
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 128

Met Gly Ser Trp Tyr Glu Phe Glu His Arg Leu Lys Ala Ile Val Ser
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 129
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 129

Met Gly Ser Trp Met Glu Phe Lys His Arg Leu Ala Ala Ile Thr Phe
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Asp Lys Ala Ala Tyr Ile Arg
50 55 60

Leu Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 130
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 130

Met Gly Ser Trp Met Glu Phe Glu Gly Arg Leu His Ala Ile Lys Arg
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Val Leu Arg Asp Gln Ala Ala Tyr Ile Arg
    50   55   60

Leu Leu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 131
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 131

Met Gly Ser Trp Ser Glu Phe Val Phe Arg Leu Asp Thr Ile Lys Ser
1   5   10   15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

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

Leu Met Leu Gln Ala Tyr Arg His Asn
65   70

<210> 132
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 132

Met Gly Ser Trp Tyr Glu Phe Asp Glu Arg Leu Ser Ala Ile Lys Leu
1   5   10   15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Ala Gln Ala Ala Tyr Ile Arg
50 55 60

Ala Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 133
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 133

Met Gly Ser Trp Met Glu Phe Asp Glu Arg Leu Trp Ala Ile Lys Lys
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg His Gln Ala Ala Tyr Ile Arg
50 55 60

Met Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 134
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 134

Met Gly Ser Trp His Glu Phe Asp Gly Arg Leu Ser Ala Ile Lys Arg
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 135
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 135

Met Gly Ser Trp Tyr Glu Phe Asp Gly Arg Leu Gln Ala Ile Ile Ala
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Phe Arg Ala Ala Tyr Ile Arg
50 55 60

Trp Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 136
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 136

Met Gly Ser Trp Phe Glu Phe Asp Lys Arg Leu Tyr Ala Ile Ile His
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Lys Ala Ala Ile Ile Arg
50 55 60

Leu Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 137
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 137

Met Gly Ser Trp Val Glu Phe Asp Asn Arg Leu Tyr Ala Ile Val Asp
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Gln Lys Ala Ala Tyr Ile Arg
50 55 60

Leu Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 138
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 138

Met Gly Ser Trp Ile Glu Phe His Gln Arg Leu Asn Ala Ile Phe Asn
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg His His Ala Ala Tyr Ile Arg
50 55 60

Glu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 139
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 139

Met Gly Ser Trp Asn Glu Phe Arg Leu Arg Leu Trp Ala Ile Thr Glu
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Cys Leu Arg Ala Glu Ala Ala Trp Ile Arg
50 55 60

Thr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 140
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 140

Met Gly Ser Trp Tyr Glu Phe Trp Leu Arg Leu Ser Ala Ile Ser Tyr
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Lys Glu Ala Ala Glu Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 141
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 141

Met Gly Ser Trp Tyr Glu Phe Gln Leu Arg Leu Trp Ala Ile His Trp
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Trp Leu Arg Met Arg Ala Ala Glu Ile Arg
    50   55   60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 142
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 142

Met Gly Ser Trp Tyr Glu Phe Ala His Arg Leu Glu Ala Ile Glu Trp
1   5   10   15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Glu Leu Arg Gln Tyr Ala Ala Ala Ile Arg
    50   55   60

Asn Tyr Leu Gln Ala Tyr Arg His Asn
65   70

<210> 143
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 143

Met Gly Ser Trp Tyr Glu Phe Asp Thr Arg Leu Gly Ala Ile Arg Asn
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Phe Gln Ala Ala Tyr Ile Arg
50 55 60

Phe Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 144
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 144

Met Gly Ser Trp Tyr Glu Phe Trp Val Arg Leu Thr Ala Ile Arg Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Gln Ala Ala Ser Ile Arg
50 55 60

Trp Val Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 145
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 145

Met Gly Ser Trp Phe Glu Phe Asp Arg Arg Leu Lys Ala Ile Asp Arg
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Met Gln Ala Ala Ile Ile Arg
50 55 60

Asn Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 146
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 146

Met Gly Ser Trp Val Glu Phe Trp Glu Arg Leu Asp Ala Ile Asp Asn
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Trp His Ala Ala Tyr Ile Arg
50 55 60

Gly Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 147
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 147

Met Gly Ser Trp Ala Glu Phe Trp Asp Arg Leu Asp Ala Ile Asp Ser
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Trp Ala Ala Tyr Ile Arg
50 55 60

Gly Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 148
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 148

Met Gly Ser Trp Ala Glu Phe Asp Leu Arg Leu Arg Ala Ile Ala Lys
1 5 10 15

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

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Leu Asp Ala Ala Tyr Ile Arg
50 55 60

Gly Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 149
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 149

Met Gly Ser Trp Ser Glu Phe Trp Asp Arg Leu Tyr Ala Ile Arg Ile
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Ser Val Ala Ala Arg Ile Arg
50 55 60

Asn Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 150
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 150

Met Gly Ser Trp Ser Glu Phe Trp Phe Arg Leu Gly Ala Ile Arg Asn
1 5 10 15

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Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

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

His Trp Leu Gln Ala Tyr Arg His Asn
65                  70
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<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 151

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Met Gly Ser Trp Ser Glu Phe Asn Asp Arg Leu Asp Ala Ile Arg Trp
1               5                   10                  15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gln Val Ala Ala Thr Ile Arg
    50                  55                  60

Tyr Arg Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 152
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<223> synthetic construct

<400> 152

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Ala Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 153
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 153

Met Gly Ser Trp Ala Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Ala Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 154
<211> 73
<212> PRT
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<220>
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<400> 154

Met Gly Ser Trp Thr Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Ala Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 155
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 155

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Lys Tyr Thr Ala Ala Ala Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 156
<211> 73
<212> PRT
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<400> 156

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 157

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Ala Ile Lys
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
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<220>
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<400> 158

Met Gly Ser Trp Ala Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<212> PRT
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<400> 159

Met Gly Ser Trp Thr Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

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<400> 160

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Val Ala Ala Val Ile Arg
50 55 60

His Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 161
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<212> PRT
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<400> 161

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ala Ser Ala Ala Ala Ile Arg
50 55 60

Ile Ala Leu Gln Ala Tyr Arg His Asn
65 70

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<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 162

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Gly Ala Ile Arg Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asn Thr Ala Ala Tyr Ile Arg
50 55 60

Thr Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 163
<211> 73
<212> PRT
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<220>
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<400> 163

Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly Ala Ile Arg Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Val Thr Ala Ala Gln Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 164
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 164

Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Thr Ile Arg
50 55 60

Arg Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 165
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 165

Met Gly Ser Trp Ser Glu Phe Trp Ala Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Thr Ile Arg
50 55 60

Arg Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 166
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 166

Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Gly Thr Ile Arg
50 55 60

Arg Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 167
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 167

Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala Thr Ile Lys
50 55 60

Arg Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 168
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 168

Met Gly Ser Trp Ser Glu Phe Trp Ala Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

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Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Gly Thr Ile Lys
50 55 60

Arg Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 169
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 169

Met Gly Ser Trp Ser Glu Phe Trp Asp Arg Leu Thr Ala Ile Arg Val
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala Ala His Ile Arg
50 55 60

Lys Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 170
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 170

Met Gly Ser Trp Thr Glu Phe Trp Thr Arg Leu Asn Ala Ile Tyr Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Phe Thr Ala Ala Ser Ile Arg
50 55 60

Met Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 171
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 171

Met Gly Ser Trp Phe Glu Phe Trp Asp Arg Leu Ala Ala Ile Arg Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Tyr Val Ala Ala Lys Ile Arg
50 55 60

Val Arg Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 172
<211> 73
<212> PRT
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<400> 172

Met Gly Ser Trp Thr Glu Phe Trp Val Arg Leu Asn Ala Ile Arg Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg His Thr Ala Ala Ile Ile Arg
50 55 60

Asn Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 173
<211> 73
<212> PRT
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<220>
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<400> 173

Met Gly Ser Trp Val Glu Phe Trp His Arg Leu Gly Ala Ile Tyr Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Arg Thr Ala Ala Leu Ile Arg
50 55 60

Gln Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 174
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 174

Met Gly Ser Trp Val Glu Phe Trp Asn Arg Leu Gly Ala Ile Tyr Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg His Thr Ala Ala Val Ile Arg
50 55 60

Leu Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 175
<211> 73
<212> PRT
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<400> 175

Met Gly Ser Trp Ser Glu Phe Trp Glu Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Arg Thr Ala Ala Thr Ile Arg
50 55 60

Ser Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 176
<211> 73
<212> PRT
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<400> 176

Met Gly Ser Trp Glu Glu Phe Asp Asn Arg Leu Glu Ala Ile Phe Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu Phe Ala Ala Thr Ile Arg
50 55 60

Ile Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 177
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 177

Met Gly Ser Trp Met Glu Phe Trp Asp Arg Leu Tyr Ala Ile Glu Phe
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Arg Val Ala Ala Thr Ile Arg
50 55 60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 178
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<212> PRT
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<220>
<223> synthetic construct

<400> 178

Met Gly Ser Trp Thr Glu Phe Trp Glu Arg Leu Tyr Ala Ile Glu Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Ser Val Ala Ala Thr Ile Arg
50 55 60

Tyr Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 179
<211> 73
<212> PRT
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<223> synthetic construct

<400> 179

Met Gly Ser Trp Asn Glu Phe Trp Glu Arg Leu Tyr Ala Ile Glu Leu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Met Thr Ala Ala Tyr Ile Arg
50 55 60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 180
<211> 73
<212> PRT
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<220>
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<400> 180

Met Gly Ser Trp Tyr Glu Phe Trp Lys Arg Leu Tyr Ala Ile Glu Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Val Ala Ala Lys Ile Arg
50 55 60

Glu Gln Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 181
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 181

Met Gly Ser Trp Thr Glu Phe Trp Ala Arg Leu Tyr Ala Ile Glu Met
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Arg Val Ala Ala Leu Ile Arg
50 55 60

Glu Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 182
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 182

Met Gly Ser Trp His Glu Phe Trp Asp Arg Leu Tyr Ala Ile Glu Phe
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Gln Val Ala Ala Lys Ile Arg
50 55 60

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Trp His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 183
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 183

Met Gly Ser Trp Asp Glu Phe Glu Phe Arg Leu Gly Ala Leu Arg Trp
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Gly Ala Ala His Ile Arg
50 55 60

His Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 184
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 184

Met Gly Ser Trp Thr Glu Phe Tyr His Arg Leu Tyr Ala Ile Arg Glu
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Gly Ala Ala His Ile Arg
50 55 60

His Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 185
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<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 185

Met Gly Ser Trp Val Glu Phe Glu Thr Arg Leu Asp Ala Ile Arg Met
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Gly Ala Ala His Ile Arg
50 55 60

Ala Leu Leu Gln Ala Tyr Arg His Asn
65 70

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<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 186

Met Gly Ser Trp Gly Glu Phe Asp Val Arg Leu Phe Ala Ile Arg Glu
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Gly Tyr Ala Ala Gln Ile Arg
50 55 60

Ser Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 187
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 187

Met Gly Ser Trp Val Glu Phe Asp Glu Arg Leu Ser Ala Ile Arg Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Leu Tyr Ala Ala Gln Ile Arg
50 55 60

Val Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 188
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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2018369639 24 Oct 2022

<223> synthetic construct

<400> 188

Met Gly Ser Trp Ser Glu Phe Asp Gly Arg Leu Gly Ala Ile Trp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asp Arg Ala Ala Gln Ile Arg
50 55 60

Glu Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 189
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 189

Met Gly Ser Trp Gly Glu Phe Glu Gly Arg Leu His Ala Ile Arg Ser
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Gly Tyr Ala Ala Trp Ile Arg
50 55 60

Ala Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 190
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 190

Met Gly Ser Trp Gly Glu Phe Asn Gly Arg Leu Gly Ala Ile Arg Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Ala Tyr Ala Ala Ser Ile Arg
50 55 60

Ala Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 191
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 191

Met Gly Ser Trp Trp Glu Phe Thr Phe Arg Leu Ala Ala Ile Glu Phe
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Ala Ile Ala Ala Glu Ile Arg
50 55 60

Lys Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 192
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 192

Met Gly Ser Trp Asp Glu Phe Gln Phe Arg Leu Ala Ala Ile Gly Phe
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Arg Gln Ala Ala Arg Ile Arg
50 55 60

His Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 193
<211> 73
<212> PRT
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<223> synthetic construct

<400> 193

Met Gly Ser Trp Tyr Glu Phe Val Thr Arg Leu His Ala Ile Asp His
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Asp Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Phe Tyr Ala Ala Gly Ile Arg
50 55 60

Met Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 194
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<212> PRT
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<223> synthetic construct

<400> 194

Met Gly Ser Trp Ser Ile Glu Phe Trp Arg Leu Glu Ala Ile Lys Phe
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Val Glu Ala Ala Ala Ile Arg
50 55 60

Arg Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 195
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 195

Met Gly Ser Trp Gly Glu Phe Glu His Arg Leu Asp Pro Ser Thr Cys
1 5 10 15

Val Trp Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Arg Gly Ala Ala Val Ile Arg
    50   55   60

His Trp Leu Gln Ala Tyr Arg His Asn
65   70

<210> 196
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 196

Met Gly Ser Trp Ile Glu Phe Ala Met Arg Leu Glu Ala Ile Glu Asn
1   5   10   15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
            20   25   30

Ser Met Ile Ala His Phe Glu Glu Leu Leu Gln Asn Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Ile His Glu Ala Phe Ala Ile His
    50   55   60

Lys Glu Leu Trp Ala Tyr Arg His Asn
65   70

<210> 197
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 197

Met Gly Ser Trp Asn Glu Phe Tyr Gln Arg Leu Glu Ala Ile Glu Asn
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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

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

Arg Glu Leu Ile Ala Tyr Arg His Asn
65 70

<210> 198
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 198

Met Gly Ser Trp Asn Glu Phe Tyr Asp Arg Leu Arg Ala Ile Lys Lys
1 5 10 15

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

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

Gly Asn Pro Glu Val Glu Ala Leu His Arg Glu Ala His Ala Ile Thr
50 55 60

His Glu Leu Trp Ala Tyr Arg His Asn
65 70

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<210> 199
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 199

Met Gly Ser Trp Gly Glu Phe Lys His Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Asp Trp Ile Ala Val Phe Glu Val Gln Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 200
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 200

Met Gly Ser Trp Tyr Glu Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Lys Phe Glu
20 25 30

Ala Trp Ile Ala Glu Phe Glu Met Ile Leu Gln Arg Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 201
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 201

Met Gly Ser Trp Tyr Glu Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Gln Tyr Ile Ala Asp Phe Glu Gly Thr Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 202
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 202

Met Gly Ser Trp Tyr Asn Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Arg Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 203
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 203

Met Gly Ser Trp Phe Gln Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Gln Trp Ile Ala Asp Phe Glu His Gln Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 204
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 204

Met Gly Ser Trp Tyr Asn Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
            20   25   30

Val Trp Ile Ala Asp Phe Glu His Gln Leu Gln Glu Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 205
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 205

Met Gly Ser Trp Asp Ala Phe Lys His Arg Leu Ala Leu Ile Lys Trp
1   5   10   15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
            20   25   30

Glu Tyr Ile Ala Glu Phe Glu Ser Asn Leu Gln Ser Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 206
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 206

Met Gly Ser Trp Asp Gly Phe Lys His Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

Asn Trp Ile Ala Glu Phe Glu Gln Arg Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 207
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 207

Met Gly Ser Trp Asn Gly Phe Lys His Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Ser Tyr Ile Ala Glu Phe Glu Ser Gly Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 208
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 208

Met Gly Ser Trp Asn Ser Phe Lys His Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Trp Tyr Ile Ala Ser Phe Glu Ser Glu Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 209
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 209

Met Gly Ser Trp Ser Asp Phe Lys Tyr Arg Leu Ala Val Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Ser Phe Ile Ala His Phe Glu Asp Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 210
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 210

Met Gly Ser Trp Ser Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Leu Phe Ile Ala Lys Phe Glu Ile Asp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 211
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 211

Met Gly Ser Trp Tyr Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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Lys Tyr Ile Ala His Phe Glu His Asp Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 212
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 212

Met Gly Ser Trp Tyr Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Lys Tyr Ile Ala Gln Phe Glu His Asp Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 213
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 213

Met Gly Ser Trp Tyr Gly Phe Lys Tyr Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

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Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Thr Tyr Ile Ala Asp Phe Glu Asp Leu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 214
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 214

Met Gly Ser Trp Ser Thr Phe Lys Tyr His Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Asp Tyr Ile Ala Gln Phe Glu Thr Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 215
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 215

Met Gly Ser Trp His Glu Phe Lys Tyr Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

His His Ile Ala Gln Phe Glu Trp Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 216
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 216

Met Gly Ser Trp Asn Met Phe Lys Tyr Arg Leu Ala His Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 217
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 217

Met Gly Ser Trp His Gly Phe Lys Tyr Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Glu Trp Ile Ala Ser Phe Glu Arg Asp Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 218
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 218

Met Gly Ser Trp His Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Gly Trp Ile Ala Gln Phe Glu Ile Thr Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 219
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 219

Met Gly Ser Trp Gln Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Trp
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asn Trp Ile Ala Glu Phe Glu Thr Lys Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 220
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 220

Met Gly Ser Trp Ser Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

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Glu Trp Ile Ala Glu Phe Glu Thr Glu Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 221
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 221

Met Gly Ser Trp Gly Tyr Phe Lys Tyr Arg Leu Ala Met Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Ser Trp Ile Ala Glu Phe Glu Gly Ser Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 222
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 222

Met Gly Ser Trp His Ala Phe Lys Tyr Lys Leu Ala Met Ile Lys Trp
1 5 10 15

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Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Glu Trp Ile Ala Glu Phe Glu Ala Leu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 223
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 223

Met Gly Ser Trp Gln His Phe Lys Tyr Arg Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Ser Phe Ile Ala Lys Phe Glu His Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 224
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 224

Met Gly Ser Trp Asn Asp Phe Lys Tyr Arg Leu Ala Ile Ile Lys Tyr
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Ser Tyr Ile Ala Ser Phe Glu His Asp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 225
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 225

Met Gly Ser Trp Gly Ala Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Arg Phe Glu
20 25 30

Glu Phe Ile Ala Asn Phe Glu His Asp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 226
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 226

Met Gly Ser Trp Tyr Asn Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Ile Trp Ile Ala Glu Phe Glu His Asp Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 227
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 227

Met Gly Ser Trp Glu Gln Phe Lys Tyr Arg Leu Ala Ile Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 228
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 228

Met Gly Ser Trp Gln Gln Phe Lys Tyr Arg Leu Ala Ile Ile Lys Tyr
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 229
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 229

Met Gly Ser Trp Ala Gly Phe Lys Tyr Arg Leu Ala Val Ile Lys Tyr
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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Gln Trp Ile Ala His Phe Glu Gly Met Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 230
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 230

Met Gly Ser Trp Thr Ala Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Ser Tyr Ile Ala His Phe Glu Asp Met Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 231
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 231

Met Gly Ser Trp Ala His Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

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Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 232
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 232

Met Gly Ser Trp Ala Asn Phe Lys Tyr Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 233
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

2018369639 24 Oct 2022

<223> synthetic construct

<400> 233

Met Gly Ser Trp Ala Thr Phe Lys Tyr Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Tyr Ile Ala Gly Phe Glu Glu Gly Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 234
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 234

Met Gly Ser Trp Thr His Phe Lys Tyr Arg Leu Ala Leu Ile Lys Trp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

Val His Ile Ala Asp Phe Glu Ala Gln Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 235
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 235

Met Gly Ser Trp Asn Thr Phe Lys Tyr His Leu Ala Val Ile Lys Phe
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 236
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 236

Met Gly Ser Trp Thr Gln Phe Lys Tyr His Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

Gln Trp Ile Ala Glu Phe Glu Lys Thr Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 237
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 237

Met Gly Ser Trp Asn Gln Phe Lys Tyr Arg Leu Ala Val Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Thr Trp Ile Ala Ala Phe Glu Glu Gln Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 238
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 238

Met Gly Ser Trp Asn Glu Phe Lys Tyr His Leu Ala Val Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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Thr Trp Ile Ala Glu Phe Glu Tyr Glu Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 239
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 239

Met Gly Ser Trp Val Gln Phe Lys Tyr His Leu Ala Val Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 240
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 240

Met Gly Ser Trp Val Asp Phe Lys Tyr His Leu Ala Val Ile Lys Phe
1 5 10 15

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Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

Thr Trp Ile Ala Asn Phe Glu Gln Glu Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 241
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 241

Met Gly Ser Trp Val Asp Phe Lys Tyr His Leu Ala Val Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Asn Trp Ile Ala His Phe Glu Ser Ile Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 242
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 242

Met Gly Ser Trp Val Glu Phe Lys Tyr His Leu Ala Val Ile Lys Phe
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 243
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 243

Met Gly Ser Trp Ser His Phe Lys Tyr His Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Lys Phe Glu
20 25 30

Phe Trp Ile Ala Glu Phe Glu His Asn Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 244
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 244

Met Gly Ser Trp Tyr His Phe Lys Tyr His Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

His Trp Ile Ala Glu Phe Glu Trp Thr Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 245
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 245

Met Gly Ser Trp Gln Gly Phe Lys Tyr His Leu Ala Leu Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

His Trp Leu Ala Glu Phe Glu His Asp Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 246
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 246

Met Gly Ser Trp Leu Ser Phe Lys His His Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Ala Trp Ile Ala Leu Phe Glu His Gln Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 247
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 247

Met Gly Ser Trp Ser Glu Phe Lys Tyr Lys Leu Ala Leu Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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Gly Trp Ile Ala Asn Phe Glu Thr Thr Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 248
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 248

Met Gly Ser Trp Ile Glu Phe Lys Tyr Lys Leu Ala Ile Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

His Trp Ile Ala Asp Phe Glu Phe Val Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 249
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 249

Met Gly Ser Trp Gln Asn Phe Lys Tyr His Leu Ala Met Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

Glu Phe Ile Ala Gln Phe Glu Ile Asn Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 250
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 250

Met Gly Ser Trp Tyr Asn Phe Lys Tyr His Leu Ala Ile Ile Lys Trp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

His Tyr Ile Ala Asp Phe Glu Arg Asn Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 251
<211> 73
<212> PRT
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<223> synthetic construct

<400> 251

Met Gly Ser Trp Tyr Gln Phe Lys Tyr His Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 252
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 252

Met Gly Ser Trp Ser His Phe Lys Tyr His Leu Ala Ile Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

Ile Trp Ile Ala Lys Phe Glu Asp Glu Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 253
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 253

Met Gly Ser Trp Val Gly Phe Lys Ala His Leu Ala Ile Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

Ile Phe Ile Ala Asp Phe Glu Ala Leu Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 254
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 254

Met Gly Ser Trp Val Asn Phe Lys Tyr Lys Leu Ala Ile Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Trp Ile Ala Glu Phe Glu Arg Thr Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 255
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 255

Met Gly Ser Trp Ser Asn Phe Lys Tyr Arg Leu Ala Val Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Trp Ile Ala Asp Phe Glu Leu His Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 256
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 256

Met Gly Ser Trp Thr Asn Phe Lys Tyr Lys Leu Ala Val Ile Lys Phe
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 257
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 257

Met Gly Ser Trp Thr Gly Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 258
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 258

Met Gly Ser Trp His Asn Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

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Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 259
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 259

Met Gly Ser Trp Phe Ala Phe Lys His Arg Leu Ala Val Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

His Trp Ile Ala Gln Phe Glu His Asp Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 260
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 260

Met Gly Ser Trp Tyr Glu Phe Lys His Arg Leu Ala Val Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asn Trp Ile Ala Gln Phe Glu His Glu Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 261
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 261

Met Gly Ser Trp Tyr Lys Phe Lys His Lys Leu Ala Val Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Trp Ile Ala Glu Phe Glu Val Thr Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 262
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 262

Met Gly Ser Trp Phe Tyr Phe Lys Gln Lys Leu Ala Phe Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 263
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 263

Met Gly Ser Trp Phe Ser Phe Lys His His Leu Ala Val Ile Lys Trp
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 264
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 264

Met Gly Ser Trp Gly Asn Phe Lys Tyr Arg Leu Ala Ile Ile Lys Phe
1 5 10 15

His Leu Glu Ala Leu Gly Ser Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Ala Trp Ile Ala Asn Phe Glu Ser Met Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 265
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 265

Met Gly Ser Trp Ser Tyr Phe Lys Tyr Gly Leu Ala Ile Ile Lys Ile
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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Arg Trp Ile Ala Ala Phe Glu His Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 266
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 266

Met Gly Ser Trp Ser Tyr Phe Lys Phe Gly Leu Ala His Ile Lys Leu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Gln Trp Ile Ala Ser Phe Glu Glu Gln Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 267
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 267

Met Gly Ser Trp Ser Tyr Phe Lys Trp Gly Leu Ala His Ile Lys Leu
1 5 10 15

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Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
            20                  25                  30

Phe Trp Ile Ala Glu Phe Glu Gly Leu Leu Gln Asp Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 268
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 268

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Met Gly Ser Trp Ile Tyr Phe Lys Tyr Gly Leu Ala His Ile Lys Thr
1               5                   10                  15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
            20                  25                  30

Gln Trp Ile Ala Glu Phe Glu Lys Met Leu Gln Asp Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 269
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 269

Met Gly Ser Trp Gly Tyr Phe Lys Tyr Gly Leu Ala Thr Ile Lys His
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Leu Trp Ile Ala Lys Phe Glu Glu Gln Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 270
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 270

Met Gly Ser Trp Glu Tyr Phe Lys Tyr Gly Leu Ala Thr Ile Lys Met
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

His Trp Ile Ala His Phe Glu His Gln Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 271
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 271

Met Gly Ser Trp Ser Tyr Phe Lys Tyr Gly Leu Ala Thr Ile Lys Glu
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Thr Trp Ile Ala Met Phe Glu Lys Gln Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 272
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 272

Met Gly Ser Trp His Tyr Phe Lys Asn Gly Leu Ala Ile Ile Lys Glu
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ile Trp Ile Ala Met Phe Glu Met Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 273
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 273

Met Gly Ser Trp Gln Tyr Phe Lys Tyr Gly Leu Ala Ile Ile Lys Ile
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ala Trp Ile Ala Thr Phe Glu Lys Gln Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 274
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 274

Met Gly Ser Trp Val Tyr Phe Lys His Gly Leu Ala Val Ile Lys Met
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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Thr Trp Ile Ala Gln Phe Glu Met Thr Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 275
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 275

Met Gly Ser Trp Val Tyr Phe Lys Tyr Gly Leu Ala Val Ile Lys Glu
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Thr Trp Ile Ala Glu Phe Glu Phe Gly Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 276
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 276

Met Gly Ser Trp Tyr Tyr Phe Lys Tyr Gly Leu Ala Val Ile Lys Gly
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
            20   25   30

Thr Trp Ile Ala Lys Phe Glu Asn His Leu Gln Ser Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 277
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 277

Met Gly Ser Trp Thr Tyr Phe Lys Tyr Gly Leu Ala Leu Ile Lys Tyr
1   5   10   15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
            20   25   30

Glu Trp Ile Ala Gln Phe Glu Val Ser Leu Gln His Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 278
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 278

Met Gly Ser Trp Asp Tyr Phe Lys Tyr Gly Leu Ala Leu Ile Lys Ile
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Val Trp Ile Ala Gln Phe Glu Met Ala Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 279
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 279

Met Gly Ser Trp Thr Tyr Phe Lys Phe Gly Leu Ala His Ile Lys Asp
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Gln Trp Ile Ala Met Phe Glu Gln Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 280
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 280

Met Gly Ser Trp Gly Tyr Phe Lys His Gly Leu Ala His Ile Lys Ser
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Val Trp Ile Ala Ala Phe Glu Asn Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 281
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 281

Met Gly Ser Trp Gly Tyr Phe Lys Thr Gly Leu Ala Ile Ile Lys Ala
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Leu Trp Ile Ala Gln Phe Glu Glu Thr Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 282
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 282

Met Gly Ser Trp Ala Tyr Phe Lys Tyr Gly Leu Ala Val Ile Lys Leu
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Arg Tyr Ile Ala Glu Phe Glu Tyr Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 283
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 283

Met Gly Ser Trp Leu Asp Phe Lys Glu Gly Leu Ala Asp Ile Lys Arg
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 284
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 284

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

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Trp Gly Ile Ala Trp Phe Glu Gly Phe Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 285
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 285

Met Gly Ser Trp Ile Val Phe Lys Gln Ser Leu Ala Trp Ile Lys Glu
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
            20   25   30

Phe Tyr Ile Ala Asn Phe Glu His Thr Leu Gln Asn Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 286
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 286

Met Gly Ser Trp Ile Tyr Phe Lys Asp Ser Leu Ala Tyr Ile Lys Lys
1   5   10   15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
            20   25   30

Tyr Tyr Ile Ala Asn Phe Glu His Glu Leu Gln Tyr Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 287
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 287

Met Gly Ser Trp Asp His Phe Lys Tyr Asn Leu Ala Trp Ile Lys Lys
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Trp Tyr Ile Ala Asn Phe Glu Lys Arg Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 288
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 288

Met Gly Ser Trp Phe Thr Phe Lys Gln Asn Leu Ala Trp Ile Lys Leu
1 5 10 15

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

Tyr Tyr Ile Ala Asp Phe Glu Asn Lys Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 289
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 289

Met Gly Ser Trp Arg Glu Phe Lys Tyr Gly Leu Ala His Ile Lys Arg
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Tyr Tyr Ile Ala Lys Phe Glu Gln Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 290
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 290

Met Gly Ser Trp Ile Gln Phe Lys Tyr Gly Leu Ala His Ile Lys Arg
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Trp Tyr Ile Ala Asp Phe Glu Gln Gln Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

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Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 291
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 291

Met Gly Ser Trp Val Glu Phe Lys His Asn Leu Ala Trp Ile Lys Val
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Tyr Tyr Ile Ala Gln Phe Glu Glu Gln Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 292
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 292

Met Gly Ser Trp Ile Ser Phe Lys Asp Asn Leu Ala Met Ile Lys Glu
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Trp Tyr Ile Ala Thr Phe Glu Val Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 293
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 293

Met Gly Ser Trp His Ile Phe Lys Asp Asn Leu Ala Thr Ile Lys Ala
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Trp Tyr Ile Ala Lys Phe Glu Glu Glu Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 294
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 294

Met Gly Ser Trp Thr Ser Phe Lys His Gly Leu Ala Gly Ile Lys Arg
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Trp Tyr Ile Ala Gln Phe Glu Arg His Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 295
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 295

Met Gly Ser Trp Gln Ser Phe Lys His Ala Leu Ala Asp Ile Lys Ile
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 296
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 296

Met Gly Ser Trp His Thr Phe Lys Glu Ala Leu Ala Gln Ile Lys Gly
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 297
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 297

Met Gly Ser Trp Thr Asp Phe Lys Thr Ser Leu Ala Asp Ile Lys Ala
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Lys Phe Glu
20 25 30

Tyr Tyr Ile Ala Ile Phe Glu Tyr Arg Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 298
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 298

Met Gly Ser Trp Thr Asn Phe Lys Glu Gly Leu Ala Glu Ile Lys Arg
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Arg Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 299
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 299

Met Gly Ser Trp His Thr Phe Lys Asp Gly Leu Ala Glu Ile Lys Ser
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 300
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 300

Met Gly Ser Trp Gln Phe Phe Lys Glu His Leu Ala Ser Ile Lys Phe
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Ala Ile Ala Asp Phe Glu Tyr His Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 301
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 301

Met Gly Ser Trp Thr Tyr Phe Lys Glu His Leu Ala Ser Ile Lys Phe
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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Asp Ala Ile Ala Glu Phe Glu Lys Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 302
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 302

Met Gly Ser Trp Ile Ile Phe Lys Gly Tyr Leu Ala His Ile Lys His
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Phe Tyr Ile Ala Ile Phe Glu Met Glu Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 303
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 303

Met Gly Ser Trp Tyr Leu Phe Gln Ser His Leu Ala His Ile Lys His
1 5 10 15

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His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Phe Thr Ile Ala Gly Phe Glu Gln Glu Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 304
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 304

Met Gly Ser Trp Tyr Ser Phe Lys Trp Thr Leu Ala Arg Ile Lys Leu
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Asn Val Ile Ala His Phe Glu Met Glu Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 305
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 305

Met Gly Ser Trp Thr Thr Leu Lys Trp Arg Leu Ala His Ile Lys Gln
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Tyr Asp Ile Ala His Phe Glu Glu Leu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 306
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 306

Met Gly Ser Trp Tyr Gly Phe Lys Trp Tyr Leu Ala Thr Ile Lys Lys
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Thr Glu Ile Ala Thr Phe Glu Leu Trp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 307
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 307

Met Gly Ser Trp Ile Glu Phe Asn Met Arg Val Leu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Tyr Glu Ala Cys Leu Asp Pro
50 55 60

Trp Ser Ser Ala Ala Tyr Arg His Asn
65 70

<210> 308
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 308

Met Gly Ser Trp Ile Glu Phe His Glu Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu Met Ala Ala Ser Ile Arg
50 55 60

His Gly Leu Gln Ala Tyr Arg His Asn
65 70

<210> 309
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 309

Met Gly Ser Trp Phe Glu Phe Tyr Glu Arg Leu Trp Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Ser Ile Arg
50 55 60

Ser Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 310
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 310

Met Gly Ser Trp Phe Glu Phe Trp Asp Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Tyr Asn Ala Ala Glu Ile Arg
50 55 60

Lys Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 311
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 311

Met Gly Ser Trp His Glu Phe Trp Ser Arg Leu Asp Ala Ile Asp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Gly Ala Ala Ala Asp Ile Arg
50 55 60

Ala Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 312
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 312

Met Gly Ser Trp Tyr Glu Phe Trp Ile Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Asp Ile Leu Arg Asp Phe Ala Ala Asp Ile Arg
50 55 60

Thr Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 313
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 313

Met Gly Ser Trp His Glu Phe Trp Asp Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Tyr Ile Arg
50 55 60

Glu Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 314
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 314

Met Gly Ser Trp Glu Glu Phe Trp Asp Arg Leu Phe Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Asn Glu Ala Ala Glu Ile Arg
50 55 60

Met Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 315
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 315

Met Gly Ser Trp Trp Glu Phe Asp Asp Arg Leu Phe Ala Ile Asp Thr
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu Trp Ala Ala Thr Ile Arg
50 55 60

Met Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 316
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 316

Met Gly Ser Trp Thr Glu Phe His Asp Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Glu Ala Ala Gln Ile Arg
50 55 60

Trp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 317
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 317

Met Gly Ser Trp Ala Glu Phe Glu Asp Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Glu Ala Ala Ala Ile Arg
50 55 60

Phe Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 318
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 318

Met Gly Ser Trp Val Glu Phe Trp Phe Arg Leu Glu Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Ala Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 319
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 319

Met Gly Ser Trp Val Glu Phe Trp Gln Arg Leu Glu Ala Ile Glu Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Glu Ile Arg
50 55 60

Trp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 320
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 320

Met Gly Ser Trp Ser Glu Phe Trp Gln Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asn Ala Ala Met Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 321
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 321

Met Gly Ser Trp Ser Glu Phe Ile Thr Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Glu Glu Ala Ala Glu Ile Arg
50 55 60

Gln His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 322
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 322

Met Gly Ser Trp Tyr Glu Phe Glu Thr Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Val Glu Ala Ala Glu Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 323
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 323

Met Gly Ser Trp Thr Glu Phe Tyr Tyr Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Val Glu Ala Ala Asn Ile Arg
50 55 60

Asp Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 324
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 324

Met Gly Ser Trp Tyr Glu Phe Val Ile Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

His Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 325
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 325

Met Gly Ser Trp Thr Glu Phe Ser Ile Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Thr Tyr Ala Ala Asn Ile Arg
50 55 60

His Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 326
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 326

Met Gly Ser Trp Thr Glu Phe Ser Ile Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Thr Tyr Ala Ala Phe Ile Arg
50 55 60

His Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 327
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 327

Met Gly Ser Trp Thr Glu Phe Val Trp Arg Leu Glu Ala Ile Trp Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu Asp Ala Ala Val Ile Arg
50 55 60

His Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 328
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 328

Met Gly Ser Trp Val Glu Phe His Glu Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Asp Ala Ala Phe Ile Arg
50 55 60

Gln Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 329
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 329

Met Gly Ser Trp Val Glu Phe His Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Tyr Ile Arg
50 55 60

Ser Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 330
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 330

Met Gly Ser Trp Ile Glu Phe Tyr Asp Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

```
Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Phe Ile Arg
    50                  55                  60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65                  70
```

<210> 331
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 331

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Met Gly Ser Trp Val Glu Phe Asp Gln Arg Leu Glu Ala Ile Tyr Asp
1               5                   10                  15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Gln Ile Arg
    50                  55                  60

Lys Trp Leu Gln Ala Tyr Arg His Asn
65                  70
```

<210> 332
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 332

Met Gly Ser Trp Val Glu Phe His Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Glu Tyr Ala Ala Gly Ile Arg
50 55 60

Trp Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 333
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 333

Met Gly Ser Trp Glu Glu Phe Ala Gln Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Tyr Val Ala Ala Gln Ile Arg
50 55 60

Tyr His Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 334
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 334

Met Gly Ser Trp Asp Glu Phe Ala Trp Arg Leu Asp Val Ile Phe Ala
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Asp Gly Leu Gln Ala Tyr Arg His Asn
65 70

<210> 335
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 335

Met Gly Ser Trp Asp Glu Phe Tyr Tyr Arg Leu Glu Ala Ile Glu Met
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His Tyr Ala Ala Gln Ile Arg
50 55 60

His Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 336
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 336

Met Gly Ser Trp Glu Glu Phe Tyr Asp Arg Leu Glu Ala Ile Tyr Asn
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu Tyr Ala Ala Asp Ile Arg
50 55 60

Glu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 337
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 337

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 338
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 338

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 339
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 339

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Thr
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 340
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 340

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1   5   10   15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 341
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 341

```
Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Lys Trp
1               5                  10                  15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50                  55                  60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65                  70
```

<210> 342
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 342

```
Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1               5                  10                  15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Lys Leu Arg Lys Ile Ala Ala Val Ile Arg
    50                  55                  60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65                  70
```

<210> 343
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 343

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Gly Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 344
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 344

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 345
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 345

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Gly Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 346
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 346

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 347
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 347

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 348
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 348

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Ala Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 349
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 349

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1   5   10   15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 350
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 350

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Glu Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 351
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 351

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Ser Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 352
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 352

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 353
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 353

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

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Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 354
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 354

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Gln Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 355
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 355

Met Gly Ser Trp Asp Glu Phe Ser Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 356
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 356

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 357
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 357

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Gln Leu Ala Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 358
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 358

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Ala Ala Ile Lys Thr
1   5   10   15

Gln Leu Ala Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val Ile Arg
    50   55   60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65   70

<210> 359
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 359

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Gln Leu Ala Ala Leu Gly Gly Glu Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 360
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 360

Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Gln Leu Ala Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Val Ile Arg
50 55 60

Glu Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 361
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 361

Met Gly Ser Trp Asp Glu Phe Glu Gln Arg Leu Ile Ala Ile Glu Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Val Ile Arg
50 55 60

Lys Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 362
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 362

Met Gly Ser Trp Val Glu Phe Asp Gln Arg Leu Gly Ala Ile Trp Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Gln Gly Ala Ala Val Ile Arg
50 55 60

Asp Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 363
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 363

Met Gly Ser Trp Val Glu Phe Asp Met Arg Leu Ser Ala Ile Trp Glu
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Glu Ile Arg
50 55 60

Glu Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 364
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 364

Met Gly Ser Trp Val Glu Phe Asp Gln Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Glu Ile Arg
50 55 60

Glu His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 365
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 365

Met Gly Ser Trp His Glu Phe Asp Gln Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Leu Tyr Ala Ala Leu Ile Arg
50 55 60

His Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 366
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 366

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Asp Ala Ile Glu Gly
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Leu Ala Ala Glu Ile Arg
50 55 60

Ala Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 367
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 367

Met Gly Ser Trp Val Glu Phe Tyr Ser Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ile Ala Ala Ala Ser Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 368
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 368

Met Gly Ser Trp Tyr Glu Phe Tyr Glu Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Asp Trp Ala Ala Trp Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 369
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 369

Met Gly Ser Trp Phe Glu Phe Asp Asp Arg Leu Trp Ala Ile Glu Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Asp Asn Ala Ala Trp Ile Arg
50 55 60

Glu Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 370
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 370

Met Gly Ser Trp Tyr Glu Phe Trp Asp Arg Leu Asp Ala Leu Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asp Ser Ala Ala Phe Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 371
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 371

Met Gly Ser Trp Met Glu Phe Val Asp Arg Leu Asp Ala Ile Glu Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ile Glu Ala Ala Phe Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 372
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 372

Met Gly Ser Trp Asp Glu Phe Val Asp Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ile Gln Ala Ala Ile Ile Arg
50 55 60

Glu Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 373
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 373

Met Gly Ser Trp Phe Glu Phe Asn Tyr Arg Leu Gly Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Gln Ile Ala Ala Glu Ile Arg
50 55 60

Glu Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 374
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 374

Met Gly Ser Trp Glu Glu Phe Phe Thr Arg Leu Asp Ala Ile Asn Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Tyr Glu Ala Ala Glu Ile Arg
50 55 60

His Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 375
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 375

Met Gly Ser Trp Tyr Glu Phe Ser Asn Arg Leu Asp Ala Ile Gly Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg His Gln Ala Ala Glu Ile Arg
50 55 60

Trp Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 376
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 376

Met Gly Ser Trp Tyr Glu Phe Trp Gly Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Met Leu Arg Glu Asp Ala Ala Glu Ile Arg
50 55 60

Gly Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 377
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 377

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Trp Ala Ile Asp Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Asp Glu Ala Ala Trp Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 378
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 378

Met Gly Ser Trp Val Glu Phe Val Asp Arg Leu Trp Ala Ile Asp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Thr Trp Ala Ala Trp Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 379
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 379

Met Gly Ser Trp Phe Glu Phe Trp Asp Arg Leu Glu Ala Ile Trp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Arg Glu Ala Ala Ile Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 380
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 380

Met Gly Ser Trp Phe Glu Phe Glu Asp Arg Leu Glu Ala Ile Tyr Gln
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Trp Ile Arg
50 55 60

Ser Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 381
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 381

Met Gly Ser Trp Phe Glu Phe His Asp Arg Leu Trp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Glu Glu Ala Ala Asp Ile Arg
50 55 60

Leu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 382
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 382

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Trp Ala Ile Asp Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val His Ala Ala Asp Ile Arg
50 55 60

Asp Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 383
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 383

Met Gly Ser Trp Phe Glu Phe Gln Asp Arg Leu Trp Ala Ile Asp Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asp His Ala Ala Met Ile Arg
50 55 60

Trp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 384
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 384

Met Gly Ser Trp Asp Glu Phe Glu Glu Arg Leu Phe Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Tyr Leu Ala Ala Asp Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 385
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 385

Met Gly Ser Trp Glu Glu Phe Trp Glu Arg Leu Asp Ala Ile Asp Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Asn Asp Ala Ala Asp Ile Arg
50 55 60

Glu Pro Leu Gln Ala Tyr Arg His Asn
65 70

<210> 386
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 386

Met Gly Ser Trp Met Glu Phe Trp Glu Arg Leu Glu Ala Ile Asp Met
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asp Asp Ala Ala Val Ile Arg
50 55 60

Asp Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 387
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 387

Met Gly Ser Trp Leu Glu Phe Met Trp Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Glu Met Ala Ala Ala Ile Arg
50 55 60

Asp Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 388
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 388

Met Gly Ser Trp Thr Glu Phe Tyr Asn Arg Leu Asp Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Glu Tyr Ala Ala Asp Ile Arg
50 55 60

Thr Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 389
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 389

Met Gly Ser Trp Trp Glu Phe Ile Trp Arg Leu Glu Ala Ile Glu Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Ser Arg Ala Ala Asp Ile Arg
50 55 60

Thr Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 390
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 390

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Tyr Tyr Ala Ala Glu Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 391
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 391

Met Gly Ser Trp Ser Glu Phe Glu Asp Arg Leu Trp Ala Ile Asp Gln
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ala Tyr Ala Ala Asp Ile Arg
50 55 60

Trp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 392
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 392

Met Gly Ser Trp Thr Glu Phe Trp Glu Arg Leu Asn Ala Ile Asp Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Leu Tyr Ala Ala Glu Ile Arg
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 393
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 393

Met Gly Ser Trp Trp Glu Phe Glu Glu Arg Leu Trp Ala Ile Asp Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Ser Trp Ala Ala Glu Ile Arg
50 55 60

Ala Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 394
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 394

Met Gly Ser Trp Trp Glu Phe Glu Asn Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Asn Tyr Ala Ala Glu Ile Arg
50 55 60

Trp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 395
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 395

Met Gly Ser Trp Val Glu Phe Glu Glu Arg Leu Trp Ala Ile Asp Glu
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Trp Ala Ala Asp Ile Arg
50 55 60

Trp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 396
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 396

Met Gly Ser Trp Val Glu Phe Glu Glu Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Asp Ala Ala Asn Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 397
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 397

Met Gly Ser Trp Met Glu Phe Glu Glu Arg Leu Trp Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ser Glu Ala Ala Trp Ile Arg
50 55 60

Met Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 398
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 398

Met Gly Ser Trp Ser Glu Phe Glu His Arg Leu Glu Ala Ile Glu Ser
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Ser Glu Ala Ala Trp Ile Arg
50 55 60

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Glu Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 399
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 399

Met Gly Ser Trp Phe Glu Phe Trp Glu Arg Leu Asp Ala Ile Glu Trp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ser Thr Ala Ala Asp Ile Arg
50 55 60

Arg Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 400
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 400

Met Gly Ser Trp Phe Glu Phe Trp Gly Arg Leu Glu Ala Ile Glu Ser
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu His Ala Ala Trp Ile Arg
50 55 60

Ala Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 401
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 401

Met Gly Ser Trp Gln Glu Phe Thr Met Arg Leu Asp Ala Ile Tyr Asn
1 5 10 15

Arg Leu Glu Thr Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gln Ser Ala Ala Asn Ile Arg
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 402
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 402

Met Gly Ser Trp Ser Glu Phe Asn Met Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

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Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg His Ser Ala Ala Arg Ile Arg
50 55 60

Leu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 403
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 403

Met Gly Ser Trp Ser Glu Phe Asn Met Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg His Ser Ala Ala Leu Ile Arg
50 55 60

Leu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 404
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 404

Met Gly Ser Trp Ile Glu Phe Asn Met Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Lys Val Ala Ala Asn Ile Arg
50 55 60

Leu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 405
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 405

Met Gly Ser Trp Tyr Glu Phe His His Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ser Ser Ala Ala Asn Ile Arg
50 55 60

Lys Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 406
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 406

Met Gly Ser Trp Tyr Glu Phe Ala Lys Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ser Ser Ala Ala Asn Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 407
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 407

Met Gly Ser Trp Thr Glu Phe Tyr Val Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Met Val Ala Ala Asn Ile Arg
50 55 60

Thr Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 408
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 408

Met Gly Ser Trp Val Glu Phe Tyr Thr Arg Leu Asp Ala Ile Tyr Gly
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gln Val Ala Ala Asn Ile Arg
50 55 60

Met Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 409
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 409

Met Gly Ser Trp Val Glu Phe His Met Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Thr Ala Ala Ala Asn Ile Arg
50 55 60

Val Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 410
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 410

Met Gly Ser Trp Tyr Glu Phe Ala Ile Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Val Trp Ala Ala Asn Ile Arg
50 55 60

Thr Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 411
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 411

Met Gly Ser Trp Asn Glu Phe Val Ile Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Met Ala Ala Ala Asn Ile Arg
    50   55   60

Met Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 412
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 412

Met Gly Ser Trp Ser Glu Phe Tyr Val Arg Val Asp Ala Ile Tyr Ala
1   5   10   15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Lys Leu Arg Val Trp Ala Ala Asn Ile Arg
    50   55   60

His Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 413
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 413

Met Gly Ser Trp Ser Glu Phe His Val Arg Leu Asp Ala Ile Tyr Ala
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Arg Leu Arg Glu Trp Ala Ala Asn Ile Arg
50 55 60

Arg Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 414
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 414

Met Gly Ser Trp Val Glu Phe His Leu Arg Leu Asp Ala Ile Tyr Gly
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val Trp Ala Ala Asn Ile Arg
50 55 60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 415
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 415

Met Gly Ser Trp Val Glu Phe Glu Met Arg Leu Asp Ala Ile Val Gly
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Arg Trp Ala Ala Asn Ile Arg
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 416
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 416

Met Gly Ser Trp Val Glu Phe Asn Ile Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg His Trp Ala Ala Ser Ile Arg
50 55 60

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Arg Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 417
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 417

Met Gly Ser Trp His Glu Phe Gly Val Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Gln Ala Ala Ala Asn Ile Arg
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 418
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 418

Met Gly Ser Trp Thr Glu Phe Asn Leu Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Ala Ser Ala Ala Ala Ile Arg
50 55 60

Val Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 419
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 419

Met Gly Ser Trp Thr Glu Phe Asn Leu Arg Leu Asp Ala Ile Tyr Gly
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Ala Ala Ala Ala Asn Ile Arg
50 55 60

Val Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 420
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 420

Met Gly Ser Trp Val Glu Phe Asn Trp Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Trp Leu Arg Val Ser Ala Ala Lys Ile Arg
    50   55   60

Gly Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 421
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 421

Met Gly Ser Trp Asn Glu Phe Ala Trp Arg Leu Asp Ala Ile Tyr Ser
1   5   10   15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Trp Leu Arg Val Ala Ala Ala Asn Ile Arg
    50   55   60

Tyr Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 422
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 422

Met Gly Ser Trp Thr Glu Phe Ala Trp Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg His Val Ala Ala Asn Ile Arg
50 55 60

Arg Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 423
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 423

Met Gly Ser Trp Val Glu Phe Ser Ile Arg Leu Asp Ala Ile Tyr Thr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Lys Gly Ala Ala Asn Ile Arg
50 55 60

Lys Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 424
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 424

Met Gly Ser Trp Val Glu Phe Tyr Ile Arg Leu Asp Ala Ile Tyr Val
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Ser Tyr Ala Ala Asn Ile Arg
50 55 60

Gln Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 425
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 425

Met Gly Ser Trp Tyr Glu Phe Ser Met Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gln Leu Arg Gly Tyr Ala Ala Asn Ile Arg
50 55 60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 426
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 426

Met Gly Ser Trp Val Glu Phe Ile Tyr Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Arg Tyr Ala Ala Asn Ile Arg
50 55 60

Asn Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 427
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 427

Met Gly Ser Trp Ile Glu Phe Glu Val Arg Leu Asp Ala Ile Tyr Asn
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Arg Leu Arg Arg Tyr Ala Ala Asn Ile Arg
50 55 60

His Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 428
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 428

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asp Ala Ile Tyr Met
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Arg Tyr Ala Ala Asn Ile Arg
50 55 60

Ala Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 429
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 429

Met Gly Ser Trp Phe Glu Phe Tyr Met Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Arg Leu Arg Thr Phe Ala Ala Asn Ile Arg
50 55 60

Lys Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 430
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 430

Met Gly Ser Trp Tyr Glu Phe Asp Tyr Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Arg Leu Arg Lys Trp Ala Ala Asn Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 431
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 431

Met Gly Ser Trp Ser Glu Phe Tyr Leu Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Lys Thr Ala Ala Asn Ile Arg
50 55 60

Glu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 432
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 432

Met Gly Ser Trp Phe Glu Phe Tyr Glu Arg Leu Asp Ala Ile Asn Trp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Gly Glu Ala Ala Ala Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 433
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 433

Met Gly Ser Trp Asn Glu Phe Glu Asp Arg Leu Asp Ala Ile Trp Trp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Val Glu Ala Ala Phe Ile Arg
50 55 60

Thr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 434
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 434

Met Gly Ser Trp Phe Tyr Phe Lys Asp Asp Leu Ala Asp Ile Asn Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Asp Asp Ile Ala Gly Phe Glu Leu Thr Leu Leu Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 435
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 435

Met Gly Ser Trp His Phe Phe Lys Asp Asp Leu Ala Trp Ile Lys Asn
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Asp Asp Ile Ala Met Phe Glu Thr Met Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 436
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 436

Met Gly Ser Trp His Trp Phe Lys Thr Asp Leu Ala Asp Ile Lys Glu
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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Asp Asp Ile Ala Glu Phe Glu Glu Phe Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 437
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 437

Met Gly Ser Trp Trp Leu Phe Lys Asp Asp Leu Ala Glu Ile Lys Tyr
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 438
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 438

Met Gly Ser Trp Tyr Glu Phe Lys Asp Asp Leu Ala Glu Ile Lys Glu
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
            20   25   30

Leu Asp Ile Ala Asp Phe Glu Trp Leu Leu Gln Leu Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 439
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 439

Met Gly Ser Trp Gln Trp Phe Lys Asp Asp Leu Ala Tyr Ile Lys Glu
1   5   10   15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
            20   25   30

Asp Met Ile Ala Asp Phe Glu Phe Glu Leu Gln Trp Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 440
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 440

Met Gly Ser Trp Ile Leu Phe Lys Asp Asp Leu Ala Trp Ile Lys Glu
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Asn Ile Ala Asp Phe Glu Glu Gln Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 441
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 441

Met Gly Ser Trp Ile Val Phe Lys Asp Asp Leu Ala Asp Ile Lys Arg
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Asp Glu Ile Ala Asp Phe Glu Trp Gln Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 442
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 442

Met Gly Ser Trp Gly His Phe Lys Gln Asp Leu Ala Trp Ile Lys Asp
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Asp Ile Ala Met Phe Glu Met Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 443
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 443

Met Gly Ser Trp Gly Tyr Phe Lys Asp Asp Leu Ala Trp Ile Lys Gly
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Trp Phe Ile Ala Val Phe Glu Glu Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 444
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 444

Met Gly Ser Trp Tyr Trp Phe Lys Asp Asp Leu Ala Glu Ile Lys Gly
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 445
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 445

Met Gly Ser Trp Met Phe Phe Lys Glu Asp Leu Ala Asp Ile Lys Trp
1 5 10 15

Ala Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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Glu Glu Ile Ala Leu Phe Glu Gln His Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 446
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 446

Met Gly Ser Trp Thr Phe Phe Lys Glu Asp Leu Ala Gly Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Glu Ile Ala Leu Phe Glu Glu Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 447
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 447

Met Gly Ser Trp Val Phe Phe Lys Asp Asp Leu Ala Asp Ile Lys Asp
1 5 10 15

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Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Ile Ala Ile Ala Leu Phe Glu Trp Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 448
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 448

Met Gly Ser Trp Thr Phe Phe Lys Asn Asp Leu Ala Glu Ile Lys Asp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 449
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 449

Met Gly Ser Trp Thr Tyr Phe Lys Asp Asp Leu Ala Asp Ile Lys Gln
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Ile Glu Ile Ala Glu Phe Glu Glu Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 450
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 450

Met Gly Ser Trp Thr Val Phe Lys Tyr Asp Leu Ala Asp Ile Lys Trp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Glu Ile Ala Glu Phe Glu Glu Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 451
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 451

Met Gly Ser Trp Tyr Trp Phe Lys Gln Asp Leu Ala His Ile Lys Ser
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 452
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 452

Met Gly Ser Trp Thr Phe Phe Lys Trp Asp Leu Ala Asp Ile Lys Ala
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Asp Leu Ala Gly Phe Glu Ala Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

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Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 453
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 453

Met Gly Ser Trp Ser Phe Phe Lys Glu Glu Leu Ala Asn Ile Gln Val
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Asp Ile Ala Asp Phe Glu Glu Asp Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 454
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 454

Met Gly Ser Trp Glu Phe Phe Lys Tyr Glu Leu Ala Asp Ile Lys Asp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Glu Asp Ile Ala Thr Phe Glu Glu Trp Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 455
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 455

Met Gly Ser Trp Gln Thr Phe Lys Asp Glu Leu Ala His Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 456
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 456

Met Gly Ser Trp Tyr Trp Phe Lys Glu Glu Leu Ala Phe Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Glu Asp Ile Ala Tyr Phe Glu Glu Met Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 457
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 457

Met Gly Ser Trp Asn Ser Phe Lys Asp Glu Leu Ala Glu Ile Lys Ala
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Glu Asp Ile Ala Trp Phe Glu Glu His Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 458
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 458

Met Gly Ser Trp Asp Leu Phe Lys Trp Glu Leu Ala Glu Ile Lys Leu
1 5 10 15

Gly Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Tyr Asp Ile Ala Trp Phe Glu Glu Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 459
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 459

Met Gly Ser Trp Ile Phe Phe Lys Gln Asp Leu Ala Glu Ile Lys Leu
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Trp Phe Glu Ser His Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 460
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 460

Met Gly Ser Trp His Leu Phe Lys Trp Thr Leu Ala Glu Ile Lys Tyr
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Thr Phe Glu Glu Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 461
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 461

Met Gly Ser Trp Val Thr Phe Lys Asp Glu Leu Ala Asp Ile Lys Asp
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 462
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 462

Met Gly Ser Trp Val Tyr Phe Lys Asp Glu Leu Ala Asp Ile Lys Asp
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Glu Asp Ile Ala Thr Phe Glu Tyr Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 463
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 463

Met Gly Ser Trp Glu Thr Phe Lys Tyr Glu Leu Ala Glu Ile Lys Asp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Asp Asp Ile Ala Glu Phe Glu Phe Glu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<211> 73
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<220>
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<400> 464

Met Gly Ser Trp Asn Thr Phe Lys Tyr Glu Leu Ala Glu Ile Lys His
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Asp Asp Ile Ala Met Phe Glu Trp Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 465
<211> 73
<212> PRT
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<220>
<223> synthetic construct

<400> 465

Met Gly Ser Trp Tyr Val Phe Lys Asp Glu Leu Ala Glu Ile Lys Gln
1 5 10 15

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Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Glu Phe Glu Thr Gln Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 466
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 466

Met Gly Ser Trp Ile Phe Phe Lys Glu Gln Leu Ala Ile Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Ala Phe Glu Asp Asp Leu Gln Phe Tyr Lys Gly Gln
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 467
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<212> PRT
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<223> synthetic construct

<400> 467

Met Gly Ser Trp Glu Phe Phe Lys Glu Val Leu Ala Glu Ile Lys Tyr
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 468
<211> 73
<212> PRT
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<220>
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<400> 468

Met Gly Ser Trp Val Phe Phe Lys Glu Asp Leu Ala Thr Ile Lys Asn
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Met Met Ile Ala Asp Phe Glu Ala Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 469
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<212> PRT
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<400> 469

Met Gly Ser Trp Glu Glu Phe Lys Glu Asp Leu Ala Glu Ile Lys Val
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Met Gly Ile Ala Asp Phe Glu Asp Gly Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 470
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<212> PRT
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<220>
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<400> 470

Met Gly Ser Trp His Trp Phe Lys Glu Asp Leu Ala Asn Ile Lys Asp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asn Ile Ala Asp Phe Glu Gly Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 471
<211> 73
<212> PRT
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<220>
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<400> 471

Met Gly Ser Trp Phe Trp Phe Lys Glu Asp Leu Ala Phe Ile Lys Glu
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Gly Ile Ala Phe Phe Glu Trp Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 472
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 472

Met Gly Ser Trp Gln Trp Phe Lys Glu Asp Leu Ala Glu Ile Lys His
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Phe Ile Ala Gln Phe Glu Phe Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 473
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 473

Met Gly Ser Trp His Trp Phe Lys Glu Asp Leu Ala Ile Ile Lys Gln
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Gln Trp Ile Ala Glu Phe Glu Trp Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 474
<211> 73
<212> PRT
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<220>
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<400> 474

Met Gly Ser Trp Asn Trp Phe Lys Glu Asp Leu Ala Ile Ile Lys Met
1 5 10 15

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Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

His Asn Ile Ala Gly Phe Glu Phe Glu Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 475
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 475

Met Gly Ser Trp Ser Trp Phe Lys Glu Asp Leu Ala Glu Ile Lys Met
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Trp Tyr Ile Ala Glu Phe Glu Phe Gln Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 476
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 476

Met Gly Ser Trp Ser Trp Phe Lys Gln Asp Leu Ala Asp Ile Lys Ile
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Asp Ile Ala Glu Phe Glu Phe Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 477
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 477

Met Gly Ser Trp Ser Trp Phe Lys Glu Asp Leu Ala Asp Ile Lys Phe
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Leu Asp Ile Ala Asp Phe Glu Gln Ala Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 478
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 478

Met Gly Ser Trp Ser Trp Phe Lys Glu Asp Leu Ala Ser Ile Lys Ala
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 479
<211> 73
<212> PRT
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<220>
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<400> 479

Met Gly Ser Trp Trp Glu Phe Lys Glu Asp Leu Ala Glu Ile Lys Trp
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

His Asp Ile Ala Lys Phe Glu Phe Glu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 480
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 480

Met Gly Ser Trp Glu Trp Phe Lys Ser Asp Leu Ala Ser Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

His Asp Ile Ala Glu Phe Glu Glu Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 481
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 481

Met Gly Ser Trp Asn Glu Phe Lys Asp Asp Leu Ala Met Ile Lys Met
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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His Asp Ile Ala Glu Phe Glu Asp Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 482
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 482

Met Gly Ser Trp Thr Phe Phe Lys Asp Asp Leu Ala Glu Ile Lys Trp
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 483
<211> 73
<212> PRT
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<400> 483

Met Gly Ser Trp Ser Asp Phe Lys Asp Asp Leu Ala Glu Ile Lys Met
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 484
<211> 73
<212> PRT
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<220>
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<400> 484

Met Gly Ser Trp Ser Met Phe Lys Asp Asp Leu Ala Glu Ile Lys Ala
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Trp Phe Glu Asp Asp Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 485
<211> 73
<212> PRT
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<223> synthetic construct

<400> 485

Met Gly Ser Trp Gln Tyr Phe Lys Asp Asp Leu Ala Glu Ile Lys Met
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Ala Asp Ile Ala Met Phe Glu Asp Asp Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 486
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 486

Met Gly Ser Trp Ser Phe Phe Lys Asp Asp Leu Ala Glu Ile Lys Tyr
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Gln Thr Ile Ala Glu Phe Glu Tyr Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 487

Met Gly Ser Trp Met Glu Phe Lys Glu Glu Leu Ala Glu Ile Lys Tyr
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 488
<211> 73
<212> PRT
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<220>
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<400> 488

Met Gly Ser Trp Ala Trp Phe Lys Glu Asp Leu Ala Glu Ile Lys Val
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 489
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 489

Met Gly Ser Trp Tyr Glu Phe Lys Phe Asp Leu Ala Glu Ile Lys Glu
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Asp Asp Ile Ala Phe Phe Glu Tyr Asp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 490
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 490

Met Gly Ser Trp Tyr Asp Phe Lys Tyr Asp Leu Ala Glu Ile Lys Met
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Phe Asp Ile Ala Phe Phe Glu Glu Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 491
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 491

Met Gly Ser Trp Tyr Ile Phe Lys Glu Asp Leu Ala Glu Ile Lys Glu
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Glu Glu Ile Ala Leu Phe Glu Met Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 492
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 492

Met Gly Ser Trp Val Leu Phe Lys Glu Glu Leu Ala Tyr Ile Lys Phe
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
            20   25   30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 493
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 493

Met Gly Ser Trp Gln Asp Phe Lys Glu Asp Leu Ala Trp Ile Lys Tyr
1   5   10   15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
            20   25   30

Tyr Asp Ile Ala Ile Phe Glu Asn Asn Leu Gln His Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50   55   60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 494
<211> 73
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<223> synthetic construct

<400> 494

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Met Gly Ser Trp Asp His Phe Lys Asn Asp Leu Ala Trp Ile Lys Lys
1               5                  10                  15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
            20                  25                  30

Ala Val Ile Ala Tyr Phe Glu Leu Tyr Leu Gln Gly Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<211> 73
<212> PRT
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<400> 495

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Met Gly Ser Trp Tyr Asp Phe Lys Glu Asp Leu Ala Asp Ile Lys Trp
1               5                  10                  15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
            20                  25                  30

Asn Val Ile Ala Tyr Phe Glu Asn Asp Leu Gln Glu Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 496

Met Gly Ser Trp Tyr Met Phe Lys Glu Glu Leu Ala Asp Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Gly Phe Glu Trp Asp Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 497
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 497

Met Gly Ser Trp Tyr Tyr Phe Lys Asp Glu Leu Ala Asp Ile Lys Trp
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Met Leu Ile Ala Gln Phe Glu Leu Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 498
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 498

Met Gly Ser Trp Met Tyr Phe Lys Asp Thr Leu Ala Asp Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Trp Ile Ala Glu Phe Glu Asp Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 499
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 499

Met Gly Ser Trp Tyr Gln Phe Lys His Asp Leu Ala Asp Ile Lys Tyr
1 5 10 15

Gly Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Asp Asp Ile Ala Asp Phe Glu Leu Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 500
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 500

Met Gly Ser Trp Tyr Val Phe Lys Asp Asp Leu Ala Asp Ile Lys Tyr
1 5 10 15

Met Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 501
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 501

Met Gly Ser Trp Asn Phe Phe Lys Tyr Asp Leu Ala Asp Ile Met Ala
1 5 10 15

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Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Glu Ile Ala Asn Phe Glu His Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 502
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 502

Met Gly Ser Trp His Trp Phe Lys Ile Val Leu Ala Asp Ile Lys Asp
1 5 10 15

Gly Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Thr Thr Ile Ala Asp Phe Glu Met Asp Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 503
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 503

Met Gly Ser Trp His Trp Phe Lys Ile Val Leu Ala Asp Ile Lys Asp
1 5 10 15

Gly Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Thr Thr Ile Ala Asp Phe Glu Met Asp Leu His His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 504
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 504

Met Gly Ser Trp Phe Met Phe Lys Glu Glu Leu Ala Asp Ile Lys Asp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 505
<211> 73
<212> PRT
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<220>
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<400> 505

Met Gly Ser Trp Phe Met Phe Lys Gln Glu Leu Ala Trp Ile Lys Glu
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Trp Asp Ile Ala Glu Phe Glu Trp Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 506
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 506

Met Gly Ser Trp Gln Ile Phe Lys Gly Glu Leu Ala Tyr Ile Lys Gln
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Phe Asp Ile Ala Glu Phe Glu Glu Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 507
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 507

Met Gly Ser Trp Asp Phe Phe Lys Glu Glu Leu Ala Glu Ile Lys His
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Phe Trp Ile Ala Asp Phe Glu Gln Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 508
<211> 73
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<213> ARTIFICIAL SEQUENCE

<220>
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<400> 508

Met Gly Ser Trp Phe Asn Phe Lys Glu Glu Leu Ala Val Ile Lys Phe
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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Trp Val Ile Ala Asp Phe Glu Asp Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 509
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 509

Met Gly Ser Trp Tyr Gln Phe Lys Thr Glu Leu Ala Trp Ile Lys Asp
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Val Ile Ala Asp Phe Glu Asp Asp Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 510
<211> 73
<212> PRT
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<220>
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<400> 510

Met Gly Ser Trp Phe Glu Phe Lys Asp Tyr Leu Ala Asp Ile Lys Trp
1 5 10 15

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Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

His Asp Ile Ala Tyr Phe Glu His Asn Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 511
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 511

Met Gly Ser Trp Val Arg Phe Lys Asp Phe Leu Ala Asp Ile Lys Met
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Tyr His Ile Ala Glu Phe Glu His Asn Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 512
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 512

Met Gly Ser Trp Trp Leu Phe Lys Glu Gln Leu Ala Leu Ile Lys Tyr
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ser Trp Ile Ala Glu Phe Glu His Gln Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 513
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 513

Met Gly Ser Trp His Val Phe Lys Thr Glu Leu Ala Asp Ile Lys Phe
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Leu Trp Ile Ala Glu Phe Glu His Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 514
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<223> synthetic construct

<400> 514

Met Gly Ser Trp Ile Trp Phe Lys Asp Trp Leu Ala Asp Ile Lys Asp
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Tyr Asp Ile Ala Leu Phe Glu Asp Gln Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 515
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 515

Met Gly Ser Trp Gly Trp Phe Lys His Glu Leu Ala Phe Ile Lys Ala
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Glu Ile Ala Glu Phe Glu Tyr Glu Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 516
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 516

Met Gly Ser Trp Thr Trp Phe Lys Asp Asn Leu Ala Trp Ile Lys Glu
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 517
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 517

Met Gly Ser Trp Thr Tyr Phe Lys Asn Asp Leu Ala Gly Ile Lys Glu
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

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Phe Glu Ile Ala Glu Phe Glu Trp Leu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 518
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 518

Met Gly Ser Trp Thr Trp Phe Lys Trp Asp Leu Ala Asp Ile Lys Gly
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Glu Glu Ile Ala Glu Phe Glu Trp Arg Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 519
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 519

Met Gly Ser Trp Leu Tyr Phe Lys Glu Tyr Leu Ala Asp Ile Lys Ser
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Tyr Glu Ile Ala Asp Phe Glu Glu Gln Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 520
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 520

Met Gly Ser Trp His Trp Phe Lys Glu Glu Leu Ala Glu Ile Lys Glu
1 5 10 15

Asp Leu Val Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Tyr Asp Ile Ala Met Phe Glu Leu Ser Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 521
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 521

Met Gly Ser Trp Asn Asp Phe Lys Glu Glu Leu Ala Trp Ile Lys Phe
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Asp Ile Ala Met Phe Glu Gln Gln Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 522
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 522

Met Gly Ser Trp Trp Asp Phe Lys Asp Trp Leu Ala Glu Ile Lys His
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 523
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 523

Met Gly Ser Trp Asp Glu Phe Lys Glu Asp Leu Ala His Ile Lys Thr
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Asp Glu Ile Ala Asp Phe Glu Met Tyr Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 524
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 524

Met Gly Ser Trp Asp Phe Phe Lys Tyr Asp Leu Ala Asn Ile Asn Glu
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Tyr Gly Ile Ala Asp Phe Glu Leu Trp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 525
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 525

Met Gly Ser Trp Tyr Gln Phe Lys Asp Asp Leu Ala His Ile Lys His
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 526
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 526

Met Gly Ser Trp Ala Glu Phe Lys His Asp Leu Ala Asp Ile Lys Arg
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Leu Ser Ile Ala Phe Phe Glu Asp Glu Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 527
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 527

Met Gly Ser Trp Val Val Phe Lys Gln Asp Leu Ala Asp Ile Asn His
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Glu Ile Ala Asp Phe Glu Trp Glu Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 528
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 528

Met Gly Ser Trp Phe Gln Phe Lys Glu Phe Leu Ala Met Ile Thr His
1 5 10 15

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Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

His Asp Ile Ala Leu Phe Glu Ser Glu Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 529
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 529

Met Gly Ser Trp His Trp Phe Lys Glu Asp Leu Ala Met Ile Thr Asp
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 530
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 530

Met Gly Ser Trp Ser Trp Phe Gln Trp Asp Leu Ala Gly Ile Lys Asp
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 531
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 531

Met Gly Ser Trp Thr Glu Phe Lys Gly Glu Leu Ala Glu Ile Lys Trp
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Glu Ile Ala Ala Phe Glu Trp Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 532
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 532

Met Gly Ser Trp Phe Glu Phe Lys Trp Thr Leu Ala Leu Ile Lys Gln
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Gln Glu Ile Ala Glu Phe Glu Trp Trp Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 533
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 533

Met Gly Ser Trp Ala Glu Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Met
20 25 30

Asp Glu Ile Met Ala Phe Glu Trp Glu Leu Trp Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Met Asn Glu Ala Phe Ala Ile Asp
50 55 60

Val Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 534
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 534

Met Gly Ser Trp Ala Glu Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Trp Glu Ile Val Ala Phe Phe Ser Glu Leu Phe Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Asp Glu Ala Ile Ala Ile Glu
50 55 60

Thr Glu Leu Val Ala Tyr Arg His Asn
65 70

<210> 535
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 535

Met Gly Ser Trp Trp Glu Phe Asp His Arg Leu Thr Ala Ile Asp Thr
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Phe Ala Glu Ala Glu Ala Ile Tyr
50 55 60

Val Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 536
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 536

Met Gly Ser Trp Trp Glu Phe Gln Phe Arg Leu Tyr Ala Ile Asp Gln
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Gln Asp Ile Ala Asp Phe Glu Trp Met Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Met Leu Glu Ala Asp Ala Ile Glu
50 55 60

Ala Glu Leu Lys Ala Tyr Arg His Asn
65 70

<210> 537
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 537

Met Gly Ser Trp Tyr Glu Phe Asp His Arg Leu Asp Ala Ile Tyr Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
            20   25   30

Tyr Gly Ile Ala Glu Phe Glu Glu Tyr Leu Gln Asp Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Ile Ser Glu Ala Trp Ala Ile Glu
    50   55   60

Trp Glu Leu Ser Ala Tyr Arg His Asn
65   70

<210> 538
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 538

Met Gly Ser Trp Tyr Glu Phe Asp Met Arg Leu Asp Ala Ile Trp Glu
1   5   10   15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
            20   25   30

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

Gly Asn Pro Glu Val Glu Ala Leu Phe Asp Glu Ala Trp Ala Ile Glu
    50   55   60

Asp Glu Leu Tyr Ala Tyr Arg His Asn
65   70

<210> 539
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 539

Met Gly Ser Trp Ser Glu Phe Asp Ser Arg Leu Asp Ala Ile Ala Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Trp Ile Ile Ala Asp Phe Glu Glu Asp Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Phe Ser Glu Ala Tyr Ala Ile Glu
50 55 60

Ile Glu Leu Asn Ala Tyr Arg His Asn
65 70

<210> 540
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 540

Met Gly Ser Trp Tyr Glu Phe Asp Asp Arg Leu Asp Ala Ile Ala Tyr
1 5 10 15

Arg Leu Asn Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Glu Ile Ala Glu Phe Glu Leu Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Val Trp Glu Ala Asp Ala Ile Glu
50 55 60

Trp Glu Leu Glu Ala Tyr Arg His Asn
65 70

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<210> 541
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 541

Met Gly Ser Trp Phe Glu Phe Asp Glu Arg Leu Asp Ala Ile Gly Ser
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Phe Tyr Ile Ala Asp Phe Glu Glu Trp Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Phe Ala Ile Asp
50 55 60

Glu Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 542
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 542

Met Gly Ser Trp Glu Glu Phe Asp Gln Arg Leu Asp Ala Ile Asp Val
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Phe Asp Ile Ala Ala Phe Glu Glu Trp Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Met Glu Ala Phe Ala Ile Thr
50 55 60

Asp Glu Leu Cys Ala Tyr Arg His Asn
65 70

<210> 543
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 543

Met Gly Ser Trp Glu Glu Phe Asp Val Arg Leu Asp Ala Ile Phe Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Phe Asp Ile Ala Trp Phe Glu Met Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Phe Asp Glu Ala Glu Ala Ile Thr
50 55 60

Asn Glu Leu Val Ala Tyr Arg His Asn
65 70

<210> 544
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 544

Met Gly Ser Trp Glu Glu Phe Asp Lys Arg Leu Asp Ala Ile Thr Arg
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Ser Thr Ile Ala Trp Phe Glu Trp Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Trp Glu Ala Tyr Ala Ile Asp
50 55 60

Tyr Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 545
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 545

Met Gly Ser Trp Tyr Glu Phe Asp His Arg Leu Glu Ala Ile Tyr Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Phe Asp Glu Ala Ala Ala Ile Gly
50 55 60

His Glu Leu Leu Ala Tyr Arg His Asn
65 70

<210> 546
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 546

Met Gly Ser Trp Asn Glu Phe Asp Asp Arg Leu Leu Ala Ile Trp Gly
1 5 10 15

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Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Glu Gln Ile Ala Gly Phe Glu Asp Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

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

Lys Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 547
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 547

Met Gly Ser Trp Val Glu Phe Asp Asp Arg Leu Asp Ala Ile Trp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Gln Ile Ala Val Phe Glu His Gln Leu Gln Asp Tyr Lys Gly Lys
35 40 45

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

Leu Glu Leu Lys Ala Tyr Arg His Asn
65 70

<210> 548
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 548

Met Gly Ser Trp Thr Glu Phe Asp Asp Arg Leu Phe Ala Ile Tyr Trp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Val Ile Ala Glu Phe Glu Asn Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Asp Glu Ala His Ala Ile Ser
50 55 60

Ile Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 549
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 549

Met Gly Ser Trp Ser Glu Phe Asp Gln Arg Leu Glu Ala Ile Trp Asn
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Arg Glu Ile Ala Tyr Phe Glu Asn Gln Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Asn Glu Ala Phe Ala Ile Val
50 55 60

Asp Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 550
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 550

Met Gly Ser Trp Tyr Glu Phe Asp Glu Arg Leu Trp Ala Ile Trp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Trp Val Ile Ala Asp Phe Glu Asn Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Phe Glu Ala Glu Ala Ile Val
50 55 60

Thr Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 551
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 551

Met Gly Ser Trp Met Glu Phe Asp Tyr Arg Leu Glu Ala Ile Trp Met
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ser Ser Ile Ala Asp Phe Glu His His Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Phe Ala Ile Gly
50 55 60

Val Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 552
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 552

Met Gly Ser Trp Tyr Glu Phe Glu Ser Arg Leu Glu Ala Ile Trp Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Gln Tyr Ile Ala Asp Phe Glu Gln His Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Trp Glu Ala Asp Ala Ile Trp
50 55 60

Leu Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 553
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 553

Met Gly Ser Trp Glu Glu Phe Tyr Met Arg Leu Val Ala Ile His Met
1 5 10 15

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

Asn Tyr Ile Ala Glu Phe Glu Glu Tyr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Thr Ile Glu Ala Asp Ala Ile Gly
50 55 60

Thr Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 554
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 554

Met Gly Ser Trp Asp Glu Phe Tyr Tyr Arg Leu Val Ala Ile Thr His
1 5 10 15

Arg Leu His Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Gly Phe Glu Trp Asp Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Lys Glu Ala Gly Ala Ile Gly
50 55 60

Met Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 555
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 555

Met Gly Ser Trp Glu Glu Phe Asp Thr Arg Leu Leu Ala Ile Phe Gly
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Met Leu Ile Ala Lys Phe Glu Asp Asp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ser Glu Glu Ala Phe Ala Ile Asp
50 55 60

His Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 556
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 556

Met Gly Ser Trp Arg Glu Phe Asp Gln Arg Leu Trp Ala Ile Asp Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Trp Met Ile Ala Thr Phe Glu Asp Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Arg Glu Ala Phe Ala Ile Asp
50 55 60

Trp Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 557
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 557

Met Gly Ser Trp Glu Glu Phe His Glu Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ser Arg Glu Ala Asp Ala Ile Asn
50 55 60

Phe Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 558
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 558

Met Gly Ser Trp Asn Glu Phe Tyr Glu Arg Leu Glu Ala Ile Asp Arg
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Trp Met Ile Ala Asp Phe Glu Asp Asp Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ile Asn Glu Ala Gly Ala Ile Gly
50 55 60

Phe Glu Leu Glu Ala Tyr Arg His Asn
65 70

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<210> 559
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 559

Met Gly Ser Trp Thr Glu Phe Thr Gln Arg Leu Glu Ala Ile Val Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asn Arg Glu Ala Val Ala Ile Asp
50 55 60

Asn Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 560
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 560

Met Gly Ser Trp Val Glu Phe Ile Met Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Trp His Ile Ala Asp Phe Glu Asp His Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Phe Glu Glu Ala Asp Ala Ile Trp
50 55 60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 561
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 561

Met Gly Ser Trp Asn Glu Phe Leu Leu Arg Leu Asp Ala Ile Glu His
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Trp Glu Ile Ala Asp Phe Glu Asp Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Val Glu Glu Ala Glu Ala Ile Asp
50 55 60

Val Glu Leu Val Ala Tyr Arg His Asn
65 70

<210> 562
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 562

Met Gly Ser Trp Tyr Glu Phe Asn Met Arg Leu Gly Ala Ile Asp Asp
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Asp Met Ile Ala Ile Phe Glu Asp Asp Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Gln Glu Ala Ala Ala Ile His
50 55 60

Gln Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 563
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 563

Met Gly Ser Trp Glu Glu Phe His Trp Arg Leu Gly Ala Ile Asp Ala
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Gly Ile Ala Asp Phe Glu Ala Ile Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Ser Glu Ala Val Ala Ile His
50 55 60

His Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 564
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 564

Met Gly Ser Trp Tyr Glu Phe Tyr Glu Arg Leu Trp Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Asp Ser Ile Ala Thr Phe Glu Pro Ser Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Val Ala Glu Ala Trp Ala Ile Phe
50 55 60

Asp Glu Leu Ala Ala Tyr Arg His Asn
65 70

<210> 565
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 565

Met Gly Ser Trp Phe Glu Phe Asp Gln Arg Leu Asp Ala Ile Thr Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Asp Val Ile Ala Leu Phe Glu Tyr His Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Val Glu Ala Trp Ala Ile Phe
50 55 60

His Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 566
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 566

Met Gly Ser Trp Ser Glu Phe Trp Phe Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Asp Asn Ile Ala Leu Phe Glu Tyr Ser Leu Gln His Tyr Lys Gly Lys
35 40 45

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

Asp Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 567
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 567

Met Gly Ser Trp Tyr Glu Phe Trp Asp Arg Leu Thr Ala Ile Glu His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Tyr Lys Glu Ala Glu Ala Ile Glu
50 55 60

Trp Glu Leu Glu Ala Tyr Arg His Asn
65 70

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<210> 568
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 568

Met Gly Ser Trp Tyr Glu Phe Asp Asp Arg Leu Trp Ala Ile Phe Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Asp Ser Ile Ala Glu Phe Glu Glu Glu Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Leu Glu Ala Trp Ala Ile Glu
50 55 60

Asn Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 569
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 569

Met Gly Ser Trp Asn Glu Phe Val Glu Arg Leu Ser Ala Ile Asp His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Gln Gln Ile Ala Glu Phe Glu Ile His Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Phe Glu Ala Asp Ala Ile Phe
50 55 60

Asp Glu Leu Leu Ala Tyr Arg His Asn
65 70

<210> 570
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 570

Met Gly Ser Trp Ser Glu Phe Val Asp Arg Leu Asp Ala Ile Phe Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Thr Ile Ala His Phe Glu Trp Asn Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Gly Glu Ala Asp Ala Ile Thr
50 55 60

Asp Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 571
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 571

Met Gly Ser Trp Ala Glu Phe Asp Ser Arg Leu Asp Ala Ile Ala Gln
1 5 10 15

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

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

Gly Asn Pro Glu Val Glu Ala Leu Ser Asn Glu Ala Asp Ala Ile Phe
50 55 60

Asn Glu Leu Lys Ala Tyr Arg His Asn
65 70

<210> 572
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 572

Met Gly Ser Trp Ala Glu Phe Asp Ser Arg Leu Ile Ala Ile Phe Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Asp Ile Ala Gln Phe Glu Gln His Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Gln Glu Ala Asp Ala Ile Thr
50 55 60

Phe Glu Leu Lys Ala Tyr Arg His Asn
65 70

<210> 573
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 573

Met Gly Ser Trp Thr Glu Phe Glu Glu Arg Leu Glu Ala Ile Trp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Trp Asp Ile Ala Tyr Phe Glu Asp Gly Leu Gln Glu Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Phe Met Glu Ala Glu Ala Ile Ile
    50   55   60

Arg Glu Leu Lys Ala Tyr Arg His Asn
65   70

<210> 574
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 574

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Ala Ala Ile Trp Asp
1   5   10   15

Arg Leu Asn Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
            20   25   30

Trp Asp Ile Ala Trp Phe Glu Glu Gly Leu Gln Glu Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Lys His Glu Ala Ser Ala Ile Gln
    50   55   60

Thr Glu Leu Phe Ala Tyr Arg His Asn
65   70

<210> 575
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 575

Met Gly Ser Trp Leu Glu Phe Glu Ser Arg Leu Trp Ala Ile Trp Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Gln Asp Ile Ala Asp Phe Glu Met Ser Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ile Arg Glu Ala Glu Ala Ile Glu
50 55 60

Thr Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 576
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 576

Met Gly Ser Trp Met Glu Phe Glu Asp Arg Leu Ile Ala Ile Trp Ala
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ile Phe Glu Ala Ile Ala Ile Asn
50 55 60

Lys Glu Leu Met Ala Tyr Arg His Asn
65 70

<210> 577
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 577

Met Gly Ser Trp Phe Glu Phe Thr Ile Arg Leu Glu Ala Ile Gln Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Asp Ile Ala Glu Phe Glu Glu Gly Leu Gln Phe Tyr Lys Gly Lys
35 40 45

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

Asn Glu Leu Val Ala Tyr Arg His Asn
65 70

<210> 578
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 578

Met Gly Ser Trp Tyr Glu Phe Val Ser Arg Leu Asp Ala Ile Glu Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Trp Asp Ile Ala Asp Phe Glu Gln Gly Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ala Gln Glu Ala Asn Ala Ile Gly
50 55 60

Ser Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 579
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 579

Met Gly Ser Trp Glu Glu Phe Asp Tyr Arg Leu Tyr Ala Ile Gln Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Trp Glu Ile Ala Asp Phe Glu His Met Leu Gln Met Tyr Lys Gly Lys
35 40 45

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

Ala Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 580
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 580

Met Gly Ser Trp Ile Glu Phe Phe His Arg Leu Asp Ala Ile Gln Asp
1 5 10 15

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

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Trp Ala Ile Ala Asp Phe Glu His Met Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gln Phe Glu Ala Phe Ala Ile Glu
50 55 60

Gly Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 581
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 581

Met Gly Ser Trp Tyr Glu Phe Ser Ser Arg Leu Asn Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Thr Asp Ile Ala Asp Phe Glu Ser Leu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Leu Asn Glu Ala Asp Ala Ile Asp
50 55 60

Tyr Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 582
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 582

Met Gly Ser Trp Phe Glu Phe Glu Tyr Arg Leu Asp Ala Ile Ile Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Ser Met Ile Ala Asn Phe Glu Tyr Ser Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Phe Glu Ala Asp Ala Ile Val
50 55 60

Asp Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 583
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 583

Met Gly Ser Trp Leu Glu Phe Glu Tyr Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Gln Asp Ile Ala Asp Phe Glu Lys Tyr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Trp Glu Glu Ala Asp Ala Ile Met
50 55 60

Trp Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 584
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 584

Met Gly Ser Trp His Glu Phe Glu Glu Arg Leu Met Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Gln Trp Ile Ala Leu Phe Glu Tyr Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Met Glu Ala Phe Ala Ile Asn
50 55 60

Asn Glu Leu Ser Ala Tyr Arg His Asn
65 70

<210> 585
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 585

Met Gly Ser Trp Tyr Glu Phe Glu Glu Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Asp Ile Ile Ala Phe Phe Glu Gln Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Met Glu Ala Glu Ala Ile Ser
50 55 60

Ile Glu Leu Asp Ala Tyr Arg His Asn
65 70

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<210> 586
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 586

Met Gly Ser Trp His Glu Phe Glu Lys Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Ser Ile Ala Trp Phe Glu Trp Asp Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Glu Glu Ala Asp Ala Ile Tyr
50 55 60

Gln Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 587
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 587

Met Gly Ser Trp Ile Glu Phe Glu Asp Arg Leu Asp Ala Ile Thr Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

His Gln Ile Ala Phe Phe Glu Glu Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu His Met Glu Ala Glu Ala Ile Met
50 55 60

Glu Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 588
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 588

Met Gly Ser Trp Met Glu Phe Glu Asp Arg Leu Met Ala Ile Val Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Trp Asn Ile Ala Met Phe Glu Glu Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Asp Glu Ala Glu Ala Ile Glu
50 55 60

Trp Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 589
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 589

Met Gly Ser Trp Glu Glu Phe Glu Asp Arg Leu Phe Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ser Val Glu Ala Phe Ala Ile Asp
50 55 60

Arg Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 590
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 590

Met Gly Ser Trp Glu Glu Phe Leu Phe Arg Leu Glu Ala Ile Gln Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ser Thr Glu Ala Lys Ala Ile Asp
50 55 60

Tyr Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 591
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 591

Met Gly Ser Trp Val Glu Phe Asp Asn Arg Leu Phe Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Gln Leu Glu Ala Phe Ala Ile Met
50 55 60

Glu Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 592
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 592

Met Gly Ser Trp Phe Glu Phe Asp Asp Arg Leu Glu Ala Ile Phe Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Phe Ala Ile Ala Glu Phe Glu Asp Ala Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Glu Glu Ala Val Ala Ile Asp
50 55 60

Glu Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 593
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 593

Met Gly Ser Trp Phe Glu Phe Asp Ala Arg Leu Met Ala Ile Asn Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Tyr His Ile Ala Leu Phe Glu Asp Gln Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Thr Leu Glu Ala Val Ala Ile Asn
50 55 60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 594
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 594

Met Gly Ser Trp Val Glu Phe Asp Ser Arg Leu Ala Ala Ile Asp Tyr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Tyr Thr Ile Ala Asn Phe Glu His Thr Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Val Tyr Glu Ala His Ala Ile Ala
50 55 60

Thr Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 595
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 595

Met Gly Ser Trp Thr Glu Phe Asp Glu Arg Leu Asp Ala Ile Asp Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

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

Ala Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 596
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 596

Met Gly Ser Trp Ile Glu Phe Asp Glu Arg Leu Asp Ala Ile Asp Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asn Glu Glu Ala Asn Ala Ile Phe
50 55 60

His Glu Leu Ser Ala Tyr Arg His Asn
65 70

<210> 597
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 597

Met Gly Ser Trp Trp Glu Phe Asp Ser Arg Leu Asp Ala Ile Asp Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Val Glu Ile Ala Asp Phe Glu Asp Trp Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Trp His Glu Ala Asp Ala Ile Val
50 55 60

Thr Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 598
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 598

Met Gly Ser Trp Tyr Glu Phe Asp Glu Arg Leu Asp Ala Ile Phe Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asp Thr Glu Ala Lys Ala Ile Ser
50 55 60

Trp Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 599
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 599

Met Gly Ser Trp Tyr Glu Phe Gln Glu Arg Leu Asp Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Tyr Thr Ile Ala Glu Phe Glu Lys Glu Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Thr Glu Ala Val Ala Ile Ser
50 55 60

Glu Glu Leu Met Ala Tyr Arg His Asn
65 70

<210> 600
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 600

Met Gly Ser Trp Glu Glu Phe Glu Asp Arg Leu Trp Ala Ile Asp Gly
1 5 10 15

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Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Gln Trp Ile Ala Thr Phe Glu Glu Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Ser Ala Ile Phe
50 55 60

Glu Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 601
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 601

Met Gly Ser Trp Phe Glu Phe Gly Asp Arg Leu Glu Ala Ile Asp Glu
1 5 10 15

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

Trp Trp Ile Ala Glu Phe Glu His His Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Asp Ala Ile Trp
50 55 60

Gly Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 602
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 602

Met Gly Ser Trp Phe Glu Phe Asn Asp Arg Leu Asp Ala Ile Ser Glu
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Thr Leu Glu Ala Asn Ala Ile Phe
50 55 60

Glu Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 603
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 603

Met Gly Ser Trp Val Glu Phe Met Asp Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Trp Glu Ile Ala Glu Phe Glu Glu His Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Leu Ala Ile Thr
50 55 60

Glu Glu Leu Ala Ala Tyr Arg His Asn
65 70

<210> 604
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 604

Met Gly Ser Trp Ile Glu Phe Met Asp Arg Leu Trp Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Glu Ile Ala Trp Phe Glu Glu Glu Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Thr Ala Ile Ser
50 55 60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 605
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 605

Met Gly Ser Trp Glu Glu Phe Asn Trp Arg Leu Arg Ala Ile Asp Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Val Glu Ala Ala Ala Ile Ala
50 55 60

Glu Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 606
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 606

Met Gly Ser Trp Trp Glu Phe Glu Ile Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Trp Glu Ala Asn Ala Ile Ile
50 55 60

Glu Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 607
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 607

Met Gly Ser Trp Tyr Glu Phe Glu Trp Arg Leu Asp Ala Ile Asp Arg
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Glu Ile Ala Asp Phe Glu Trp Met Leu Gln Asn Tyr Lys Gly Lys
35 40 45

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

Thr Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 608
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 608

Met Gly Ser Trp Tyr Glu Phe Val Tyr Arg Leu Arg Ala Ile Asp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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

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

Phe Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 609
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 609

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Tyr Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Arg Glu Ile Ala Gln Phe Glu Ile Trp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Asp Glu Ala Thr Ala Ile Asn
50 55 60

Ser Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 610
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 610

Met Gly Ser Trp Asp Glu Phe Glu Phe Arg Leu Glu Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Tyr Glu Ile Ala Gln Phe Glu Phe Met Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Met Glu Ala Trp Ala Ile Glu
50 55 60

Asn Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 611
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 611

Met Gly Ser Trp Glu Glu Phe Glu Trp Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Tyr Glu Ile Ala Ile Phe Glu Asn Glu Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Ser Glu Ala Tyr Ala Ile Glu
50 55 60

Arg Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 612
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 612

Met Gly Ser Trp Tyr Glu Phe Phe Asp Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Ala Glu Ile Ala Glu Phe Glu Met Glu Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Val Glu Ala His Ala Ile Glu
50 55 60

Met Glu Leu Phe Ala Tyr Arg His Asn
65 70

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<210> 613
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 613

Met Gly Ser Trp Tyr Glu Phe Met Gly Arg Leu Glu Ala Ile Asp Glu
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

His Glu Ile Ala Glu Phe Glu Trp Ser Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Phe Glu Ala Gly Ala Ile Pro
50 55 60

Trp Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 614
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 614

Met Gly Ser Trp Val Glu Phe Ser Asn Arg Leu Asp Ala Ile Trp Glu
1 5 10 15

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

Trp Glu Ile Ala Glu Phe Glu Trp Glu Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Ala Glu Ala Asp Ala Ile Glu
50 55 60

Trp Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 615
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 615

Met Gly Ser Trp Glu Glu Phe His Met Arg Leu Ile Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asp Tyr Glu Ala His Ala Ile Trp
50 55 60

Arg Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 616
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 616

Met Gly Ser Trp Trp Glu Phe Lys Tyr Arg Leu Asp Ala Ile Cys Phe
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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Asp Glu Ile Ala Tyr Phe Glu Glu Asp Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Tyr Glu Ala Leu Ala Ile Trp
50 55 60

Asp Glu Leu Ala Ala Tyr Arg His Asn
65 70

<210> 617
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 617

Met Gly Ser Trp Asp Glu Phe Ala Met Arg Leu Glu Ala Ile Gln Ala
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Asp Glu Ile Ala Phe Phe Glu Thr Met Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Ala Ala Ile Glu
50 55 60

Ala Glu Leu Gly Ala Tyr Arg His Asn
65 70

<210> 618
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 618

Met Gly Ser Trp Trp Glu Phe Asn Ala Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Trp Tyr Glu Ala Tyr Ala Ile Glu
50 55 60

Lys Glu Leu Asn Ala Tyr Arg His Asn
65 70

<210> 619
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 619

Met Gly Ser Trp Ile Glu Phe Trp Asn Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Asp Glu Ile Ala Glu Phe Glu Ile Tyr Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Lys His Glu Ala Glu Ala Ile Asn
50 55 60

Lys Glu Leu Met Ala Tyr Arg His Asn
65 70

<210> 620
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 620

Met Gly Ser Trp Asn Glu Phe Val Ile Arg Leu Phe Ala Ile Asp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Asp Glu Ile Ala Thr Phe Glu Tyr Glu Leu Gln Arg Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Glu Ala Ile Val
50 55 60

Ser Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 621
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 621

Met Gly Ser Trp Tyr Glu Phe Leu Ala Arg Leu Tyr Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

His Trp Ile Ala Asp Phe Glu Glu Gln Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Thr Asp Glu Ala Val Ala Ile Gly
50 55 60

Glu Glu Leu Ser Ala Tyr Arg His Asn
65 70

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<210> 622
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 622

Met Gly Ser Trp Leu Glu Phe Glu Thr Arg Leu His Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Glu His Ile Ala Trp Phe Glu Glu Asp Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Phe Glu Ala Asp Ala Ile Gly
50 55 60

Trp Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 623
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 623

Met Gly Ser Trp Phe Glu Phe Glu Thr Arg Leu Glu Ala Ile Asp Leu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Asp Val Ile Ala Phe Phe Glu Asp Trp Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Lys Met Glu Ala Trp Ala Ile Gly
50 55 60

Glu Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 624
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 624

Met Gly Ser Trp His Glu Phe Trp Gln Arg Leu Glu Ala Ile Glu Gly
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Met Ala Glu Ala Glu Ala Ile Asp
50 55 60

Asn Glu Leu Arg Ala Tyr Arg His Asn
65 70

<210> 625
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 625

Met Gly Ser Trp Tyr Glu Phe Glu Gln Arg Leu Glu Ala Ile Glu Trp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Glu Asp Ile Ala Asp Phe Glu Glu Trp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gln Tyr Glu Ala Tyr Ala Ile Ala
50 55 60

Glu Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 626
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 626

Met Gly Ser Trp Tyr Glu Phe Glu Asn Arg Leu Phe Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asp Asn Glu Ala Glu Ala Ile Asp
50 55 60

Ile Glu Leu Ala Ala Tyr Arg His Asn
65 70

<210> 627
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 627

Met Gly Ser Trp Tyr Glu Phe Glu Gln Arg Leu Gly Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asp Glu Glu Ala Trp Ala Ile Asp
50 55 60

Asp Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 628
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 628

Met Gly Ser Trp Trp Glu Phe Glu Gln Arg Leu Asp Ala Ile Glu Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

His Ile Ile Ala Asp Phe Glu Asp Glu Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Trp Glu Ala Phe Ala Ile Asp
50 55 60

Gly Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 629
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 629

Met Gly Ser Trp Phe Glu Phe Pro Tyr Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

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

Gln Phe Ile Ala Trp Phe Glu Met Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Trp Phe Glu Ala Asn Ala Ile Val
50 55 60

Glu Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 630
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 630

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu Glu Ala Ile Glu Ile
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ser Phe Ile Ala His Phe Glu Asp Asp Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Met Asp Glu Ala Asn Ala Ile Val
50 55 60

Phe Glu Leu Asp Ala Tyr Arg His Asn
65 70

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<210> 631
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 631

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Phe Met Ile Ala Met Phe Glu Gln His Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ile Pro Glu Ala Gly Ala Ile Asp
50 55 60

Lys Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 632
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 632

Met Gly Ser Trp Asp Glu Phe Asp Ala Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Met Gly Glu Ala Asn Ala Ile Val
50 55 60

Met Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 633
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 633

Met Gly Ser Trp Tyr Glu Phe Trp Arg Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Thr Asp Ile Ala Gly Phe Glu Trp Met Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu His Glu Ala Trp Ala Ile Asn
50 55 60

Ser Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 634
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 634

Met Gly Ser Trp His Glu Phe Ile Trp Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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Thr Glu Ile Ala Thr Phe Glu Ala Gln Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Ile Ala Ile Ala
50 55 60

Trp Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 635
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 635

Met Gly Ser Trp Tyr Glu Phe Tyr Trp Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Lys Ala Ile Ala Thr Phe Glu Asp Gln Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Thr Glu Ala Leu Ala Ile His
50 55 60

Ala Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 636
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 636

Met Gly Ser Trp Phe Glu Phe Gln Trp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Glu Glu Glu Ala Met Ala Ile Gln
50 55 60

Thr Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 637
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 637

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Trp Ala Ile Glu Gln
1 5 10 15

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

Asn Ser Ile Ala Lys Phe Glu Asp Met Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu His Glu Glu Ala Asp Ala Ile Ile
50 55 60

Trp Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 638
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 638

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Trp Ala Ile Asp Arg
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Gln Met Ile Ala His Phe Glu Gln Ile Leu Gln Val Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu His Phe Glu Ala His Ala Ile Gly
50 55 60

Met Glu Leu Ala Ala Tyr Arg His Asn
65 70

<210> 639
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 639

Met Gly Ser Trp Trp Glu Phe Leu Asp Arg Leu Glu Ala Ile Glu Tyr
1 5 10 15

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

Trp Glu Ile Ala Met Phe Glu Asp His Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu His Ser Glu Ala His Ala Ile Ile
50 55 60

Ser Glu Leu Ser Ala Tyr Arg His Asn
65 70

<210> 640
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 640

Met Gly Ser Trp Ala Glu Phe Glu Asp Arg Leu Ala Ala Ile Glu Arg
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Ser Ser Ile Ala Trp Phe Glu Pro Asp Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Met Tyr Glu Ala Glu Ala Ile Phe
50 55 60

Ser Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 641
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 641

Met Gly Ser Trp Trp Glu Phe Tyr Asp Arg Leu Thr Ala Ile Glu Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Gly Ile Ala Asp Phe Glu Tyr Asp Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Phe Trp Glu Ala Trp Ala Ile Gln
50 55 60

Ser Glu Leu Thr Ala Tyr Arg His Asn
65 70

<210> 642
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 642

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Ala Ala Ile Glu Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Glu Ile Ala Tyr Phe Glu His Gly Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Ser Glu Ala Met Ala Ile Ile
50 55 60

Asp Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 643
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 643

Met Gly Ser Trp Trp Glu Phe Ser Trp Arg Leu Glu Ala Ile Glu Thr
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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Met Asp Ile Ala Trp Phe Glu Gln Asp Leu Gln Leu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Glu Glu Ala Tyr Ala Ile Tyr
50 55 60

Glu Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 644
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 644

Met Gly Ser Trp Glu Glu Phe Phe Phe Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Glu Val Ile Ala Tyr Phe Glu Gln Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Tyr Val Glu Ala Tyr Ala Ile Gln
50 55 60

Glu Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 645
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 645

Met Gly Ser Trp Phe Glu Phe Glu Glu Arg Leu Asn Ala Ile Ser Trp
1 5 10 15

Arg Leu His Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Glu Asp Ile Ala Trp Phe Glu Asp Asp Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Asn Glu Ala Tyr Ala Ile Trp
50 55 60

Glu Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 646
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 646

Met Gly Ser Trp Phe Glu Phe Glu Glu Arg Leu Glu Ala Ile Ile Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Met Ala Ile Ser
50 55 60

Lys Glu Leu Lys Ala Tyr Arg His Asn
65 70

<210> 647
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 647

Met Gly Ser Trp Ala Glu Phe Asp Asp Arg Leu Glu Ala Ile Glu Tyr
1 5 10 15

Arg Leu His Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Glu Gly Ile Ala Gly Phe Glu His Ala Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Thr Glu Ala Gly Ala Ile Asn
50 55 60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 648
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 648

Met Gly Ser Trp Asp Glu Phe Glu Glu Arg Leu Gln Ala Ile Glu Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ser Thr Glu Ala Gln Ala Ile Gln
50 55 60

Asp Glu Leu Trp Ala Tyr Arg His Asn
65 70

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<210> 649
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 649

Met Gly Ser Trp Trp Glu Phe Thr Asp Arg Leu Asp Ala Ile Phe Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Glu Tyr Glu Ala Asn Ala Ile Gln
50 55 60

Tyr Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 650
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 650

Met Gly Ser Trp Trp Glu Phe Thr Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Ala Asp Glu Ala Asp Ala Ile Glu
50 55 60

Ser Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 651
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 651

Met Gly Ser Trp Val Glu Phe Phe Trp Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

Phe Glu Ile Ala Asp Phe Glu Ala Trp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu His Ser Glu Ala Asp Ala Ile Gln
50 55 60

Leu Glu Leu Arg Ala Tyr Arg His Asn
65 70

<210> 652
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 652

Met Gly Ser Trp Val Glu Phe Tyr Asn Arg Leu Asp Ala Ile Glu Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Glu Leu Ile Ala Gln Phe Glu Phe Ala Leu Gln Asp Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Glu Asp Glu Ala Asp Ala Ile Trp
    50   55   60

Glu Glu Leu Met Ala Tyr Arg His Asn
65   70

<210> 653
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 653

Met Gly Ser Trp Glu Glu Phe Tyr Tyr Arg Leu His Ala Ile Asp Asn
1   5   10   15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
            20   25   30

Trp His Ile Ala Asp Phe Glu Leu Glu Leu Gln Asp Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Ser Glu Glu Ala Thr Ala Ile Phe
    50   55   60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65   70

<210> 654
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 654

Met Gly Ser Trp Arg Glu Phe His Asp Arg Leu Phe Ala Ile Asp Gly
1   5   10   15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
            20   25   30

Trp Asp Ile Ala Asp Phe Glu Phe Glu Leu Gln Asp Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Ser Trp Glu Ala Asp Ala Ile Met
    50   55   60

Gln Glu Leu Gly Ala Tyr Arg His Asn
65   70

<210> 655
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 655

Met Gly Ser Trp Glu Glu Phe Asp Glu Arg Leu Trp Ala Ile Ser Asp
1   5   10   15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
            20   25   30

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

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

Thr Glu Leu Trp Ala Tyr Arg His Asn
65   70

<210> 656
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 656

Met Gly Ser Trp Glu Glu Phe Glu Gln Arg Leu Trp Ala Ile Asp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Tyr Glu Ile Ala Glu Phe Glu Met Asp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Phe Tyr Glu Ala His Ala Ile Asn
50 55 60

Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 657
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 657

Met Gly Ser Trp Asp Glu Phe His Gln Arg Leu Ala Ala Ile Gly Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Trp Glu Ile Ala Thr Phe Glu Trp Asp Leu Gln Val Tyr Lys Gly Lys
35 40 45

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

Glu Glu Leu Met Ala Tyr Arg His Asn
65 70

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<210> 658
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 658

Met Gly Ser Trp Val Glu Phe Glu Tyr Arg Leu Asp Ala Ile Ser Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Met Phe Glu Ala Glu Ala Ile Asp
50 55 60

Asp Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 659
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 659

Met Gly Ser Trp Asp Glu Phe Asp Thr Arg Leu Asp Ala Ile Phe Ser
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Gly Glu Ile Ala Glu Phe Glu Gly Ser Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Phe Glu Ala His Ala Ile Asp
50 55 60

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Glu Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 660
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 660

Met Gly Ser Trp His Glu Phe Asp Asp Arg Leu Asp Ala Ile Met Ser
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Leu Ala Glu Ala Tyr Ala Ile Asp
50 55 60

Trp Glu Leu Glu Ala Tyr Arg His Asn
65 70

<210> 661
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 661

Met Gly Ser Trp Tyr Glu Phe Phe Asp Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Trp Ala Ile Asp
    50   55   60

Glu Glu Leu Tyr Ala Tyr Arg His Asn
65   70

<210> 662
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 662

Met Gly Ser Trp Phe Glu Phe Leu Tyr Arg Leu Asp Ala Ile Glu Asp
1   5   10   15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
            20   25   30

Gln Glu Ile Ala Lys Phe Glu Ser Glu Leu Gln Ser Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala His Ala Ile Asp
    50   55   60

Met Glu Leu Glu Ala Tyr Arg His Asn
65   70

<210> 663
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 663

Met Gly Ser Trp Leu Glu Phe Glu Asp Arg Leu Val Ala Ile Asp His
1   5   10   15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Asn Trp Glu Ala Asp Ala Ile His
50 55 60

Ala Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 664
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 664

Met Gly Ser Trp Tyr Glu Phe Glu Ser Arg Leu Asp Ala Ile Val Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Tyr Glu Ile Ala Lys Phe Glu Trp Glu Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asn Trp Glu Ala Gly Ala Ile Glu
50 55 60

Phe Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 665
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 665

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Asp Ala Ile Leu Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Arg Asp Ile Ala Phe Phe Glu Ser Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala Met Ala Ile Asp
50 55 60

Asp Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 666
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 666

Met Gly Ser Trp Gly Glu Phe Met Asp Arg Leu Glu Ala Ile Asp Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Ser Asp Ile Ala Glu Phe Glu Gln Glu Leu Gln Met Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Trp Asp Glu Ala Met Ala Ile Arg
50 55 60

Asp Glu Leu Phe Ala Tyr Arg His Asn
65 70

<210> 667
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 667

Met Gly Ser Trp Glu Glu Phe Asp Asp Arg Leu Asp Ala Ile Glu His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Glu Ala Glu Ala Glu Ala Ile Ala
50 55 60

Asp Glu Leu Trp Ala Tyr Arg His Asn
65 70

<210> 668
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 668

Met Gly Ser Trp Tyr Glu Phe Ala Asp Arg Leu Asp Ala Ile Met Asp
1 5 10 15

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

Trp Glu Ile Ala Ala Phe Glu Glu Phe Leu Gln Met Tyr Lys Gly Lys
35 40 45

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

Asp Glu Leu Met Ala Tyr Arg His Asn
65 70

<210> 669
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 669

Met Gly Ser Trp Asn Glu Phe Trp Glu Arg Leu Asp Ala Ile Glu Trp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Leu Asp Ile Ala Trp Phe Glu Glu Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Ile Phe Glu Ala His Ala Ile Thr
50 55 60

Leu Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 670
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 670

Met Gly Ser Trp Tyr Glu Phe Asp Ala Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Phe Glu Ile Ala Gly Phe Glu Glu Ala Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Leu Lys Glu Ala Glu Ala Ile Thr
50 55 60

Asp Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 671
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 671

Met Gly Ser Trp Asp Glu Phe Ser Glu Arg Leu Asp Ala Ile Trp Gly
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

Phe His Ile Ala Glu Phe Glu His Glu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gln Gly Glu Ala Ala Ala Ile Ile
50 55 60

Asn Glu Leu Tyr Ala Tyr Arg His Asn
65 70

<210> 672
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 672

Met Gly Ser Trp Asp Glu Phe Trp Asp Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Arg Val Ile Ala Trp Phe Glu Asn Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Asp Asn Glu Ala Asp Ala Ile Arg
50 55 60

Ile Glu Leu His Ala Tyr Arg His Asn
65 70

<210> 673
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 673

Met Gly Ser Trp Asp Glu Phe Asp Asp Arg Leu Glu Ala Ile Val Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Phe Glu Ile Ala Gln Phe Glu His Gln Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Asp Glu Ala Asp Ala Ile Trp
50 55 60

Ile Glu Leu Asp Ala Tyr Arg His Asn
65 70

<210> 674
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 674

Met Gly Ser Trp Glu Glu Phe Thr Ile Arg Leu Gly Ala Ile Tyr Trp
1 5 10 15

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

Trp Phe Ile Ala Glu Phe Glu Tyr Glu Leu Gln Pro Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Val Ile Glu Ala Asn Ala Ile Asp
50 55 60

Gly Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 675
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 675

Met Gly Ser Trp Phe Glu Phe Glu Trp Arg Leu Asp Ala Ile Glu Asn
1 5 10 15

Arg Leu Asn Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Tyr His Ile Ala Ala Phe Glu Asp Ser Leu Gln His Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Glu Trp Glu Ala His Ala Ile Gln
50 55 60

Ser Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 676
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 676

Met Gly Ser Trp Tyr Glu Phe Asp Asp Arg Leu Glu Ala Ile Trp Asp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Thr Ala Ala Asp Ile Arg
50 55 60

Ala Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 677
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 677

Met Gly Ser Trp Gly Glu Phe Trp Ala Arg Leu Glu Ala Ile Trp Ile
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Asp Ile Arg
50 55 60

Arg Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 678
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 678

Met Gly Ser Trp Ile Glu Phe Glu Val Arg Leu Asp Ala Ile Trp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Asp Glu Ala Ala Asp Ile Arg
50 55 60

Gln Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 679
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 679

Met Gly Ser Trp Thr Glu Phe Asp Arg Arg Leu Asp Ala Ile Trp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Asp Ile Arg
50 55 60

Asp Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 680
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 680

Met Gly Ser Trp Thr Glu Phe Asp Met Arg Leu Asp Ala Ile Trp Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu Glu Ala Ala Thr Ile Arg
50 55 60

Gly Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 681
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 681

Met Gly Ser Trp Glu Glu Phe His Asp Arg Leu Met Ala Ile Glu Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Tyr Glu Ala Ala Asp Ile Arg
50 55 60

Asp Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 682
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 682

Met Gly Ser Trp Val Glu Phe Arg Asp Arg Leu Asp Ala Ile Glu Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Tyr Glu Ala Ala Glu Ile Arg
50 55 60

Met Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 683
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 683

Met Gly Ser Trp Met Glu Phe Ile Asp Arg Leu Asp Ala Ile Glu His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Glu Ile Arg
50 55 60

Met Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 684
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 684

Met Gly Ser Trp Thr Glu Phe Val Trp Arg Leu Asp Ala Ile Glu Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Glu Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 685
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 685

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu Tyr Ala Ile Glu Val
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Gln Glu Ala Ala Glu Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 686
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 686

Met Gly Ser Trp Tyr Glu Phe Tyr Asp Arg Leu Asp Ala Ile Glu Trp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Gln Ile Arg
50 55 60

Asp Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 687
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 687

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu Asp Ala Ile Glu His
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Phe Ile Arg
50 55 60

Asp Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 688
<211> 73
<212> PRT
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<220>
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<400> 688

Met Gly Ser Trp Phe Glu Phe Val Asp Arg Leu Thr Ala Ile Gln Val
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Glu Ala Ala Leu Ile Arg
50 55 60

Tyr Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 689
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 689

Met Gly Ser Trp Phe Glu Phe Leu Asp Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Val Ile Arg
50 55 60

Asp Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 690
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 690

Met Gly Ser Trp Tyr Glu Phe Met Val Arg Leu Asp Ala Ile Glu Glu
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Ser Ile Arg
50 55 60

Tyr His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 691
<211> 73
<212> PRT
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<220>
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<400> 691

Met Gly Ser Trp Tyr Glu Phe Glu Asp Arg Leu Asp Ala Ile Gln Trp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Ser Ala Ala Asn Ile Arg
50 55 60

Gln His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 692
<211> 73
<212> PRT
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<223> synthetic construct

<400> 692

Met Gly Ser Trp Ser Glu Phe Glu Tyr Arg Leu Phe Ala Ile Glu Asn
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Met Ile Arg
50 55 60

Gln Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 693
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 693

Met Gly Ser Trp Val Glu Phe Glu Tyr Arg Leu Asp Ala Ile Thr Glu
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Glu Glu Ala Ala Phe Ile Arg
50 55 60

Gln Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 694
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 694

Met Gly Ser Trp Trp Glu Phe Leu Asp Arg Leu Asp Ala Ile Glu Met
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Glu Ala Ala Leu Ile Arg
50 55 60

Asn Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 695
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 695

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Asp Ala Ile Glu Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu Glu Ala Ala Phe Ile Arg
50 55 60

Ile Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 696
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 696

Met Gly Ser Trp Trp Glu Phe Glu Ser Arg Leu Asp Ala Ile Phe Met
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Glu Asp Ala Ala Phe Ile Arg
50 55 60

Glu Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 697
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 697

Met Gly Ser Trp Val Glu Phe Trp His Arg Leu Asp Ala Ile Lys Ala
1 5 10 15

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

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Asp Phe Arg
50 55 60

Leu Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 698
<211> 73
<212> PRT
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<220>
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<400> 698

Met Gly Ser Trp Tyr Glu Phe Tyr Asn Arg Leu Ser Ala Ile Tyr Ala
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 699
<211> 73
<212> PRT
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<220>
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<400> 699

Met Gly Ser Trp Tyr Glu Phe Tyr Asp Arg Leu Ser Ala Ile Tyr Ala
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

Tyr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 700
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 700

Met Gly Ser Trp Asn Glu Phe Tyr Asp Arg Leu Ser Ala Ile Tyr Phe
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

Met Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 701
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 701

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Met Gly Ser Trp Asn Glu Phe Tyr Asp Arg Leu Ser Ala Ile Tyr Phe
1               5                  10                  15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu His Leu Arg Trp Tyr Ala Ala Asp Ile Arg
    50                  55                  60

Met Ile Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 702
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 702

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Met Gly Ser Trp Glu Glu Phe Tyr Asp Arg Leu Gly Ala Ile Phe Ala
1               5                  10                  15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Asp Ile Arg
    50                  55                  60

Met Ile Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 703
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 703

Met Gly Ser Trp Val Glu Phe Tyr Asp Arg Leu His Ala Ile Tyr Phe
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

Leu Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 704
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 704

Met Gly Ser Trp Lys Glu Phe Asp Asn Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Trp Tyr Ala Ala Asp Ile Arg
50 55 60

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Met Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 705
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 705

Met Gly Ser Trp Val Glu Phe Trp Asp Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg His Tyr Ala Ala Asp Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 706
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 706

Met Gly Ser Trp Tyr Glu Phe Ala Asp Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Tyr Tyr Ala Ala Asp Ile Arg
50 55 60

Trp Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 707
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 707

Met Gly Ser Trp Tyr Glu Phe Glu Glu Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Gln Glu Ala Ala Asp Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 708
<211> 73
<212> PRT
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<220>
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<400> 708

Met Gly Ser Trp Thr Glu Phe Glu Trp Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

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Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Asp Glu Ala Ala Asp Ile Arg
50 55 60

Gln Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 709
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 709

Met Gly Ser Trp Ile Glu Phe Glu Ser Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Leu Glu Ala Ala Asp Ile Arg
50 55 60

Glu Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 710
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 710

Met Gly Ser Trp Phe Glu Phe Glu Asp Arg Leu Asp Ala Ile Trp Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Met Asp Ala Ala Met Ile Arg
50 55 60

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 711
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 711

Met Gly Ser Trp Glu Glu Phe Glu Asp Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Tyr Asp Ala Ala Tyr Ile Arg
50 55 60

Glu Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 712
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 712

Met Gly Ser Trp Ile Glu Phe Glu Asp Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Tyr Glu Ala Ala Glu Ile Arg
50 55 60

Tyr Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 713
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 713

Met Gly Ser Trp Tyr Glu Phe Trp Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Tyr Ser Ala Ala Glu Ile Arg
50 55 60

Tyr Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 714
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 714

Met Gly Ser Trp Val Glu Phe Glu Ser Arg Leu Ala Ala Ile Glu His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu Tyr Ala Ala Glu Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 715
<211> 73
<212> PRT
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<220>
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<400> 715

Met Gly Ser Trp Trp Glu Phe Glu His Arg Leu Phe Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Asp Tyr Ala Ala Glu Ile Arg
50 55 60

Asp Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 716
<211> 73
<212> PRT
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<220>
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<400> 716

Met Gly Ser Trp Tyr Glu Phe Asp Ser Arg Leu Met Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Gln Glu Ala Ala Glu Ile Arg
50 55 60

Met Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 717
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 717

Met Gly Ser Trp Tyr Glu Phe Glu Trp Arg Leu Met Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg His Glu Ala Ala Glu Ile Arg
50 55 60

Asp Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 718
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 718

Met Gly Ser Trp Tyr Glu Phe Tyr Asn Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Gln Glu Ala Ala Asp Ile Arg
50 55 60

Gly Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 719
<211> 73
<212> PRT
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<223> synthetic construct

<400> 719

Met Gly Ser Trp Trp Glu Phe His Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Ile Glu Ala Ala Asp Ile Arg
50 55 60

Arg Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 720
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 720

Met Gly Ser Trp Tyr Glu Phe Trp Asp Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Leu Glu Ala Ala Asp Ile Arg
50 55 60

Arg Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 721
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 721

Met Gly Ser Trp Tyr Glu Phe Glu Glu Arg Leu Trp Ala Ile Glu Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Tyr Glu Ala Ala Trp Ile Arg
50 55 60

Asp Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 722
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 722

Met Gly Ser Trp Tyr Glu Phe Glu Asn Arg Leu Glu Ala Ile Glu Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Glu Glu Ala Ala Phe Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 723
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 723

Met Gly Ser Trp Tyr Glu Phe Glu Tyr Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu Glu Ala Ala Trp Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 724
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 724

Met Gly Ser Trp Tyr Glu Phe Glu Asn Arg Leu Gly Ala Ile Gly Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Tyr Ile Arg
50 55 60

Ala Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 725
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 725

Met Gly Ser Trp Tyr Glu Phe Glu His Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Glu Ala Ala Trp Ile Arg
50 55 60

Leu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 726
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 726

Met Gly Ser Trp Tyr Glu Phe Glu Trp Arg Leu Asp Ala Ile Tyr Asp
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Glu Ile Arg
50 55 60

Ala Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 727
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 727

Met Gly Ser Trp Val Glu Phe Glu Asn Arg Leu Glu Ala Ile Glu Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Asp Ala Ala Gln Ile Arg
50 55 60

Met Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 728
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 728

Met Gly Ser Trp Tyr Glu Phe Glu Glu Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Glu Gln Ala Ala Phe Ile Arg
50 55 60

Thr Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 729
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 729

Met Gly Ser Trp Phe Glu Phe Glu Trp Arg Leu Glu Ala Ile Phe Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Ala Glu Ala Ala Glu Ile Arg
50 55 60

Leu Arg Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 730
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 730

Met Gly Ser Trp Trp Glu Phe Glu Asp Arg Leu Met Ala Ile Tyr Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Ala Glu Ala Ala Leu Ile Arg
50 55 60

Glu Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 731
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 731

Met Gly Ser Trp Phe Glu Phe Glu Asp Arg Leu Tyr Ala Ile Glu Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Trp Gly Ala Ala Thr Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 732
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 732

Met Gly Ser Trp Ile Glu Phe Trp Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asp Glu Ala Ala Trp Ile Arg
50 55 60

Asp Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 733
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 733

Met Gly Ser Trp Phe Glu Phe Trp Asp Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asp Glu Ala Ala Trp Ile Arg
50 55 60

Gly Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 734
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 734

Met Gly Ser Trp Glu Glu Phe Thr Asp Arg Leu Trp Ala Ile Glu Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Phe Ile Arg
50 55 60

Lys Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 735
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 735

Met Gly Ser Trp Val Glu Phe Val Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Phe Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 736
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 736

Met Gly Ser Trp Phe Glu Phe Val Asp Arg Leu Glu Ala Ile Glu Met
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Trp Arg Ala Ala Met Ile Arg
50 55 60

Tyr Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 737
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 737

Met Gly Ser Trp Trp Glu Phe Glu Met Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Trp Glu Ala Ala Phe Ile Arg
50 55 60

Asp Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 738
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 738

Met Gly Ser Trp Phe Glu Phe Glu Ile Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Asp Glu Ala Ala Glu Ile Arg
50 55 60

Gln Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 739
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 739

Met Gly Ser Trp Tyr Glu Phe Tyr Gln Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Asp Glu Ala Ala Glu Ile Arg
50 55 60

Val Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 740
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 740

Met Gly Ser Trp Ile Glu Phe Glu Asp Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gln Glu Ala Ala Glu Ile Arg
50 55 60

Leu Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 741
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 741

Met Gly Ser Trp His Glu Phe Tyr Asp Arg Leu Asp Ala Ile Tyr Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Leu Leu Ala Ala Glu Ile Arg
50 55 60

Lys Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 742
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 742

Met Gly Ser Trp His Glu Phe Ile Thr Arg Leu Glu Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Trp Ala Ala Glu Ile Arg
50 55 60

Phe Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 743
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 743

Met Gly Ser Trp Met Glu Phe Phe Asp Arg Leu Val Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Met Trp Ala Ala Glu Ile Arg
50 55 60

Phe Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 744
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 744

Met Gly Ser Trp Val Glu Phe Ser Gly Arg Leu Ile Ala Ile Asp Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Met Trp Ala Ala Glu Ile Arg
50 55 60

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 745
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 745

Met Gly Ser Trp Val Glu Phe His His Arg Leu Phe Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Met Val Ala Ala Glu Ile Arg
50 55 60

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 746
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 746

Met Gly Ser Trp His Glu Phe Met Glu Arg Leu Ile Ala Ile Asp Gly
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Val Ala Ala Phe Ile Arg
50 55 60

Asp Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 747
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 747

Met Gly Ser Trp Lys Glu Phe Ile Gln Arg Leu Asp Ala Ile His Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Val Ala Ala Phe Ile Arg
50 55 60

Phe Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 748
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 748

Met Gly Ser Trp Ser Glu Phe Ile Phe Arg Leu Asp Ala Ile His Ser
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Phe Ile Ala Ala Glu Ile Arg
50 55 60

Leu Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 749
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 749

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 750
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 750

Met Gly Ser Trp Leu Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 751
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 751

Met Gly Ser Trp Phe Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 752
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 752

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 753
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 753

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 754
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 754

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Asp His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 755
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 755

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 756
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 756

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 757
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 757

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 758
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 758

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 759
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 759

Met Gly Ser Trp Phe Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 760
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 760

Met Gly Ser Trp Leu Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 761
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 761

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 762
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 762

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 763
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 763

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 764
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 764

Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 765
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 765

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 766
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 766

Met Gly Ser Trp Phe Glu Phe Tyr Glu Arg Leu Asn Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Ala His Ala Ala Ser Ile Arg
50 55 60

Thr Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 767
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 767

Met Gly Ser Trp Ile Glu Phe Tyr Trp Arg Leu Glu Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

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Trp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 768
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 768

Met Gly Ser Trp Ser Glu Phe Val Lys Arg Leu Asp Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Ala Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 769
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 769

Met Gly Ser Trp Glu Glu Phe Tyr Tyr Arg Leu Glu Ala Ile Asp Ala
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val His Ala Ala His Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 770
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 770

Met Gly Ser Trp Val Glu Phe His Tyr Arg Leu Gln Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val His Ala Ala His Ile Arg
50 55 60

Lys Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 771
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 771

Met Gly Ser Trp Val Glu Phe Val Gly Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg His His Ala Ala Glu Ile Arg
50 55 60

Asn Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 772
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 772

Met Gly Ser Trp Asn Glu Phe Met Asp Arg Leu Asn Ala Ile Asp Asn
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Lys Gln Ala Ala Ser Ile Arg
50 55 60

Leu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 773
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 773

Met Gly Ser Trp Asn Glu Phe Phe Gln Arg Leu Asn Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Gln His Ala Ala Asn Ile Arg
50 55 60

Trp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 774
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 774

Met Gly Ser Trp Tyr Glu Phe Val Val Arg Leu Phe Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 775
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<400> 775

Met Gly Ser Trp Tyr Glu Phe Tyr Leu Arg Leu Asp Ala Ile Asp His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Lys Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 776
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 776

Met Gly Ser Trp Tyr Glu Phe Arg Ala Arg Leu Leu Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Asn Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 777
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 777

Met Gly Ser Trp Thr Glu Phe Trp His Arg Leu Glu Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 778
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 778

Met Gly Ser Trp Thr Glu Phe Gln Asn Arg Leu Asn Ala Ile Asp His
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala Lys Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 779
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 779

Met Gly Ser Trp Ser Glu Phe Phe Lys Arg Leu Glu Ala Ile Asp Arg
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 780
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 780

Met Gly Ser Trp Tyr Glu Phe Gln Gln Arg Leu Glu Ala Ile Asp Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 781
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 781

Met Gly Ser Trp Thr Glu Phe Glu Lys Arg Leu His Ala Ile Asp Tyr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 782
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 782

Met Gly Ser Trp Thr Glu Phe His Gln Arg Leu Asp Ala Ile Asp Glu
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Phe Leu Arg Glu His Ala Ala Lys Ile Arg
50 55 60

Met Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 783
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 783

Met Gly Ser Trp Leu Glu Phe Ser Gln Arg Leu Thr Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asn Leu Arg Glu His Ala Ala Lys Ile Arg
50 55 60

Asn Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 784
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 784

Met Gly Ser Trp Thr Glu Phe Val Asn Arg Leu Tyr Ala Ile Asp Ser
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gly Leu Arg Thr His Ala Ala Lys Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 785
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 785

Met Gly Ser Trp Met Glu Phe Val Asp Arg Leu Ser Ala Ile Asp Arg
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu His Ala Ala Asn Ile Arg
50 55 60

Gln Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 786
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 786

Met Gly Ser Trp Val Glu Phe Val Ser Arg Leu Tyr Ala Ile Asp Phe
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Glu His Ala Ala Gln Ile Arg
50 55 60

Asp Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 787
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 787

Met Gly Ser Trp Ser Glu Phe His Thr Arg Leu Asp Ala Ile Asp Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Arg His Ala Ala Ala Ile Arg
50 55 60

Phe Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 788
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 788

Met Gly Ser Trp Leu Glu Phe His Ser Arg Leu Asp Ala Ile Asp Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

His Tyr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 789
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 789

Met Gly Ser Trp Thr Glu Phe Tyr Gln Arg Leu Asp Ala Ile Asp Thr
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gly Leu Arg Gln Gln Ala Ala Gln Ile Arg
50 55 60

Ala Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 790
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 790

Met Gly Ser Trp Ala Glu Phe Ser Asp Arg Leu Asn Ala Ile Asp Gln
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Glu His Ala Ala Glu Ile Arg
50 55 60

Lys Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 791
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 791

Met Gly Ser Trp Met Glu Phe Asn His Arg Leu Gln Ala Ile Asp Gly
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

Ala Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 792
<211> 73
<212> PRT
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<220>
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<400> 792

Met Gly Ser Trp Tyr Glu Phe Tyr Lys Arg Leu Glu Ala Ile Asp Asn
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 793
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 793

Met Gly Ser Trp Tyr Glu Phe Tyr Tyr Arg Leu Glu Ala Ile Asp Asn
1 5 10 15

Arg Leu Ile Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu His Ala Ala Lys Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 794
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 794

Met Gly Ser Trp Tyr Glu Phe Val Ser Arg Leu Glu Ala Ile Asp Asp
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Met Leu Arg Gln His Ala Ala Ala Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 795
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 795

Met Gly Ser Trp Tyr Glu Phe Ser His Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Pro Leu Arg Glu His Ala Ala Tyr Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 796
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 796

Met Gly Ser Trp Phe Glu Phe Phe Glu Arg Leu Ala Ala Ile Glu Asp
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Ala Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 797
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 797

Met Gly Ser Trp Ile Glu Phe Lys Tyr Arg Leu Asp Ala Ile Glu Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ile His Ala Ala Ala Ile Arg
50 55 60

Thr Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 798
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 798

Met Gly Ser Trp Tyr Glu Phe Met Tyr Arg Leu Asp Ala Ile Glu Tyr
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ile His Ala Ala Met Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 799
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 799

Met Gly Ser Trp Val Glu Phe Val Thr Arg Leu Glu Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Ala His Ala Ala His Ile Arg
50 55 60

His Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 800
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 800

Met Gly Ser Trp Tyr Glu Phe Val Ile Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Val His Ala Ala His Ile Arg
50 55 60

Val Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 801
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 801

Met Gly Ser Trp Val Glu Phe Val Glu Arg Leu Asp Ala Ile Glu Phe
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Asn His Ala Ala His Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 802
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 802

Met Gly Ser Trp Ser Glu Phe Val His Arg Leu Asp Ala Ile Glu Val
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Tyr His Ala Ala Lys Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 803
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 803

Met Gly Ser Trp Ser Glu Phe Tyr Tyr Arg Leu Ala Ala Ile Glu Ser
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Arg Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Arg Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 804
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 804

Met Gly Ser Trp Tyr Glu Phe Tyr Leu Arg Leu Ser Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val Gln Ala Ala His Ile Arg
50 55 60

Thr Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 805
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 805

Met Gly Ser Trp Tyr Glu Phe Tyr Asp Arg Leu Asp Ala Ile Glu Asp
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Asp Gln Ala Ala Tyr Ile Arg
50 55 60

Thr Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 806
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 806

Met Gly Ser Trp His Glu Phe Trp Val Arg Leu Glu Ala Ile Glu Ser
1 5 10 15

Arg Leu Phe Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val Gln Ala Ala His Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 807
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 807

Met Gly Ser Trp Val Glu Phe Tyr His Arg Leu Glu Ala Ile Glu Gln
1 5 10 15

Arg Leu Met Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu Gln Ala Ala Ala Ile Arg
    50   55   60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65   70

<210> 808
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 808

Met Gly Ser Trp Val Glu Phe Tyr Glu Arg Leu Asn Ala Ile Glu Tyr
1   5   10   15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala Tyr Ile Arg
    50   55   60

Gln Trp Leu Gln Ala Tyr Arg His Asn
65   70

<210> 809
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

<223> synthetic construct

<400> 809

Met Gly Ser Trp Val Glu Phe Tyr His Arg Leu Asp Ala Ile Phe Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Ala Asn Ala Ala Gly Ile Arg
50 55 60

Ser Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 810
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 810

Met Gly Ser Trp Ser Glu Phe Thr Asp Arg Leu Phe Ala Ile Glu Asp
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Met His Ala Ala Ser Ile Arg
50 55 60

Leu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 811
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 811

Met Gly Ser Trp His Glu Phe Tyr Asp Arg Leu Tyr Ala Ile Trp Asp
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gly Leu Arg Asn Ala Ala Ala Val Ile Arg
50 55 60

Ile Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 812
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 812

Met Gly Ser Trp Phe Glu Phe Ser Asn Arg Leu Tyr Ala Ile Trp His
1 5 10 15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Thr Gln Ala Ala Phe Ile Arg
50 55 60

Ile Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 813
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 813

Met Gly Ser Trp Phe Glu Phe Ser Asp Arg Leu Tyr Ala Ile Trp Glu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Phe Gln Ala Ala Phe Ile Arg
50 55 60

Tyr Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 814
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 814

Met Gly Ser Trp Phe Glu Phe Glu Asp Arg Leu Phe Ala Ile Trp Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Gln Ser Ala Ala Ser Ile Arg
50 55 60

Trp Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 815
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 815

Met Gly Ser Trp His Glu Phe Ser Glu Arg Leu Phe Ala Ile Trp Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Gln Ser Ala Ala Phe Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 816
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 816

Met Gly Ser Trp Gly Glu Phe Thr Val Arg Leu Tyr Ala Ile Asp Arg
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Glu Leu Arg Arg Phe Ala Ala Ile Ile Arg
    50   55   60

Ala Phe Leu Gln Ala Tyr Arg His Asn
65   70

<210> 817
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 817

Met Gly Ser Trp Tyr Glu Phe Asp His Arg Leu Met Ala Ile Ser Phe
1   5   10   15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Thr Leu Arg Arg Arg Ala Ala Asn Ile Arg
    50   55   60

His Leu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 818
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 818

Met Gly Ser Trp Ser Ile Phe Lys Tyr His Leu Ala Asp Ile Lys Leu
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Phe Leu Ile Ala Asp Phe Glu Phe Thr Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 819
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 819

Met Gly Ser Trp His His Phe Lys Tyr Phe Leu Ala Asp Ile Lys Ser
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 820
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 820

Met Gly Ser Trp Leu Tyr Phe Lys Tyr Asn Leu Ala Val Ile Lys His
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Met Ser Ile Ala Asp Phe Glu Tyr Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 821
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 821

Met Gly Ser Trp Phe Tyr Phe Lys Tyr Glu Leu Ala Trp Ile Lys His
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Thr His Ile Ala Phe Phe Glu His Gln Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 822
<211> 73
<212> PRT
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<220>
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<400> 822

Met Gly Ser Trp Ala Asp Phe Lys Trp Thr Leu Ala Tyr Ile Lys His
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Met Glu Ile Ala Tyr Phe Glu Gln Ser Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 823
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 823

Met Gly Ser Trp Ala Tyr Phe Lys Gly Gln Leu Ala Tyr Ile Lys Ser
1 5 10 15

Gly Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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Leu Arg Ile Ala Tyr Phe Glu His Trp Leu Gln Asn Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 824
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 824

Met Gly Ser Trp Glu Asn Phe Lys Asp Thr Leu Ala Trp Ile Lys Glu
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

His Arg Ile Ala Ile Phe Glu His Tyr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 825
<211> 73
<212> PRT
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<220>
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<400> 825

Met Gly Ser Trp Val Leu Phe Lys Asp Tyr Leu Ala Asp Ile Lys His
1 5 10 15

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Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

His Leu Ile Ala Asn Phe Glu Gly Asp Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 826
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 826

Met Gly Ser Trp Ser Leu Phe Lys His Arg Leu Ala Asn Ile Lys Val
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Thr Phe Ile Ala Tyr Phe Glu Lys Asp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 827
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 827

Met Gly Ser Trp Glu His Phe Lys Val Glu Leu Ala Gly Ile Lys Ala
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 828
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 828

Met Gly Ser Trp Ile Tyr Phe Lys Asp Glu Leu Ala Gly Ile Lys Lys
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 829
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 829

Met Gly Ser Trp Val Leu Phe Lys Gln Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Glu Gln Ile Ala Arg Phe Glu His Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 830
<211> 73
<212> PRT
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<220>
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<400> 830

Met Gly Ser Trp Val Leu Phe Lys Gln Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Trp Glu Ile Ala Ala Phe Glu Gln Arg Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 831
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 831

Met Gly Ser Trp Phe Leu Phe Lys Ser Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Tyr Gln Ile Ala Glu Phe Glu Phe Trp Leu Gln Ser Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 832
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 832

Met Gly Ser Trp Leu Leu Phe Lys Ser Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Trp Asn Ile Ala Glu Phe Glu Lys Asn Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 833
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 833

Met Gly Ser Trp Leu Leu Phe Lys Ser Asp Leu Ala Trp Ile Lys Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Glu Ser Ile Ala Met Phe Glu His Trp Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 834
<211> 73
<212> PRT
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<220>
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<400> 834

Met Gly Ser Trp Leu Tyr Phe Lys Ser Asp Leu Ala Trp Ile Lys Trp
1 5 10 15

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Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Glu Ala Ile Ala Glu Phe Glu Gln Ala Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 835
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 835

Met Gly Ser Trp Lys Leu Phe Lys Tyr Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 836
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 836

Met Gly Ser Trp Tyr Leu Phe Lys Asn Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Met Val Ile Ala Met Phe Glu Asp His Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 837
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 837

Met Gly Ser Trp Val Tyr Phe Lys Ala His Leu Ala Phe Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 838
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 838

Met Gly Ser Trp Met Tyr Phe Lys Ser His Leu Ala Trp Ile Lys Trp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 839
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 839

Met Gly Ser Trp Thr Leu Phe Lys Trp Asp Leu Ala Phe Ile Lys Trp
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 840
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 840

Met Gly Ser Trp Ile Leu Phe Lys Glu Asp Leu Ala Phe Ile Lys Trp
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Thr Thr Ile Ala Asn Phe Glu Ser Asp Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 841
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 841

Met Gly Ser Trp Tyr Phe Phe Lys Ser Arg Leu Ala Tyr Ile Lys Val
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

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Trp Glu Ile Ala His Phe Glu Glu Trp Leu Gln Arg Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 842
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 842

Met Gly Ser Trp Tyr Ile Phe Lys Ser Glu Leu Ala Trp Ile Lys Trp
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 843
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 843

Met Gly Ser Trp Tyr Ile Phe Lys Gln Glu Leu Ala Ser Ile Lys Leu
1 5 10 15

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Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

Ala Glu Ile Ala Trp Phe Glu Trp Trp Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 844
<211> 73
<212> PRT
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<220>
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<400> 844

Met Gly Ser Trp Val Arg Phe Lys Thr Glu Leu Ala Tyr Ile Lys Glu
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Ser Glu Ile Ala Ile Phe Glu His Ser Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 845
<211> 73
<212> PRT
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<220>

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<223> synthetic construct

<400> 845

Met Gly Ser Trp Tyr Leu Phe Lys Thr Glu Leu Ala Ala Ile Lys Tyr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ser Phe Glu
20 25 30

Tyr Glu Ile Ala Trp Phe Glu His Ile Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 846
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 846

Met Gly Ser Trp Tyr Trp Phe Lys Tyr Glu Leu Ala Glu Ile Lys Trp
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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2018369639

<210> 847
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 847

Met Gly Ser Trp Trp Val Phe Lys Lys Thr Leu Ala Glu Ile Lys Trp
1 5 10 15

Thr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Ala Glu Ile Ala Phe Phe Glu Phe Ile Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 848
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 848

Met Gly Ser Trp Val Tyr Phe Lys Asp His Leu Ala Glu Ile Lys Ser
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Tyr Asp Ile Ala Trp Phe Glu Phe Ile Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 849
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 849

Met Gly Ser Trp Val Tyr Phe Lys His Arg Leu Ala Glu Ile Lys Asp
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Thr Asp Ile Ala Trp Phe Glu Trp Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 850
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 850

Met Gly Ser Trp Ile Ile Phe Lys Thr Asp Leu Ala Arg Ile Lys Asn
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

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Arg Asp Ile Ala Trp Phe Glu Phe Met Leu Gln Ile Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 851
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 851

Met Gly Ser Trp Met His Phe Lys Gln Asp Leu Ala Glu Ile Lys Gly
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Met Asp Ile Ala Trp Phe Glu Tyr Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 852
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 852

Met Gly Ser Trp Gln Ile Phe Lys Gln Asp Leu Ala Ala Ile Lys Asp
1 5 10 15

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Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Phe Asp Ile Ala Trp Phe Glu His Met Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 853
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 853

Met Gly Ser Trp Leu Ala Phe Lys Glu Asp Leu Ala His Ile Lys Ser
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

His Asp Ile Ala Trp Phe Glu Tyr Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 854
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 854

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Met Gly Ser Trp Phe Val Phe Lys Glu Asp Leu Ala Gly Ile Lys Phe
1               5                  10                  15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
            20                  25                  30

Thr Asp Ile Ala Trp Phe Glu Tyr Met Leu Gln Tyr Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 855
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 855

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Met Gly Ser Trp Thr His Phe Lys Glu Asp Leu Ala His Ile Lys Asp
1               5                  10                  15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20                  25                  30

Leu Asp Ile Ala Trp Phe Glu Phe Met Leu Gln Tyr Tyr Lys Gly Lys
        35                  40                  45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
    50                  55                  60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65                  70
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<210> 856
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 856

Met Gly Ser Trp Tyr Tyr Phe Lys Glu Arg Leu Ala Ala Ile Lys Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Ala Asp Ile Ala Trp Phe Glu Phe Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 857
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 857

Met Gly Ser Trp Tyr Thr Phe Lys Gly Ser Leu Ala Glu Ile Lys Asn
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Ser Asp Ile Ala Trp Phe Glu Phe Met Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 858
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 858

Met Gly Ser Trp Phe Thr Phe Lys Asp Asp Leu Ala Gln Ile Lys Asn
1 5 10 15

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

Met Ser Ile Ala Trp Phe Glu Phe Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 859
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 859

Met Gly Ser Trp Val Leu Phe Lys Gln Asp Leu Ala Met Ile Lys Gln
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

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Tyr Asp Ile Ala Trp Phe Glu His Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 860
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 860

Met Gly Ser Trp Val Glu Phe Lys Arg Asp Leu Ala Asn Ile Lys Gln
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Met Gln Ile Ala Trp Phe Glu His Thr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 861
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 861

Met Gly Ser Trp Ser Tyr Phe Lys Glu Asp Leu Ala Asn Ile Lys Ser
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Trp Phe Glu
20 25 30

Ser Ser Ile Ala Trp Phe Glu His Thr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 862
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 862

Met Gly Ser Trp Ser Ile Phe Lys Gln Asp Leu Ala Asp Ile Lys Asp
1 5 10 15

Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Met Phe Glu
20 25 30

Met Asp Ile Ala Trp Phe Glu His Thr Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 863
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 863

Met Gly Ser Trp Glu Ile Phe Lys Asp Asp Leu Ala Ser Ile Lys Lys
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Ser Asp Ile Ala Trp Phe Glu Leu Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 864
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 864

Met Gly Ser Trp Ser Ile Phe Lys Asp Asp Leu Ala Val Ile Lys Glu
1 5 10 15

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

Gln Asp Ile Ala Trp Phe Glu His Leu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 865
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

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<400> 865

Met Gly Ser Trp Ser Val Phe Lys Asp Asp Leu Ala Gln Ile Lys Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Leu Asp Ile Ala Trp Phe Glu Tyr Val Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 866
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 866

Met Gly Ser Trp Ala Val Phe Lys Asp Ser Leu Ala His Ile Lys Asp
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

Met Asp Ile Ala Trp Phe Glu Tyr Val Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 867
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 867

Met Gly Ser Trp Ile Ala Phe Lys Asp His Leu Ala Ile Ile Lys Gln
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Arg Phe Glu
20 25 30

Phe Glu Ile Ala Trp Phe Glu Trp Met Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 868
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 868

Met Gly Ser Trp Ile His Phe Lys Asn Asp Leu Ala Val Ile Lys Asp
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Arg Phe Glu
20 25 30

Ile Met Ile Ala Trp Phe Glu Asp Ala Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 869
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 869

Met Gly Ser Trp Met Val Phe Lys Gln Asp Leu Ala Glu Ile Lys Ala
1 5 10 15

Asn Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asp Phe Glu
20 25 30

Phe Ala Ile Ala Trp Phe Glu Tyr Glu Leu Gln Trp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 870
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 870

Met Gly Ser Trp Lys Asn Phe Lys Leu Glu Leu Ala Leu Ile Lys Ser
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 871
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 871

Met Gly Ser Trp His Ser Phe Lys Gln Asp Leu Ala Tyr Ile Lys Tyr
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gln Phe Glu
20 25 30

Glu Leu Ile Ala Phe Phe Glu Tyr Tyr Leu Gln Thr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 872
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 872

Met Gly Ser Trp Val Val Phe Lys Ser Ser Leu Ala Gln Ile Lys Ile
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Val Lys Ile Ala His Phe Glu Gln Glu Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 873
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 873

Met Gly Ser Trp Asp Gln Phe Lys Asn Ser Leu Ala Ser Ile Lys Arg
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ile Phe Glu
20 25 30

Val Lys Ile Ala His Phe Glu His Phe Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 874
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 874

Met Gly Ser Trp Asn Asn Phe Lys Ser Ser Leu Ala Ser Ile Lys Gln
1 5 10 15

Val Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Val Phe Glu
20 25 30

Leu Gln Ile Ala His Phe Glu Arg Glu Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 875
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 875

Met Gly Ser Trp Val Glu Phe Gly His Arg Leu Trp Ala Ile Asp Gln
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Gln Arg Ala Ala Phe Ile Arg
50 55 60

Phe Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 876
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 876

Met Gly Ser Trp Ala Glu Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Leu
20 25 30

Gly Glu Ile Trp Ala Phe Glu Met Glu Leu Ala Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Gly Arg Glu Ala Ala Ala Ile Arg
50 55 60

Met Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 877
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 877

Met Gly Ser Trp Tyr Glu Phe Asp Leu Arg Leu His Ala Ile Tyr Asp
1 5 10 15

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

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Asp Asn Ala Ala Tyr Ile Arg
50 55 60

Gln Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 878
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 878

Met Gly Ser Trp His Glu Phe His Asp Arg Leu Gln Ala Ile His Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ile Ala Ala Ala His Ile Arg
50 55 60

Gln Val Leu Gln Ala Tyr Arg His Asn
65 70

<210> 879
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 879

Met Gly Ser Trp Asn Tyr Phe Lys Asp His Leu Ala Trp Ile Lys Asn
1 5 10 15

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Ser Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala His Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 880
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 880

Met Gly Ser Trp Leu Trp Phe Lys Ile Phe Leu Ala Glu Ile Lys Tyr
1 5 10 15

Phe Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Asp
20 25 30

Phe Glu Ile His Ala Phe His Val Glu Leu Phe Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Glu Val Ala Ala Glu Ile Arg
50 55 60

Trp Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 881
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 881

Met Gly Ser Trp Thr Glu Phe Gln Ser Arg Leu Asp Ala Ile His Ser
1 5 10 15

Arg Leu Arg Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Leu Leu Arg Asp Asp Ala Ala Phe Ile Arg
50 55 60

His Phe Leu Gln Ala Tyr Arg His Asn
65 70

<210> 882
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 882

Met Gly Ser Trp Val Val Phe Lys Val Asp Leu Ala Thr Ile Lys Tyr
1 5 10 15

Ile Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Gly Glu Ile Ala Gly Phe Glu Tyr Ser Leu Gln Phe Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 883
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 883

Met Gly Ser Trp Thr Ile Phe Lys Glu Trp Leu Ala Phe Ile Lys Thr
1 5 10 15

Asp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Phe Phe Glu
20 25 30

Gly Trp Ile Ala Ser Phe Glu Met Glu Leu Gln Lys Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 884
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 884

Met Gly Ser Trp Glu Glu Phe Glu Leu Arg Leu Asn Ala Ile Glu Glu
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Tyr Phe Glu Ala Asp Ala Ile Phe
50 55 60

Glu Glu Leu Val Ala Tyr Arg His Asn
65 70

<210> 885
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 885

Met Gly Ser Trp Val Val Phe Lys Gln Arg Leu Ala Tyr Ile Lys Asp
1 5 10 15

Leu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 886
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 886

Met Gly Ser Trp Val Glu Phe Tyr Glu Arg Leu Asp Ala Ile Asp Arg
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val His Ala Ala Ser Ile Arg
50 55 60

Ala Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 887
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 887

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ala His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 888
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 888

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Val His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 889
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 889

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ala His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 890
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 890

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Lys Ala His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 891
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 891

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Gln Ala His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 892
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 892

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Ala His Ala Ala Gly Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 893
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
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<400> 893

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala His Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 894
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 894

Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 895
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 895

Met Gly Ser Trp Ser Glu Phe Tyr Asp Arg Leu Asn Ala Ile Asp Ala
1 5 10 15

Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Glu His Ala Ala Ala Ile Arg
50 55 60

Glu Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 896
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 896

Met Gly Ser Trp Val Glu Phe Glu Ala Arg Leu Ser Ala Ile Tyr Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Ser Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 897
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 897

Met Gly Ser Trp Val Glu Phe Phe Val Arg Leu Asp Ala Ile Trp Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Phe His Ala Ala Gly Ile Arg
50 55 60

Gln Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 898
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 898

Met Gly Ser Trp Thr Glu Phe Asn Leu Arg Leu Asp Ala Ile Tyr Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Trp His Ala Ala Gly Ile Arg
50 55 60

Gln Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 899
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 899

Met Gly Ser Trp Met Glu Phe Tyr Asp Arg Leu Asp Ala Ile Trp Val
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Phe His Ala Ala Gly Ile Arg
50 55 60

Glu Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 900
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 900

Met Gly Ser Trp His Glu Phe Asn Gly Arg Leu Trp Ala Ile Tyr Ala
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Gly Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 901
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 901

Met Gly Ser Trp Tyr Glu Phe Val Gln Arg Leu His Ala Ile Asn Asp
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Tyr Thr Leu Gln Ala Tyr Arg His Asn
65 70

<210> 902
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 902

Met Gly Ser Trp Ala Glu Phe Tyr Gln Arg Leu Asn Ala Ile Trp Asn
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Val Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Gly Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 903
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 903

Met Gly Ser Trp Val Glu Phe Asn Glu Arg Leu His Ala Ile Tyr Leu
1 5 10 15

Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Trp Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 904
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 904

Met Gly Ser Trp Asn Glu Phe Lys Leu Glu Leu Ala Phe Ile Lys Asp
1 5 10 15

Trp Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Asn Phe Glu
20 25 30

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Glu Ala Ile Ala Glu Phe Glu Ala Gly Leu Gln Gly Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 905
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 905

Met Gly Ser Trp Met Glu Phe Glu Ala Arg Leu Glu Ala Ile Trp Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ser Leu Arg Phe His Ala Ala Gly Ile Arg
50 55 60

Gln His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 906
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 906

Met Gly Ser Trp Val Glu Phe Glu Asp Arg Leu Asn Ala Ile Trp Trp
1 5 10 15

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Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Arg His Ala Ala Gly Ile Arg
50 55 60

Thr Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 907
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 907

Met Gly Ser Trp His His Phe Lys Met His Leu Ala Gly Ile Lys Leu
1 5 10 15

Gln Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Glu Phe Glu
20 25 30

Glu Trp Ile Ala Asp Phe Glu Gly Ala Leu Gln Asp Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 908
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 908

Met Gly Ser Trp Ala Glu Phe Phe Ala Arg Leu Asp Ala Ile Trp Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Phe His Ala Ala Gly Ile Arg
50 55 60

Gln Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 909
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 909

Met Gly Ser Trp Ala Glu Phe Phe Ala Arg Leu Asp Ala Ile Trp Asp
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Phe His Ala Ala Gly Ile Arg
50 55 60

Gln Lys Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 910
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 910

Met Gly Ser Trp Ala Glu Phe Phe Ala Arg Leu Asp Ala Ile Trp Glu
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Lys Phe His Ala Ala Gly Ile Arg
50 55 60

Gln Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 911
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 911

Met Gly Ser Trp His Glu Phe Arg Trp Arg Leu Phe Ala Ile Trp Gln
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Leu Asp Ala Ala Leu Ile Arg
50 55 60

Val Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 912
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 912

Met Gly Ser Trp Ala Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1 5 10 15

Lys Leu Gly Glu Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 913
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 913

Met Gly Ser Trp Ala Glu Phe Arg Trp Ala Leu His Ala Ile Trp Leu
1 5 10 15

Lys Leu Gly Glu Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 914
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 914

Met Gly Ser Trp Ala Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1 5 10 15

Lys Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 915
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 915

Met Gly Ser Trp Ala Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1 5 10 15

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Gln Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65   70

<210> 916
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 916

Met Gly Ser Trp Ala Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1   5   10   15

Arg Leu Gly Ala Leu Gly Gly Thr Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65   70

<210> 917
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 917

Met Gly Ser Trp Ala Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 918
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 918

Met Gly Ser Trp Ala Glu Phe Arg Trp Lys Leu Glu Ala Ile Trp Leu
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 919
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 919

Met Gly Ser Trp Ala Glu Phe Arg Trp Lys Leu Gly Ala Ile Trp Leu
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 920
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 920

Met Gly Ser Trp Tyr Glu Phe Arg Trp Arg Leu His Ala Ile Trp Leu
1 5 10 15

Arg Leu Gly Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Trp Leu Arg Gln Asp Ala Ala Gln Ile Arg
50 55 60

Tyr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 921
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 921

Met Gly Ser Trp His Glu Phe Leu Arg Arg Leu Leu Ala Ile Glu Met
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu His Leu Arg Val Arg Ala Ala Ser Ile Arg
50 55 60

Gln Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 922
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 922

Met Gly Ser Trp Trp Gly Phe Lys Val Asn Leu Ala Trp Ile Lys Trp
1 5 10 15

Lys Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Tyr Phe Glu
20 25 30

Leu Trp Ile Ala Asn Phe Glu His Ser Leu Gln Glu Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 923
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 923

Met Gly Ser Trp Val Asn Phe Lys Thr His Leu Ala Arg Ile Lys Val
1 5 10 15

His Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Leu Phe Glu
20 25 30

His Asp Ile Ala Asn Phe Glu Gln Val Leu Gln Gln Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 924
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 924

Met Gly Ser Trp Leu Val Phe Lys Asp Glu Leu Ala Gly Ile Lys Asn
1 5 10 15

Tyr Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Thr Phe Glu
20 25 30

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

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 925
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 925

Met Gly Ser Trp Lys Thr Phe Lys Ile Glu Leu Ala Gly Ile Lys Leu
1 5 10 15

Glu Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Gly Phe Glu
20 25 30

Asn Ala Ile Ala Gln Phe Glu Ser Ser Leu Gln Tyr Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg
50 55 60

Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 926
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 926

Met Gly Ser Trp Trp Glu Phe Lys Val Arg Leu Ser Ala Ile Gln Tyr
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Glu Gln Ala Ala Leu Ile Arg
50 55 60

Thr Ile Leu Gln Ala Tyr Arg His Asn
65 70

<210> 927
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 927

Met Gly Ser Trp Trp Glu Phe His Ile Arg Leu His Ala Ile Asn Tyr
1 5 10 15

Arg Leu Ala Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Glu Leu Ala Ala Lys Ile Arg
50 55 60

Gly Asp Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 928
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 928

Met Gly Ser Trp Trp Glu Phe Gln Val Arg Leu Arg Ala Ile Gln Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Gly Leu Ala Ala Gln Ile Arg
50 55 60

Phe Asp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 929
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 929

Met Gly Ser Trp Trp Glu Phe Lys Ile Arg Leu Tyr Ala Ile Glu Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Tyr Asn Leu Gln Ala Tyr Arg His Asn
65 70

<210> 930
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 930

Met Gly Ser Trp Phe Glu Phe Asn Ile Arg Leu His Ala Ile Glu Tyr
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asn Tyr Ala Ala Ser Ile Arg
50 55 60

Lys Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 931
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 931

Met Gly Ser Trp Phe Glu Phe Glu Ile Arg Leu Arg Ala Ile Glu Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Leu Ala Ala Glu Ile Arg
50 55 60

Tyr Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 932
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 932

Met Gly Ser Trp Phe Glu Phe Lys Ile Arg Leu Tyr Ala Ile Gln Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asn Leu Ala Ala Glu Ile Arg
50 55 60

His Ser Leu Gln Ala Tyr Arg His Asn
65 70

<210> 933
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 933

Met Gly Ser Trp Trp Glu Phe Lys Val Arg Leu Arg Ala Ile Glu Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Val Leu Ala Ala Ser Ile Arg
50 55 60

Ile His Leu Gln Ala Tyr Arg His Asn
65 70

<210> 934
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 934

Met Gly Ser Trp Ser Glu Phe Trp Phe Arg Leu His Ala Ile Leu Tyr
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Thr Leu Arg Asp Ala Ala Ala Glu Ile Arg
50 55 60

Val Ala Leu Gln Ala Tyr Arg His Asn
65 70

<210> 935
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 935

Met Gly Ser Trp Ile Glu Phe Trp Val Arg Leu Asn Ala Ile Leu Tyr
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ala Leu Arg Asp Ser Ala Ala Glu Ile Arg
50 55 60

Arg Trp Leu Gln Ala Tyr Arg His Asn
65 70

<210> 936
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 936

Met Gly Ser Trp Val Glu Phe Trp Ile Arg Leu Asn Ala Ile Lys Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Glu Leu Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 937
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 937

Met Gly Ser Trp Thr Glu Phe Trp Trp Arg Leu Ser Ala Ile Val Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Glu Leu Arg Asp Met Ala Ala Asp Ile Arg
50 55 60

Ser Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 938
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 938

Met Gly Ser Trp Trp Glu Phe Tyr Leu Arg Leu Arg Ala Ile Ser Tyr
1 5 10 15

Arg Leu Gln Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

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Lys Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 939
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 939

Met Gly Ser Trp Trp Glu Phe His Val Arg Leu Arg Ala Ile Glu Tyr
1 5 10 15

Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Gln Leu Arg Leu Ile Ala Ala Asn Ile Arg
50 55 60

His Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 940
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 940

Met Gly Ser Trp Trp Glu Phe His Val Arg Leu Lys Ala Ile Glu Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Tyr Ile Ala Ala Asn Ile Arg
50 55 60

Gln Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 941
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 941

Met Gly Ser Trp Trp Glu Phe Lys Val Arg Leu Lys Ala Ile Glu Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Tyr Ile Ala Ala Asn Ile Arg
50 55 60

Gln Leu Leu Gln Ala Tyr Arg His Asn
65 70

<210> 942
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 942

Met Gly Ser Trp Trp Glu Phe Gln Val Arg Leu Ala Ala Ile Glu Tyr
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

Gly Asn Pro Glu Val Glu Asn Leu Arg Gln Leu Ala Ala His Ile Arg
    50   55   60

Ser Val Leu Gln Ala Tyr Arg His Asn
65   70

<210> 943
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 943

Met Gly Ser Trp Trp Glu Phe Gln Val Arg Leu Ser Ala Ile Glu Tyr
1   5   10   15

Arg Leu Thr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
            20   25   30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
        35   40   45

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

Ser Leu Leu Gln Ala Tyr Arg His Asn
65   70

<210> 944
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>

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<223> synthetic construct

<400> 944

Met Gly Ser Trp Trp Glu Phe Asn Ile Arg Leu His Ala Ile Asp Tyr
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

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

Ala Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 945
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 945

Met Gly Ser Trp Trp Glu Phe Arg Val Arg Leu Glu Ala Ile Asp Tyr
1 5 10 15

Arg Leu Lys Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Met Lys Ala Ala Thr Ile Arg
50 55 60

Ala Ile Leu Gln Ala Tyr Arg His Asn
65 70

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<210> 946
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 946

Met Gly Ser Trp Tyr Glu Phe Asp Ile Arg Leu Glu Ala Ile Lys Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Tyr Leu Arg Lys Lys Ala Ala Val Ile Arg
50 55 60

Ser Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 947
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 947

Met Gly Ser Trp Trp Glu Phe Arg Ile Arg Leu Glu Ala Ile Trp Tyr
1 5 10 15

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

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Ile Phe Ala Ala Asn Ile Arg
50 55 60

Ser Lys Leu Gln Ala Tyr Arg His Asn
65 70

<210> 948
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 948

Met Gly Ser Trp Trp Glu Phe Asn Val Arg Leu Gln Ala Ile Lys Tyr
1 5 10 15

Arg Leu Ser Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Lys Thr Ala Ala His Ile Arg
50 55 60

Trp Gln Leu Gln Ala Tyr Arg His Asn
65 70

<210> 949
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 949

Met Gly Ser Trp Trp Glu Phe Asn Val Arg Leu Ser Ala Ile Arg Tyr
1 5 10 15

Arg Leu Leu Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

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Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Asp Leu Arg Ala Ser Ala Ala Gln Ile Arg
50 55 60

Ala Met Leu Gln Ala Tyr Arg His Asn
65 70

<210> 950
<211> 73
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 950

Met Gly Ser Trp Trp Glu Phe Asn Met Arg Leu Ser Ala Ile Lys Tyr
1 5 10 15

Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu
20 25 30

Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys Gly Lys
35 40 45

Gly Asn Pro Glu Val Glu Ile Leu Arg Arg Leu Ala Ala Asp Ile Arg
50 55 60

Glu Arg Leu Gln Ala Tyr Arg His Asn
65 70

<210> 951
<211> 170
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 951

Asp Glu Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr Ala Ile
1 5 10 15

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```
Glu Trp Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu Ala Ala
            20                  25                  30

Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala Tyr Lys
        35                  40                  45

Gly Lys Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala Ala Val
    50                  55                  60

Ile Arg Ser Asn Leu Gln Ala Tyr Arg His Asn Gly Gly Gly Gly Ser
65                  70                  75                  80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Met Leu Gln Met Ala
                85                  90                  95

Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys
            100                 105                 110

Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys
        115                 120                 125

Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn
    130                 135                 140

Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

His His His His His His His His His His
                165                 170
```

<210> 952
<211> 175
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 952

```
Asp Glu Gly Gly Gly Gly Ser Met Gly Ser Trp Ala Glu Phe Lys Gln
1               5                   10                  15
```

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Arg Leu Ala Ala Ile Lys Thr Arg Leu Gln Ala Leu Gly Gly Ser Glu
20 25 30

Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu
35 40 45

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

Lys Glu Ala Ala Ala Ile Arg Asp Glu Leu Gln Ala Tyr Arg His Asn
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
85 90 95

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
100 105 110

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
115 120 125

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
130 135 140

Val Lys Gly Thr Asn Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser His His His His His His His His His His
165 170 175

<210> 953
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 953

Asp Glu His His His His His His His His His His Lys Leu Glu Asn
1 5 10 15

```
Leu Tyr Phe Gln Gly Gly Gly Gly Gly Ser Met Gly Ser Trp Asp Glu
            20                  25                  30

Phe Gly Arg Arg Leu Tyr Ala Ile Glu Trp Arg Leu Tyr Ala Leu Gly
        35                  40                  45

Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe
    50                  55                  60

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

Lys Leu Arg Glu Ile Ala Ala Val Ile Arg Ser Asn Leu Gln Ala Tyr
                85                  90                  95

Arg His Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln
        115                 120                 125

Asp Lys Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala
    130                 135                 140

Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr
145                 150                 155                 160

Leu Gln Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu
                165                 170                 175

Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala
            180                 185                 190

Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu
        195                 200                 205

Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met
    210                 215                 220
```

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```
Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala
225                 230                 235                 240

Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val
                245                 250                 255

Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys
            260                 265                 270

Gln Ala Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile
        275                 280                 285

Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala
    290                 295                 300

Val Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln
305                 310                 315                 320

Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys
                325                 330                 335

Thr Arg Ala Ala Leu Gly Val
            340


<210>  954
<211>  343
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  synthetic construct

<400>  954

Asp Glu His His His His His His His His His His Lys Leu Glu Asn
1               5                   10                  15

Leu Tyr Phe Gln Gly Gly Gly Gly Gly Ser Met Gly Ser Trp Ser Glu
            20                  25                  30

Phe Trp Val Arg Leu Gly Ala Ile Arg Glu Arg Leu Asp Ala Leu Gly
        35                  40                  45
```

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```
Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe
    50                  55                  60

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

Lys Leu Arg Tyr Thr Ala Ala Thr Ile Arg Arg Phe Leu Gln Ala Tyr
                85                  90                  95

Arg His Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln
        115                 120                 125

Asp Lys Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala
    130                 135                 140

Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr
145                 150                 155                 160

Leu Gln Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu
                165                 170                 175

Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala
            180                 185                 190

Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu
        195                 200                 205

Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met
    210                 215                 220

Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala
225                 230                 235                 240

Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val
                245                 250                 255

Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys
            260                 265                 270
```

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Gln Ala Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile
275 280 285

Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala
290 295 300

Val Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln
305 310 315 320

Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys
325 330 335

Thr Arg Ala Ala Leu Gly Val
340

<210> 955
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 955

Asp Glu His His His His His His His His His His Lys Leu Glu Asn
1 5 10 15

Leu Tyr Phe Gln Gly Gly Gly Gly Gly Ser Met Gly Ser Trp Ala Glu
20 25 30

Phe Lys Gln Arg Leu Ala Ala Ile Lys Thr Arg Leu Glu Ala Leu Gly
35 40 45

Gly Ser Glu Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe
50 55 60

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

Ala Leu Arg Lys Glu Ala Ala Ala Ile Arg Asp Glu Leu Gln Ala Tyr
85 90 95

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```
Arg His Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110

Gly Ser Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln
        115                 120                 125

Asp Lys Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala
    130                 135                 140

Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr
145                 150                 155                 160

Leu Gln Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu
                165                 170                 175

Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala
            180                 185                 190

Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu
        195                 200                 205

Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met
    210                 215                 220

Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala
225                 230                 235                 240

Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val
                245                 250                 255

Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys
            260                 265                 270

Gln Ala Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile
        275                 280                 285

Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala
    290                 295                 300
```

```
Val Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln
305                 310                 315                 320

Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys
                325                 330                 335

Thr Arg Ala Ala Leu Gly Val
            340
```

<210> 956
<211> 438
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 956

```
Asp Glu Gly Gly Gly Gly Ser Met Gly Ser Trp Asp Glu Phe Gly Arg
1               5                   10                  15

Arg Leu Tyr Ala Ile Glu Trp Gln Leu Tyr Ala Leu Gly Gly Thr Glu
            20                  25                  30

Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu
        35                  40                  45

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

Glu Ile Ala Ala Val Ile Arg Glu Asn Leu Gln Ala Tyr Arg His Asn
65                  70                  75                  80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                85                  90                  95

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
            100                 105                 110

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
        115                 120                 125
```

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```
Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
    130                 135                 140

Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser
145                 150                 155                 160

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
                165                 170                 175

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
            180                 185                 190

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
        195                 200                 205

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
    210                 215                 220

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
225                 230                 235                 240

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
                245                 250                 255

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
            260                 265                 270

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
        275                 280                 285

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
    290                 295                 300

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg
305                 310                 315                 320

Ala Ala Leu Gly Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                325                 330                 335

Gly Gly Gly Ser Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr
            340                 345                 350
```

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```
Ala Ile Glu Trp Gln Leu Tyr Ala Leu Gly Gly Thr Glu Ala Glu Leu
        355                 360                 365

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
    370                 375                 380

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala
385                 390                 395                 400

Ala Val Ile Arg Glu Asn Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
                405                 410                 415

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His His His His
            420                 425                 430

His His His His His His
        435
```

<210> 957
<211> 438
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 957

```
Asp Glu Gly Gly Gly Gly Ser Met Gly Ser Trp Ser Glu Phe Trp Val
1               5                   10                  15

Arg Leu Gly Ala Ile Arg Glu Arg Leu Asp Ala Leu Gly Gly Ser Glu
            20                  25                  30

Ala Glu Leu Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu
        35                  40                  45

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

Tyr Thr Ala Ala Thr Ile Arg Arg Phe Leu Gln Ala Tyr Arg His Asn
65                  70                  75                  80
```

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2018369639

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                85                  90                  95

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
            100                 105                 110

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
        115                 120                 125

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
    130                 135                 140

Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser
145                 150                 155                 160

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
                165                 170                 175

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
            180                 185                 190

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
        195                 200                 205

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
    210                 215                 220

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
225                 230                 235                 240

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
                245                 250                 255

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
            260                 265                 270

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
        275                 280                 285
```

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```
Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
    290                 295                 300

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg
305                 310                 315                 320

Ala Ala Leu Gly Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                325                 330                 335

Gly Gly Gly Ser Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly
            340                 345                 350

Ala Ile Arg Glu Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu
        355                 360                 365

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
    370                 375                 380

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala
385                 390                 395                 400

Ala Thr Ile Arg Arg Phe Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
                405                 410                 415

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His His His His
            420                 425                 430

His His His His His His
        435


<210>  958
<211>  338
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  synthetic construct

<400>  958

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1               5                   10                  15
```

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```
Phe Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Gly Ser Gly
            20                  25                  30

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

Ala Ile Lys Thr Arg Leu Glu Ala Leu Gly Gly Ser Glu Ala Glu Leu
    50                  55                  60

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
65                  70                  75                  80

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Ala Leu Arg Lys Glu Ala
                85                  90                  95

Ala Ala Ile Arg Asp Glu Leu Gln Ala Tyr Arg His Asn Gly Gln Ala
            100                 105                 110

Gly Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
        115                 120                 125

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
    130                 135                 140

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
145                 150                 155                 160

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
                165                 170                 175

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
            180                 185                 190

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
        195                 200                 205

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
    210                 215                 220

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys
225                 230                 235                 240
```

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Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
245 250 255

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
260 265 270

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
275 280 285

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
290 295 300

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
305 310 315 320

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
325 330 335

Pro Arg

<210> 959
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 959

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Gly Ser Gly
20 25 30

Gly Gly Gly Ser Met Gly Ser Trp Asp Glu Phe Gly Arg Arg Leu Tyr
35 40 45

Ala Ile Glu Trp Arg Leu Tyr Ala Leu Gly Gly Ser Glu Ala Glu Leu
50 55 60

```
Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
65                  70                  75                  80

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Lys Leu Arg Glu Ile Ala
                85                  90                  95

Ala Val Ile Arg Ser Asn Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro
        115                 120                 125

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    130                 135                 140

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
145                 150                 155                 160

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                165                 170                 175

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
            180                 185                 190

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        195                 200                 205

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    210                 215                 220

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
225                 230                 235                 240

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                245                 250                 255

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            260                 265                 270
```

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```
Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        275                 280                 285

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    290                 295                 300

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
305                 310                 315                 320

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                325                 330                 335

Met Gln Ala Leu Pro Pro Arg
            340
```

<210> 960
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 960

```
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1               5                   10                  15

Phe Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Gly Ser Gly
            20                  25                  30

Gly Gly Gly Ser Met Gly Ser Trp Ser Glu Phe Trp Val Arg Leu Gly
        35                  40                  45

Ala Ile Arg Glu Arg Leu Asp Ala Leu Gly Gly Ser Glu Ala Glu Leu
    50                  55                  60

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
65                  70                  75                  80

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Lys Leu Arg Tyr Thr Ala
                85                  90                  95
```

```
Ala Thr Ile Arg Arg Phe Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro
        115                 120                 125

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    130                 135                 140

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
145                 150                 155                 160

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                165                 170                 175

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
            180                 185                 190

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        195                 200                 205

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    210                 215                 220

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
225                 230                 235                 240

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                245                 250                 255

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            260                 265                 270

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        275                 280                 285

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    290                 295                 300

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
305                 310                 315                 320
```

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
325 330 335

Met Gln Ala Leu Pro Pro Arg
340

<210> 961
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 961

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Gly Ser Gly
20 25 30

Gly Gly Gly Ser Met Gly Ser Trp Phe Glu Phe Tyr Asp Arg Leu Asn
35 40 45

Ala Ile Asp Ala Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu
50 55 60

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
65 70 75 80

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Asn Leu Arg Val His Ala
85 90 95

Ala Ala Ile Arg Glu Trp Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro
115 120 125

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
130 135 140

```
Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
145                 150                 155                 160

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                165                 170                 175

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
            180                 185                 190

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        195                 200                 205

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    210                 215                 220

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
225                 230                 235                 240

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                245                 250                 255

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            260                 265                 270

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        275                 280                 285

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    290                 295                 300

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
305                 310                 315                 320

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                325                 330                 335

Met Gln Ala Leu Pro Pro Arg
            340
```

<210> 962
<211> 343
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 962

```
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1               5                  10                  15

Phe Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Gly Ser Gly
            20                  25                  30

Gly Gly Gly Ser Met Gly Ser Trp Leu Glu Phe Tyr His Arg Leu Asn
        35                  40                  45

Ala Ile Asp Ser Arg Leu Trp Ala Leu Gly Gly Ser Glu Ala Glu Leu
    50                  55                  60

Ala Ala Phe Glu Lys Glu Ile Ala Ala Phe Glu Ser Glu Leu Gln Ala
65                  70                  75                  80

Tyr Lys Gly Lys Gly Asn Pro Glu Val Glu Ser Leu Arg Asp His Ala
                85                  90                  95

Ala His Ile Arg Glu Trp Leu Gln Ala Tyr Arg His Asn Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro
        115                 120                 125

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    130                 135                 140

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
145                 150                 155                 160

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                165                 170                 175
```

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```
Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
            180                 185                 190

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        195                 200                 205

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    210                 215                 220

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
225                 230                 235                 240

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                245                 250                 255

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            260                 265                 270

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        275                 280                 285

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    290                 295                 300

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
305                 310                 315                 320

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                325                 330                 335

Met Gln Ala Leu Pro Pro Arg
            340
```

<210> 963
<211> 668
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 963

```
Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp
1               5                  10                  15

Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly
            20                  25                  30

Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn
        35                  40                  45

Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly
    50                  55                  60

Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn
65                  70                  75                  80

Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly
                85                  90                  95

Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg
            100                 105                 110

Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu
        115                 120                 125

Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu
    130                 135                 140

Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu
145                 150                 155                 160

Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile
                165                 170                 175

Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser
            180                 185                 190

His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys
        195                 200                 205

Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His Thr Pro Lys
    210                 215                 220
```

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```
Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg Glu Gly Asp
225                 230                 235                 240

Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro Glu Tyr Thr
                245                 250                 255

Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys Gln Asn Thr
            260                 265                 270

Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser Gly Lys Tyr
        275                 280                 285

Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser Glu Glu Val
    290                 295                 300

Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val Gln Ile Leu
305                 310                 315                 320

His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu Cys Met Ser
                325                 330                 335

Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His Asn Gly Lys
            340                 345                 350

Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro Lys Ile Leu
        355                 360                 365

Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn Ile Leu Gly
    370                 375                 380

Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln Tyr Pro Pro
385                 390                 395                 400

Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly
                405                 410                 415

Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val
            420                 425                 430
```

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```
Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu
        435                 440                 445

Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala
    450                 455                 460

Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu
465                 470                 475                 480

Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro
                485                 490                 495

Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe
            500                 505                 510

Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly
        515                 520                 525

Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro
    530                 535                 540

Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln
545                 550                 555                 560

Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg
                565                 570                 575

Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser
            580                 585                 590

Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr
        595                 600                 605

Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys
    610                 615                 620

Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys
625                 630                 635                 640

Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu
                645                 650                 655
```

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Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg
660 665

<210> 964
<211> 22
<212> PRT
<213> Homo sapiens

<400> 964

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp Gln
1 5 10 15

Leu Thr Gly Ser Ala Ala
20

<210> 965
<211> 204
<212> PRT
<213> Homo sapiens

<400> 965

Ser Gly Pro Val Lys Glu Leu Val Gly Ser Val Gly Gly Ala Val Thr
1 5 10 15

Phe Pro Leu Lys Ser Lys Val Lys Gln Val Asp Ser Ile Val Trp Thr
20 25 30

Phe Asn Thr Thr Pro Leu Val Thr Ile Gln Pro Glu Gly Gly Thr Ile
35 40 45

Ile Val Thr Gln Asn Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly
50 55 60

Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile
65 70 75 80

Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln
85 90 95

Glu Tyr Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr
100 105 110

```
Met Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
        115                 120                 125

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys Ala
    130                 135                 140

Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu Pro Ile
145                 150                 155                 160

Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys Val Ala Arg
                165                 170                 175

Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu Ala Arg Lys Leu
            180                 185                 190

Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser Met
        195                 200
```

<210> 966
<211> 335
<212> PRT
<213> Homo sapiens

<400> 966

```
Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp Gln
1               5                   10                  15

Leu Thr Gly Ser Ala Ala Ser Gly Pro Val Lys Glu Leu Val Gly Ser
            20                  25                  30

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

Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu Val Thr Ile Gln
    50                  55                  60

Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn Arg Asn Arg Glu Arg
65                  70                  75                  80

Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys
```

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```
                85                  90                  95

Lys Asn Asp Ser Gly Ile Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu
            100                 105                 110

Gln Gln Pro Ser Thr Gln Glu Tyr Val Leu His Val Tyr Glu His Leu
        115                 120                 125

Ser Lys Pro Lys Val Thr Met Gly Leu Gln Ser Asn Lys Asn Gly Thr
    130                 135                 140

Cys Val Thr Asn Leu Thr Cys Cys Met Glu His Gly Glu Glu Asp Val
145                 150                 155                 160

Ile Tyr Thr Trp Lys Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn
                165                 170                 175

Gly Ser Ile Leu Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr
            180                 185                 190

Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro
        195                 200                 205

Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser
    210                 215                 220

Ser Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu
225                 230                 235                 240

Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu
                245                 250                 255

Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro
            260                 265                 270

Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro
        275                 280                 285

His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr
    290                 295                 300
```

Ser Thr Val Glu Ile Pro Lys Lys Met Glu Asn Pro His Ser Leu Leu
305 310 315 320

Thr Met Pro Asp Thr Pro Arg Leu Phe Ala Tyr Glu Asn Val Ile
325 330 335

<210> 967
<211> 630
<212> PRT
<213> Homo sapiens

<400> 967

Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser
1 5 10 15

Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln
20 25 30

Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser
35 40 45

Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile
50 55 60

Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val
65 70 75 80

Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp
85 90 95

Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro
100 105 110

Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
115 120 125

Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr
130 135 140

Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr
145 150 155 160

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```
Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met
                165                 170                 175

Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser
            180                 185                 190

Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro
        195                 200                 205

Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly
    210                 215                 220

Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly
225                 230                 235                 240

Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr
                245                 250                 255

Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser
            260                 265                 270

Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser
        275                 280                 285

Cys Thr Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp
    290                 295                 300

Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys
305                 310                 315                 320

Tyr Gly Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser
                325                 330                 335

Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu
            340                 345                 350

Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala
        355                 360                 365
```

```
Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile
    370                 375                 380

Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu
385                 390                 395                 400

Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn
                405                 410                 415

Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly
            420                 425                 430

Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His
        435                 440                 445

Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe
    450                 455                 460

Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp
465                 470                 475                 480

Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly
                485                 490                 495

His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe
            500                 505                 510

Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu
        515                 520                 525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
    530                 535                 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545                 550                 555                 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
                565                 570                 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
            580                 585                 590
```

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
595 600 605

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln
610 615 620

Arg Ala Ser Pro Leu Thr
625 630

<210> 968
<211> 229
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 968

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
1 5 10 15

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
20 25 30

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
35 40 45

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

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
65 70 75 80

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
85 90 95

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
100 105 110

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
115 120 125

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Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
130 135 140

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
145 150 155 160

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
165 170 175

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
180 185 190

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
195 200 205

Glu Val Cys Phe Ala Glu Glu Gly Pro Lys Leu Ile Ser Lys Thr Arg
210 215 220

Ala Ala Leu Gly Val
225

<210> 969
<211> 204
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 969

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

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

Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys
35 40 45

Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu
50 55 60

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```
Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys
65                  70                  75                  80

Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys
                85                  90                  95

Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val
            100                 105                 110

Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe
        115                 120                 125

His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Thr Met Lys
    130                 135                 140

Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu
145                 150                 155                 160

Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys
                165                 170                 175

Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln
            180                 185                 190

Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly Val
        195                 200


<210>  970
<211>  204
<212>  PRT
<213>  ARTIFICIAL SEQUENCE

<220>
<223>  synthetic construct

<400>  970

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

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

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Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys
35 40 45

Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu
50 55 60

Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys
65 70 75 80

Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys
85 90 95

Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val
100 105 110

Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe
115 120 125

His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Thr Met Lys
130 135 140

Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu
145 150 155 160

Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys
165 170 175

Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Pro
180 185 190

Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly Val
195 200

<210> 971
<211> 207
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

24 Oct 2022
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<400> 971

Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu
1 5 10 15

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

Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile
35 40 45

Thr Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu
50 55 60

Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly
65 70 75 80

His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly
85 90 95

Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser
100 105 110

Leu Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys
115 120 125

Phe Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln
130 135 140

Thr Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln
145 150 155 160

Ile Thr Glu Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser Gly Leu
165 170 175

Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu
180 185 190

Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly Val
195 200 205

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<210> 972
<211> 207
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 972

```
Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu
1               5                  10                  15

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

Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile
        35                  40                  45

Thr Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu
    50                  55                  60

Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly
65                  70                  75                  80

His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly
                85                  90                  95

Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser
            100                 105                 110

Leu Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys
        115                 120                 125

Phe Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln
    130                 135                 140

Thr Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln
145                 150                 155                 160

Ile Thr Glu Glu Gln Leu Glu Ala Val Ile Ala Asp Phe Ser Gly Leu
                165                 170                 175
```

Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu
180 185 190

Glu Gly Pro Lys Leu Ile Ser Lys Thr Arg Ala Ala Leu Gly Val
195 200 205

<210> 973
<211> 213
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 973

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
1 5 10 15

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
20 25 30

Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser
35 40 45

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
50 55 60

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
65 70 75 80

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
85 90 95

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
100 105 110

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
115 120 125

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
130 135 140

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```
Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
145                 150                 155                 160

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
                165                 170                 175

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
            180                 185                 190

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Arg
        195                 200                 205

Ala Ala Leu Gly Val
    210
```

<210> 974
<211> 213
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 974

```
Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
1               5                   10                  15

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
            20                  25                  30

Asn Ala Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser
        35                  40                  45

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
    50                  55                  60

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
65                  70                  75                  80

Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
                85                  90                  95
```

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Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
100 105 110

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
115 120 125

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
130 135 140

Gln Gly Val Ala Leu Gln Thr Met Lys Gln Glu Phe Leu Ile Asn Leu
145 150 155 160

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Val Ile
165 170 175

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
180 185 190

Glu Val Cys Phe Ala Glu Glu Gly Pro Lys Leu Ile Ser Lys Thr Arg
195 200 205

Ala Ala Leu Gly Val
210

<210> 975
<211> 5
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

<400> 975

Gly Gly Gly Gly Gly
1 5

<210> 976
<211> 8
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> synthetic construct

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<400> 976

Gly Gly Gly Gly Gly Gly Gly Gly
1 5