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(54) Title: BISPECIFIC T CELL ENGAGERS

Scfv-Fc x Fab-Fc molecules

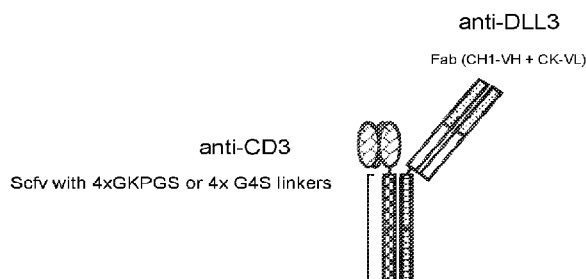


FIG. 1A

(57) **Abstract:** Provided are bispecific T Cell Engagers. More specifically, the invention is directed to bispecific molecules that bind to DLL3, MUC17 or CLD18 and activate CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137). Also provided are methods of treating an ailment such as cancer using an antibody (or fragment) against DLL3, MUC17 or CLD18 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 and/or CD137.



Bispecific T cell Engagers

RELATED APPLICATIONS

[0001] This application claims priority to U.S. provisional patent application serial number 62/968,999 filed on January 31, 2020, U.S. provisional patent application serial number 62/981,048 filed on February 25, 2020 and U.S. provisional patent application serial number 62/991,070 filed on March 17, 2020. The contents of the aforementioned applications are incorporated herein by reference.

REFERENCE TO SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 1, 2021, is named GB1-002US_SL.txt and is 979,504 bytes in size.

FIELD OF INVENTION

[0003] This invention relates generally to cancer therapies, and more specifically, to novel compounds comprising anti-DLL3, CLDN18.2 and Muc17 antibodies or immunoreactive fragments thereof for the treatment of cancer.

BACKGROUND

[0004] Cancer is generally defined as a group of diseases involving abnormal cell growth with the potential to invade or spread to other parts of the body. In 2019, roughly 1.8 million people were diagnosed with cancer in the United States. Each year, an estimated 606,880 people will die from cancer in the United States. Lung and bronchus cancer is responsible for the most deaths. Colorectal cancer and pancreatic cancer are the second and third most common causes of cancer death respectively.

[0005] Cancer has been linked to several factors including smoking, obesity, poor diet, lack of physical activity and excessive consumption of alcohol. Other factors include certain infections, exposure to ionizing radiation and environmental pollutants. Certain cancers have been linked to infections such as *Helicobacter pylori*, hepatitis B, hepatitis C, human papillomavirus infection, Epstein–Barr virus and human immunodeficiency virus (HIV).

[0006] Conventional cancer treatments are directed at removing cancerous tissue and preventing it from spreading. Such treatment options include surgery, chemotherapy,

radiation therapy, hormonal therapy, targeted therapy and palliative care. Treatments are usually pursued based on the type, location and grade of the cancer as well as the patient's health and preferences. These options have limitations. They can be ineffective, particularly when cancer has metastasized. Moreover, chemotherapy and radiation therapy have a range of side-effects related to cell toxicity.

[0007] Because cancer cells divide faster than most normal cells, they can be sensitive to chemotherapy drugs. However, chemotherapy drugs will also attack other cells in the body, especially fast-dividing cells such as blood cells and the cells lining the mouth, stomach, and intestines. Accordingly, there is a need for improved medications and methods of treating cancer that are more targeted and have less deleterious side effects.

[0008] A promising area for the development of treatments includes targeted therapies using antibodies. For example, the use of antibody drug conjugates can be used to target a drug toward a tumor. Immunoconjugates are antibodies conjugated (joined) to a second molecule, usually a toxin, radioisotope or label. Immunoconjugates can provide for relatively high concentrations of drug within the tumor whereas systemic administration of unconjugated (i.e., untargeted) drug to achieve the same tumor concentration can lead to levels that are toxic to normal cells.

[0009] Another promising area is development of treatments that harness the immune system to attack and kill tumor cells. Checkpoint inhibitors, such as anti-CTLA4, anti-PD1 and anti-PDL1 therapies have changed the way cancer is treated. Similarly, the direct activation of cytotoxic T cells by bispecific T cell engagers or CAR-T engineered T cells, has led to previously unseen cures in many types of cancers.

[0010] Delta-like ligand 3 (DLL3) is an inhibitory notch ligand that is expressed at relatively low levels in normal tissues. It is expressed at high levels in small cell lung cancer (SCLC) and other neuroendocrine tumors, thus presenting potential therapeutic target in cancer diagnosis and treatment.

[0011] Mucin 17, also referred to as MUC17, is a member of the mucin family that is composed of more than 20 members. Mucins are large, highly glycosylated membrane bound proteins. They generally function in mucosal areas to protect epithelial cells from their environment, as well as to regulate proliferation and survival of cells. MUC17 is expressed in pancreatic, appendiceal, and some colon cancers and thus is a target antigen for these cancers. Thus, MUC17 is a candidate for targeting of therapies such as antibody

drug conjugates, T cell engagers, and CAR-T cells.

[0012] Claudin-18 (CLDN18) is a protein in humans that is encoded by the CLDN18 gene. It belongs to the group of claudins, a family of proteins that form components of tight cell junction strands in epithelial cells. Studies have demonstrated that Isoform 2 (Claudin 18.2 or CLDN18.2) is abundant in gastric tumors. It has exposed extracellular loops and is available for monoclonal antibody binding. These biological characteristics have led to the development of monoclonal antibodies against claudin 18.2, such as claudiximab (IMAB362).

[0013] CD3, CD28 and CD137 are receptors present on T-cells. T cells can be activated through CD3, CD28 and CD137, by antigen-presenting cells that utilize the activation signals MHC Class I and II, CD80 and CD86, and 4-1BBL, respectively. CD3 is part of the T cell receptor (TCR) and is the signaling component for the receptor. There are three CD3 subunits, epsilon, delta and gamma. Epsilon associates with both delta and zeta and together they are responsible for signaling. CD3 signaling is considered signal 1 that is required to activate T cells. The co-receptors, CD28 and CD137, are considered signal 2. Both signal 1 and signal 2 are required for full activation, proliferation and survival of T cells.

[0014] The present invention discloses bispecific T Cell Engagers. The bispecific molecules can bind to DLL3, MUC17 and/or CLDN18.2 and activate CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137). Also provided are methods of treating an ailment such as cancer using antibodies and antibody conjugates, pharmaceutical compositions thereof, and articles of manufacture.

SUMMARY

[0015] The inventions described and claimed herein have many attributes and embodiments including, but not limited to, those set forth or described or referenced in this brief summary. The inventions described and claimed herein are not limited to, or by, the features or embodiments identified in this summary, which is included for purposes of illustration only and not restriction.

[0016] An aspect of the invention is an antibody against DLL3. The antibody can be a fragment such as an antigen binding fragment (Fab) or a single chain variable fragment (Scfv).

[0017] An aspect of the invention is an agonist antibody that activates CD3, CD28

and/or CD137.

[0018] An aspect of the invention is a bispecific molecule that includes an antibody (or fragment) against DLL3 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0019] An aspect of the invention is a method of treating an ailment such as cancer using an antibody (or fragment) against DLL3 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0020] An aspect of the invention is a method of treating an ailment that uses two or more of the bispecific molecules described herein in combination with one another.

[0021] An aspect on the invention is a method of activating T-cell cytotoxicity against DLL3 expressing cells.

[0022] An aspect of the invention is a method of activating T-cell cytotoxicity using a bispecific molecule the includes an antibody (or fragment) against DLL3 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0023] An aspect of the invention is a humanized antibody which binds to human DLL3 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 56 – 74 or 75.

[0024] The disclosed methods can utilize any DLL3 antibody, including for example, an anti-DLL3 antibody comprising three CDRs of a heavy chain variable region amino acid sequence of SEQ ID NO: 1 – 27 or 29.

[0025] An aspect of the invention is a humanized antibody which binds to human DLL3 protein comprising a light chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 76 – 90 or 91.

[0026] The disclosed methods can utilize any DLL3 antibody, including for example, an anti-DLL3 antibody comprising three CDRs of a light chain variable region amino acid sequence of SEQ ID NO: 32 – 54 or 55.

[0027] An aspect of the invention is an antibody against MUC17. The antibody can be

a fragment such as an antigen binding fragment (Fab) or a single chain variable fragment (Scfv).

[0028] An aspect of the invention is an agonist antibody that activates CD3, CD28 and/or CD137.

[0029] An aspect of the invention is a bispecific molecule that includes an antibody (or fragment) against MUC17 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0030] An aspect of the invention is a method of treating an ailment such as cancer using an antibody (or fragment) against MUC17 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0031] An aspect of the invention is a method of treating an ailment that uses two or more of the bispecific molecules described herein in combination with one another.

[0032] An aspect on the invention is a method of activating T-cell cytotoxicity against MUC17 expressing cells.

[0033] An aspect of the invention is a method of activating T-cell cytotoxicity using a bispecific molecule the includes an antibody (or fragment) against MUC17 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0034] An aspect of the invention is a humanized antibody which binds to human MUC17 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 127 – 245 or 246.

[0035] The disclosed methods can utilize any MUC17 antibody, including for example, an anti-MUC17 antibody comprising three CDRs of a heavy chain variable region amino acid sequence of SEQ ID NO: 92 – 111 or 112.

[0036] The disclosed methods can utilize any MUC17 antibody, including for example, an anti-MUC17 antibody comprising three CDRs of a light chain variable region amino acid sequence of SEQ ID NO: 113 – 125 or 126.

[0037] An aspect of the invention is a humanized antibody which binds to human MUC17 protein comprising a light chain variable domain having at least 95%, at least 96%,

at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 147 – 168 or 169.

[0038] The disclosed methods can utilize any MUC17 antibody, including for example, an anti-MUC17 antibody comprising three CDRs of a heavy chain variable region amino acid sequence of SEQ ID NO: 92 – 111 or 112.

[0039] The disclosed methods can utilize any MUC17 antibody, including for example, an anti-MUC17 antibody comprising three CDRs of a light chain variable region amino acid sequence of SEQ ID NO: 113 – 125 or 126.

[0040] An aspect of the invention is a method of treating an ailment such as cancer using an antibody (or fragment) against CLDN18.2 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0041] An aspect on the invention is a method of activating T-cell cytotoxicity against CLDN18.2 expressing cells.

[0042] An aspect of the invention is a method of activating T-cell cytotoxicity using a bispecific molecule the includes an antibody (or fragment) against CLDN18.2 paired with an antibody (or fragment) of an agonist antibody that activates CD3, CD28 or CD137.

[0043] The disclosed methods can utilize any CLDN18.2 antibody, including for example, an anti-CLDN18.2 antibody comprising three CDRs of a heavy chain variable region amino acid sequence of SEQ ID NO: 170 – 186 or 187.

[0044] An aspect of the invention is a humanized antibody which binds to human CLDN18.2 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 197 – 205 or 206.

[0045] The disclosed methods can utilize any CLDN18.2 antibody, including for example, an anti-CLDN18.2 antibody comprising three CDRs of a light chain variable region amino acid sequence of SEQ ID NO: 188 – 195 or 196.

[0046] An aspect of the invention is a humanized antibody which binds to human CLDN18.2 protein comprising a light chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 207 – 212 or 213.

[0047] The disclosed methods can utilize any CLDN18.2 antibody, including for example, an anti-CLDN18.2 antibody comprising three CDRs of a heavy chain variable region amino acid sequence of SEQ ID NO: 170 – 186 or 187.

[0048] The disclosed methods can utilize any CLDN18.2 antibody, including for example, an anti-CLDN18.2 antibody comprising three CDRs of a light chain variable region amino acid sequence of SEQ ID NO: 188 – 195 or 196.

[0049] In some embodiments, the targeting domains are linked to one another by peptide bonds via peptide linkers or through covalent conjugates using appropriate crosslinking technologies known in the art.

[0050] In some embodiments, the targeting domains comprise antibody variable regions. In some embodiments, the targeting domains are in the form of a single domain antibody (sdAb), a fragment variable (Fv) heterodimer, a single chain Fv (scFv), a Fab fragment, a TriFab, or a combination thereof.

[0051] In some embodiments, the bispecific molecules are administered with a checkpoint inhibitor.

[0052] In some embodiments, the bispecific molecules are administered with an anti-PD1 and/or anti-PDL1 antagonists.

[0053] Other features and advantages of aspects of the present invention will become apparent from the following more detailed description, taken in conjunction with the accompanying drawings, which illustrate, by way of example, the principles of aspects of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0054] The accompanying drawings illustrate aspects of the present invention. In such drawings:

[0055] FIG. 1A to 1F depict Scfv-Fc x Fab-Fc formats for the bispecific molecules of the invention.

[0056] FIG. 1A depicts an anti-CD3, anti-DLL3 (Scfv-Fc x Fab-Fc) molecule

- [0057]** FIG. 1B depicts an anti-CD28, anti-DLL3 (Scfv-Fc x Fab-Fc) molecule
- [0058]** FIG. 1C depicts an anti-DLL3, anti-CD3 (Scfv-Fc x Fab-Fc) molecule
- [0059]** FIG. 1D depicts an anti-DLL3, anti-CD28 (Scfv-Fc x Fab-Fc) molecule
- [0060]** FIG. 1E depicts an anti-CD137, anti-DLL3 (Scfv-Fc x Fab-Fc) molecule
- [0061]** FIG. 1F depicts an anti-DLL3, anti-CD137 (Scfv-Fc x Fab-Fc) molecule
- [0062]** FIG. 2A to 2C depict several scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention.
- [0063]** FIG. 2A depicts an anti-DLL3, anti-CD3 (scfv-scfv-Fc x Fc) molecule.
- [0064]** FIG. 2B depicts an anti-DLL3, anti-CD28 (scfv-scfv-Fc x Fc) molecule
- [0065]** FIG. 2C depicts an anti-DLL3, anti-CD137 (scfv-scfv-Fc x Fc) molecule
- [0066]** FIG. 2D to 2F depict several scfv-scfv-Fc x Fab-Fc formats for the bispecific molecules of the invention.
- [0067]** FIG. 2D depicts an anti-DLL3, anti-CD3, anti-DLL3 (scfv-scfv-Fc x Fab-Fc) molecule.
- [0068]** FIG. 2E depicts an anti-DLL3, anti-CD28, anti-DLL3 (scfv-scfv-Fc x Fab-Fc) molecule.
- [0069]** FIG. 2F depicts an anti-DLL3, anti-CD137, anti-DLL3 (scfv-scfv-Fc x Fab-Fc) molecule.
- [0070]** FIG. 3A is a graph that demonstrates the binding of anti-DLL3 antibodies to human DLL3 expressing CHO cells.
- [0071]** FIG. 3B is a graph of that demonstrates the binding of anti-DLL3 antibodies to CHO cells expressing cynomolgus DLL3.
- [0072]** FIG. 4 is a graph of that demonstrates the binding of anti-DLL3 scfv-Fc to human DLL3 expressing CHO cells.
- [0073]** FIG. 5 is a graph showing DLL3Fab-Fc x CD3scfv-Fc mediated killing of huDLL3 expressing CHO cells by human T cells

[0074] FIG. 6 is a graph showing DLL3Fab-Fc x CD3scfv-Fc mediated activation of human T-cells in the presence of huDLL3 expressing CHO cells.

[0075] FIG. 7 is a graph showing DLL3scfv-CD3scfv-Fc x Fc killing of huDLL3 expressing CHO cells by human T cells.

[0076] FIG. 8 is a graph showing DLL3scfv-CD3scfv-Fc x Fc mediated activation of human T-cells in the presence of huDLL3 expressing CHO cells.

[0077] FIG. 9A – 9C are graphs showing DLL3Fab-Fc x DLL3scfv-CD3scfv-Fc mediated killing of huDLL3 expressing NCI-H82 cells by human T cells.

[0078] FIG. 10A and 10B are graphs showing Anti-CD3 variants of DLL3Fab-Fc x CD3scfv-Fc and DLL3scfv-CD3scfv-Fc formatted molecules mediating the killing of huDLL3 expressing NCI-H82 cells by human T cells.

[0079] FIG. 11A – 11F are graphs showing DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc.

[0080] FIG. 12 is a chart of HPLC-size exclusion chromatography analysis of HEK293 transiently expressed and Protein A purified bispecifics using various CD3 variants.

[0081] FIG 13 is a graph showing the killing of NC1-H82 tumor cells of peripheral blood mononuclear cells (PBMCs) with variants of 3D22I.

[0082] FIG 14 is a graph showing the expression of CD25 by PBMCs when stimulated with variants of 3D22I in the presence of NC1-H82 tumor cells.

[0083] FIG 15 is a graph showing DLL3 scfv x CD3scfv x DLL3 Fab variant 3D45I more potently stimulates killing of NCI-H82 cells by PBMCs than 3D39I.

[0084] FIG 16 is a graph showing DLL3 scfv x CD3scfv x DLL3 Fab variant 3D45I more potently stimulates expression of CD25 by PBMCs in the presence of NCI-H82 cells than 3D39I.

[0085] FIG 17 is a graph showing CD28scfv-Fc x DLL3Fab-Fc bispecific molecules in combination with 50M of CD3-DLL3 benchmark, 3DBM, activate T-cells to secrete IL-2 better than 3DBM alone.

[0086] FIG 18 is a graph showing CD28scfv-Fc (C50S) x DLL3-Fab-Fc variants 28D13 and 28D15, with the free cysteine in the anti-CD28 molecule engineered out, induce IL-2 secretion by PBMCs similarly to the parental molecule, 28D10, when combined with 50pM benchmark, 3DBM in the presence of NCI-H82 cells.

[0087] FIG 19A is a graph showing Urelumab increases IFN γ secretion when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule.

[0088] FIG 19B is a graph showing 4-1BB Fab-Fc x DLL3scfv-Fc bispecific 4D3 increases IFN γ secretion when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule.

[0089] FIG. 20A depicts an anti-CD137, anti-DLL3 Fab molecule.

[0090] FIG. 21A to 21F depict Scfv-Fc x Fab-Fc formats for the bispecific molecules of the invention. FIG. 21A depicts an anti-CD3, anti-MUC17 (Scfv-Fc x Fab-Fc) molecule

[0091] FIG. 21B depicts an anti-CD28, anti-MUC17 (Scfv-Fc x Fab-Fc) molecule

[0092] FIG. 21C depicts an anti-MUC17, anti-CD3 (Scfv-Fc x Fab-Fc) molecule

[0093] FIG. 21D depicts an anti-MUC17, anti-CD28 (Scfv-Fc x Fab-Fc) molecule

[0094] FIG. 21E depicts an anti-CD137, anti-MUC17 (Scfv-Fc x Fab-Fc) molecule

[0095] FIG. 21F depicts an anti-MUC17, anti-CD137 (Scfv-Fc x Fab-Fc) molecule

[0096] FIG. 22A to 22F depict several scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. FIG. 22A depicts an anti-MUC17, anti-CD3 (scfv-scfv-Fc x Fc) molecule.

[0097] FIG. 22B depicts an anti-MUC17, anti-CD28 (scfv-scfv-Fc x Fc) molecule.

[0098] FIG. 22C depicts an anti-MUC17, anti-CD137 (scfv-scfv-Fc x Fc) molecule.

[0099] FIG. 22D depicts an anti-MUC17, anti-CD3, anti-MUC17 (scfv-scfv-Fc x Fab-Fc) molecule.

[00100] FIG. 22E depicts an anti-MUC17, anti-CD28, anti-MUC17 (scfv-scfv-Fc x Fab-Fc) molecule.

[00101] FIG. 22F depicts an anti-MUC17, anti-CD137, anti-MUC17 (scfv-scfv-Fc x Fab-Fc) molecule.

[00102] FIG. 23 is a graph that demonstrates MUC17xCD3 Bispecifics bind CHOK1 cells expressing MUC17.

[00103] FIG. 24 is a graph that demonstrates MUC17xCD3 Bispecifics bind to ASPC1 tumor cells.

[00104] FIG. 25 is a graph showing MUC17xCD3 Bispecific molecules activate human PBMC T cells to kill MUC17 expressing CHO cells.

[00105] FIG. 26A is a graph showing MUC17xCD3 Bispecifics of various formats of antibody 1MU32A activating PBMC T cells to kill of ASPC1 cells.

[00106] FIG. 26B is a graph showing MUC17xCD3 Bispecifics of various formats of antibody 1MU32A increase the levels of the T cell activation marker CD25 in the presence of ASPC1 cells.

[00107] FIG. 26C – 26F depict the bispecific molecules 3M46C, 3M64C, 3M62C and 3M66C.

[00108] FIG. 27A is a graph showing MUC17xCD3 Bispecifics of various formats of antibody 1MU11A activating PBMC T cells to kill of ASPC1 cells

[00109] FIG. 27B is a graph showing MUC17xCD3 Bispecifics of various formats of antibody 1MU11A increase the levels of the T cell activation marker CD25 in the presence of ASPC1 cells.

[00110] FIG. 27C – 27F depict the bispecific molecules 3M55C, 3M63C, 3M61C and 3M65C.

[00111] FIG. 28A is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3, in combination with 10pM of MUC17xCD3 Bispecific molecule 3M62C activate T-cells to secrete IL-2 in the presence of ASPC1 cells.

[00112] FIG. 28B is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3, in combination with 10pM of MUC17xCD3 Bispecific molecule 3M62C activate T-cells to express CD25 in the presence of ASPC1 cells.

[00113] FIG. 28C – 28F depict the bispecific molecules 28M1, 28M2, 28M3 and 3M62C.

[00114] FIG. 29A is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3, in combination with 20pM of MUC17xCD3 Bispecific molecule 3M55C activate T-cells to secrete IL-2 in the presence of ASPC1 cells.

[00115] FIG. 29B is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3, in combination with 20pM of MUC17xCD3 Bispecific molecule 3M55C activate T-cells to express CD25 in the presence of ASPC1 cells.

[00116] FIG. 29C – 29F depict the bispecific molecules 28M1, 28M2, 28M3 and 3M55C.

[00117] FIG. 30A is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3 alone do not activate T-cells to secrete IL-2 in the presence of ASPC1 cells.

[00118] FIG. 30B is a graph showing CD28xMuc17 Bispecific molecules, 28M1, 28M2, and 28M3 alone do not activate T-cells to express CD25 in the presence of ASPC1 cells.

[00119] FIG. 31 is a graph showing Bioactivity of multiple CD3 variants: PBMC killing of ASPC1 cells expressing Muc17.

[00120] FIG. 32 is a graph showing hu1MU11A and hu1MU32A retain Muc17 binding activity in the Scfv format.

[00121] FIG. 33 is a graph showing CD137 Fab x Muc17 scfv bispecific molecules 4M1 increases IFN γ secretion by PBMC when combined with 2pM 3M8B7 benchmark and in the presence of ASPC1 cells.

[00122] FIG. 34 is a graph showing CD137 Fab x Muc17 scfv bispecific molecules 4M2 increase IFN γ secretion by PBMC when combined with 2pM 3M8B7 benchmark and in the presence of ASPC1 cells.

[00123] FIG. 35 is a graph showing Muc17xCD137 bispecific 4M2 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of CHO cells expressing Muc17.

[00124] FIG. 36 is a graph showing Muc17xCD137 bispecific 4M7 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of

CHO cells expressing Muc17.

[00125] FIG. 37 is a graph showing Muc17xCD137 bispecific 4M8 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of CHO cells expressing Muc17.

[00126] FIG. 38A and 38B depict Muc17xCD137 and DLL3xCD137 molecules.

[00127] FIG. 39A to 39E depict Muc17x CD137 formats for the bispecific molecules of the invention.

[00128] FIG. 40A to 40D depict several scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. FIG. 40A depicts an anti-CLDN18.2, anti-CD3 (scfv-scfv-Fc x Fc) molecule.

[00129] FIG. 40B depicts an anti-CLDN18.2, anti-CD28 (scfv-scfv-Fc x Fc) molecule

[00130] FIG. 40C depicts an anti-CD3, anti-CLDN18.2 (scfv-scfv-Fc x Fc) molecule.

[00131] FIG. 40D depicts an anti-CD28, anti-CLDN18.2 (scfv-scfv-Fc x Fc) molecule.

[00132] FIG. 41A to 41F depict several scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. FIG. 41A depicts an anti-CLDN18.2, anti-CD3 (scfv-scfv-Fc x Fc) molecule.

[00133] FIG. 41B depicts an anti-CLDN18.2, anti-CD28 (scfv-scfv-Fc x Fc) molecule.

[00134] FIG. 41C depicts an anti-CLDN18.2, anti-CD137 (scfv-scfv-Fc x Fc) molecule.

[00135] FIG. 41D depicts an anti-CLDN18.2, anti-CD3 (scfv-scfv-Fc x Fc) molecule.

[00136] FIG. 41E depicts an anti-CLDN18.2, anti-CD28 (scfv-scfv-Fc x Fc) molecule.

[00137] FIG. 41F depicts an anti-CLDN18.2, anti-CD137 (scfv-scfv-Fc x Fc) molecule.

[00138] FIG. 42 is a graph that demonstrates CLDN18.2xCD3 Bispecifics bind to CHO cells expressing huCLND18.2.

[00139] FIG. 43A is a graph showing T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules in the presence of CLDN18.2 expressing CHO cells.

[00140] FIG. 43B is a graph showing the killing of CHO cells expressing huCLDN18.2 by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules.

[00141] FIG. 44A is a graph showing T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules in the presence of CLDN18.2 expressing SNU-601 tumor cells.

[00142] FIG. 44B is a graph showing the killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules.

[00143] FIG. 45A is a graph showing T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules in the presence of CLDN18.2 expressing SNU-601 tumor cells.

[00144] FIG. 45B is a graph showing the killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules.

[00145] FIG. 46A is a graph showing T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules in the presence of CLDN18.2 expressing SNU-601 tumor cells.

[00146] FIG. 46B is a graph showing the killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules with CD3 variant molecules.

[00147] FIG. 47 is a graph showing CD3xCLDN18.2 binding to LDN18.2-CHO cells.

[00148] FIG. 48A and 48B are graphs showing that all four CD28xCLDN18.2 T-cell engagers in combination with 10pM 3C18C potentially activates PBMCs in the presence of SNU-601 cells.

[00149] FIG. 49A and 49B are graphs showing that all four CD28xCLDN18.2 T-cell engagers in combination with 10pM 3C22C potentially activate PBMCs in the presence of SNU-601 cells.

[00150] FIG. 50A and 50B are graphs showing that all four CD28xCLDN18.2 T-cell engagers in combination with 20pM 3C22C potentially activate PBMCs in the presence of SNU-601 cells.

[00151] FIG. 51A and 51B are graphs showing that all four CD28xCLDN18.2 T-cell engagers in combination with 2pM 3C27C potentially activates PBMCs in the presence of

SNU-601 cells.

[00152] FIG. 52A and 52B are graphs showing that the four CD28xCLDN18.2 T-cell engagers alone do not activate PBMCs.

[00153] FIG. 53A and 53B are graphs showing that the four CD3xCLDN18.2 T-cell engagers alone activate PBMCs to express CD25 but secrete IL-2 to a much lower extent.

[00154] FIG. 54 is a graph showing CD3xCLDN18.2 bispecific 3C22C stimulates PBMC mediated killing of GSU cells more potently than 3 lots of the benchmark, 3CBM.

[00155] FIG. 55 is a graph showing CD3xCLDN18.2 bispecific 3C22C stimulates PBMC to express CD25 in the presence of GSU cells more potently than 3 lots of the benchmark, 3CBM.

[00156] FIG. 56 is a graph showing 3C27I is more potent at killing SNU-601 cells than 3C18I, 3C22I, or 3C26I.

[00157] FIG. 57 is a graph showing CD28xCLDN18.2 T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCCLDN18.2 bispecific, 3C18C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells.

[00158] FIG. 58 is a graph showing CD28xCLDN18.2 T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 bispecific, 3C22C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells.

[00159] FIG. 59 is a graph showing CD28xCLDN18.2 T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 Bispecific, 3C26C, activate PBMCs to produce IL-2 when co-cultured with SNU-601.

[00160] FIG. 60 is a graph showing CD28xCLDN18.2 T cell engagers, 28C1, 28C2, 28C3, and 28C4 alone do not activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells.

[00161] FIG. 61 is a graph showing CLDN18.2xCD28 bispecific molecules 28C7 and 28C10 in combination with 5pM of the CD3 bispecific 3C22I activates T-cells to secrete IL-2.

[00162] FIG. 62 is a graph showing CLDN18.2 x CD28 bispecific molecules 28C5, 28C6, 28C7 and 28C8 induced IL-2 secretion by PBMCs when in the presence of CHO

cells expressing CLDN18.2 but not with parental CHO cells.

[00163] FIG. 63 is a graph showing CD137 x CLDN18.2 bispecific molecules 4C1 and 4C2 in combination with 10pM of the CD3 bispecific 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells.

[00164] FIG. 64 is a graph showing CD137 x CLDN 18.2 bispecific molecules 4C1 and 4C2 in combination with 10pM of the CD3 bispecific 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells.

[00165] FIG. 65 and 66 are graphs showing CD137x CLDN 18.2 bispecific molecules 4C5 and 4C6 in combination with 3C22I activate T-cells to secrete IFNg.

[00166] FIG. 67 is a graph showing CD137x CLDN 18.2 bispecific molecules 4C1 and 4C5 in combination with 80pM 3C27I increase the activation of CD8 cells in the presence of mitomycin treated CHO cells expressing CLDN18.2.

[00167] FIG. 68A and 69B depict CLDN x CD137 formats for the bispecific molecules of the invention.

[00168] FIG. 69A and 69B depict alternative formats for the bispecific molecules of the invention.

Definitions

[00169] Reference in this specification to "one embodiment/aspect" or "an embodiment/aspect" means that a particular feature, structure, or characteristic described in connection with the embodiment/aspect is included in at least one embodiment/aspect of the disclosure. The use of the phrase "in one embodiment/aspect" or "in another embodiment/aspect" in various places in the specification are not necessarily all referring to the same embodiment/aspect, nor are separate or alternative embodiments/aspects mutually exclusive of other embodiments/aspects. Moreover, various features are described which may be exhibited by some embodiments/aspects and not by others. Similarly, various requirements are described which may be requirements for some embodiments/aspects but not other embodiments/aspects. Embodiment and aspect can in certain instances be used interchangeably.

[00170] The terms used in this specification generally have their ordinary meanings in the art, within the context of the disclosure, and in the specific context where each term is

used. Certain terms that are used to describe the disclosure are discussed below, or elsewhere in the specification, to provide additional guidance to the practitioner regarding the description of the disclosure. It will be appreciated that the same thing can be said in more than one way.

[00171] Consequently, alternative language and synonyms may be used for any one or more of the terms discussed herein. Nor is any special significance to be placed upon whether or not a term is elaborated or discussed herein. Synonyms for certain terms are provided. A recital of one or more synonyms does not exclude the use of other synonyms. The use of examples anywhere in this specification including examples of any terms discussed herein is illustrative only, and is not intended to further limit the scope and meaning of the disclosure or of any exemplified term. Likewise, the disclosure is not limited to various embodiments given in this specification.

[00172] Without intent to further limit the scope of the disclosure, examples of instruments, apparatus, methods and their related results according to the embodiments of the present disclosure are given below. Note that titles or subtitles may be used in the examples for convenience of a reader, which in no way should limit the scope of the disclosure. Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains. In the case of conflict, the present document, including definitions, will control.

[00173] As applicable, the terms "about" or "generally", as used herein in the specification and appended claims, and unless otherwise indicated, means a margin of +/- 20%. Also, as applicable, the term "substantially" as used herein in the specification and appended claims, unless otherwise indicated, means a margin of +/- 10%. It is to be appreciated that not all uses of the above terms are quantifiable such that the referenced ranges can be applied.

[00174] The term "subject" or "patient" refers to any single animal, more preferably a mammal (including such non-human animals as, for example, dogs, cats, horses, rabbits, zoo animals, cows, pigs, sheep, and non-human primates) for which treatment is desired. Most preferably, the patient herein is a human. In an embodiment, a "subject" of diagnosis or treatment is a prokaryotic or a eukaryotic cell, a tissue culture, a tissue or an animal, *e.g.* a mammal, including a human.

[00175] As used herein, the term "comprising" is intended to mean that the compositions

and methods include the listed elements, but do not exclude other unlisted elements. “Consisting essentially of” when used to define compositions and methods, excludes other elements that alters the basic nature of the composition and/or method, but does not exclude other unlisted elements. Thus, a composition consisting essentially of the elements as defined herein would not exclude trace amounts of elements, such as contaminants from any isolation and purification methods or pharmaceutically acceptable carriers, such as phosphate buffered saline, preservatives, and the like, but would exclude additional unspecified amino acids. “Consisting of” excludes more than trace elements of other ingredients and substantial method steps for administering the compositions described herein. Embodiments defined by each of these transition terms are within the scope of this disclosure and the inventions embodied therein.

[00176] The term “active agent” or “active ingredient” refers to a substance, compound, or molecule, which is biologically active or otherwise, induces a biological or physiological effect on a subject to which it is administered to. In other words, “active agent” or “active ingredient” refers to a component or components of a composition to which the whole or part of the effect of the composition is attributed. An active agent can be a primary active agent, or in other words, the component(s) of a composition to which the whole or part of the effect of the composition is attributed. An active agent can be a secondary agent, or in other words, the component(s) of a composition to which an additional part and/or other effect of the composition is attributed.

[00177] In an embodiment, a “pharmaceutical composition” is intended to include the combination of an active agent, such as an anti-DLL3, anti-MUC17 or anti-CLDN18.2 antibody and antibody conjugates, with a carrier, inert or active, in a sterile composition suitable for diagnostic or therapeutic use *in vitro*, *in vivo* or *ex vivo*. In one aspect, the pharmaceutical composition is substantially free of endotoxins or is non-toxic to recipients at the dosage or concentration employed.

[00178] In an embodiment, “an effective amount” refers, without limitation, to the amount of the defined component sufficient to achieve the desired therapeutic result. In an embodiment, that result can be effective cancer treatment.

[00179] In an embodiment, as used herein, the terms “treating,” “treatment” and the like are used herein, without limitation, to mean obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disorder or sign or symptom thereof, and/or may be therapeutic in terms of amelioration of the symptoms of the disease or infection, or a partial or complete cure for a

disorder and/or adverse effect attributable to the disorder.

[00180] As used herein, the term "recombinant" refers to polypeptides or polynucleotides that do not exist naturally and which may be created by combining polynucleotides or polypeptides in arrangements that would not normally occur together. The term can refer to a polypeptide produced through a biological host, selected from a mammalian expression system, an insect cell expression system, a yeast expression system, and a bacterial expression system.

[00181] The term "Delta-like 3" or "DLL3" refers to a protein which in humans is encoded by the DLL3 gene. Mutations in the gene cause the autosomal recessive genetic disorder Jarcho-Levin syndrome. DLL3 is expressed normally on the inside of cells and at low levels on normal tissues. However, lung tumor cells overexpress the gene and cell surface DLL3 levels are increased.

[00182] The term "Mucin 17" or "MUC17" refers to a member of the mucin family that includes more than 20 members. Mucins are large, highly glycosylated membrane bound proteins. They are expressed almost exclusively in the intestine. Their general function is to protect epithelial cells from their environment, as well as to regulate proliferation and survival of cells. MUC17 is highly expressed in pancreatic adenocarcinoma tissue (at protein level). MUC17 is expressed in pancreatic, appendiceal, and some colon cancers. Its expression is not detectable in normal pancreas, in pancreatitis or in cell lines derived from other cancers.

[00183] The term "Claudin-18" or "CLD 18" refers to a protein that in humans is encoded by the CLDN18 gene. CLDN18 belongs to the large claudin family of proteins, which form tight junction strands in epithelial cells. "Claudin 18.2" or "CLDN18.2" denotes isoform 2 which is abundant in tumors, particularly those of the gastric system.

[00184] The term "CD" or "cluster of differentiation molecules" refers to cell surface markers that are useful for the identification and characterization of leukocytes such as CD3, CD28 and CD137. CD3 is the signaling component of the T cell receptor (TCR) complex. Because CD3 is required for T cell activation, drugs (often monoclonal antibodies) that target it are being investigated as immunostimulants for the treatment of cancer.

[00185] CD28 is the major costimulatory molecule required in the generation of T cell-mediated immune responses. Upon interaction with its ligands CD80 and CD86, CD28

transduces activation signals that lead to the expression of anti-apoptotic proteins and enhance the synthesis of several cytokines including IL-2. CD28 costimulatory receptor is present on all T-cells. Agonist antibodies directed against CD28 have led to severe adverse events in the clinic, in contrast to antibodies directed against the other CD28 family members CTLA-4, PD-1, or their B7 ligands, which function as checkpoint inhibitors to overcome tumor immune tolerance and can be used in cancer immunotherapy.

[00186] CD137 is a member of the tumor necrosis factor (TNF) receptor family. Its alternative names are tumor necrosis factor receptor superfamily member 9 (TNFRSF9), 4-1BB and induced lymphocyte activation. Agonistic anti-CD137 antibody acts as an activating costimulatory molecule especially important for effector/memory T cells and promotes the survival and proliferation of T lymphocytes. For example, BBK-4, Urelumab and Utomilumab (PF-05082566) targets this receptor to stimulate a more intense immune system attack on cancers.

[00187] PD-1 (Programmed cell death protein 1 or CD279) is a protein on the surface of cells that has a role in regulating the immune system's response to the cells of the human body by down-regulating the immune system and promoting self-tolerance by suppressing T cell inflammatory activity. Engagement of PD-1 by either of its ligands, PD-L1 or PD-L2, on an adjacent cell inhibits TCR signaling and TCR-mediated proliferation, transcriptional activation and cytokine production. This prevents autoimmune diseases, but it can also prevent the immune system from killing cancer cells. Therapeutic antibodies designed to block the PD-1/PD-L1 interaction have potential for the treatment of cancer.

[00188] Programmed death-ligand 1 (PD-L1) also known as cluster of differentiation 274 (CD274) or B7 homolog 1 (B7-H1) is a protein that in humans is encoded by the CD274 gene. PD-L1 binds to its receptor, PD-1, found on activated T cells, B cells, and myeloid cells, to modulate activation or inhibition.

[00189] As used herein, the term "antibody" refers to a polypeptide or a polypeptide complex that specifically recognizes and binds to an antigen through one or more immunoglobulin variable regions. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding and is

encoded by the variable domain. An antibody can be a whole antibody, an antigen binding fragment or a single chain thereof.

[00190] An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to variable domains of the light and heavy chain respectively.

[00191] Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain VL-CL joined to VH-CH1 by a disulfide bond. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990)).

[00192] Accordingly, in either aspect of the invention, the term antibody also embraces minibodies, scFvs, diabodies, triabodies and the like. ScFvs and Diabodies are small bivalent biospecific antibody fragments with high avidity and specificity. Their high signal to noise ratio is typically better due to a better specificity and fast blood clearance increasing their potential for diagnostic and therapeutic targeting of specific antigen (Sundaresan *et al.*, *J Nucl Med* 44:1962-9 (2003)). In addition, these antibodies are advantageous because they can be engineered if necessary as different types of antibody fragments ranging from a small single chain Fv (scFv) to an intact IgG with varying isoforms (Wu & Senter, *Nat. Biotechnol.* 23:1137-1146 (2005)). In some embodiments, the antibody fragment is part of a scFv-scFv or diabody. In some embodiments, in either aspect, the invention provides high avidity antibodies for use according to the invention.

[00193] The term "agonist antibody" refers to an antibody that stimulates or activates an organ. An antibody can act as an agonist of a receptor, essentially replacing the activity of the normal ligand. The agonist activity can occur when the antibody binds the receptor in a manner that mimics the binding of the physiological ligand resulting in antibody-mediated

agonism. For example, agonistic antibodies against the thyrotropin receptor in Grave's disease stimulate the thyroid gland to release thyroid hormones that produce hyperthyroidism. Agonistic antibodies may also stimulate when clustered, either via the Fc portion of the antibody engaging an Fc receptor in trans or cis, or through antigen mediated clustering. The latter clustering mechanism requires antigen engagement by one half of a bispecific molecule and engagement of the stimulatory receptor by the second half of a bispecific molecule. Exemplary stimulatory receptors are CD3, CD28 and 4-1BB, which stimulate T cells.

[00194] The terms "antibody fragment" or "antigen-binding fragment" are used with reference to a portion of an antibody, such as Fab', Fab, Fv, scFv and the like. Regardless of structure, an antibody fragment binds with the same antigen that is recognized by the intact antibody. The term "antibody fragment" also includes diabodies and any synthetic or genetically engineered proteins comprising immunoglobulin variable regions that act like an antibody by binding to a specific antigen to form a complex.

[00195] The term "antigen-binding fragment" or "Fab" refers to a region on an antibody that binds to antigens. It includes one constant and one variable domain of each of the heavy and the light chain (i.e. four domains: VH, CH1, VL and CL1.). The variable domain contains the paratope (the antigen-binding site), that includes a set of complementary determining regions at the amino terminal end of the monomer. Each arm of the Y thus binds an epitope on the antigen.

[00196] The term "Fc region" or "fragment crystallizable region" refers to the tail region of an antibody CH2-CH3 that interacts with cell surface receptors called Fc receptors and some proteins of the complement system. This "effector function" allows antibodies to activate the immune system leading to cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, (e.g. C1q).

[00197] In IgG, IgA and IgD antibody isotypes, the Fc region has two identical protein fragments, derived from the second and third constant domains of the antibody's two heavy chains. IgM and IgE Fc regions have three heavy chain constant domains (CH domains 2–4) in each polypeptide chain whereas IgG is composed of 2 CH domains, 2 and 3. The Fc regions of IgGs bear a highly conserved N-glycosylation site. Glycosylation of the Fc fragment is essential for Fc receptor-mediated activity. The N-glycans attached to this site

are predominantly core-fucosylated diantennary structures of the complex type. In addition, small amounts of these N-glycans also bear bisecting GlcNAc and α -2,6 linked sialic acid residues.

[00198] A particular IgG subclass can be preferred for a particular use. For example, IgG1 is more effective than IgG2 and IgG4 at mediating ADCC and CDC. Thus, IgG2 Fc can be preferred when effector function is undesirable. However, IgG2 Fc-containing molecules are generally more difficult to manufacture and can be less stable than IgG1 Fc-containing molecules. Further, the effector function of an antibody can be increased, or decreased, by introducing one or more mutations into the Fc (see, for example, Strohl, Curr. Opin. Biotech., 20:685-691, 2009). Exemplary IgG1 Fc molecules having increased effector function include those having the following substitutions:

S239D/I332E, S239D/A330S/I332E, S239D/A330L/I332E, S298A/D333A/K334A, P2471/A339D, P2471/A339Q, D280H/K290S, D280H/K290S/S298D, D280H/K290S/S298V, F243L/R292P/Y300L, F243L/R292P/Y300L/P396L, F243L/R292P/Y300L/V3051/P396L, G236A/S239D/I332E, K326A/E333A, K326W/E333S, K290E/S298G/T299A, K290N/S298G/T299A, K290E/S298G/T299A/K326E, K290N/S298G/T299A/K326E

[00199] Fucosylation is another method of increasing effector function of IgG Fc-containing proteins. Removal of the core fucose from the biantennary complex-type oligosaccharides attached to the Fc greatly increases ADCC effector function without altering antigen binding or CDC effector function. There are different ways to reduce or abolish fucosylation of Fc-containing molecules. These include recombinant expression in certain mammalian cell lines including a FUT8 knockout cell line, variant CHO line Lec13, rat hybridoma cell line YB2/0, a cell line comprising a small interfering RNA specifically against the FUT8 gene, and a cell line co-expressing β -1,4-N-acetylglucosaminyltransferase III and Golgi α -mannosidase II. Alternatively, the Fc-containing molecule can be expressed in a non-mammalian cell such as a plant cell, yeast, or prokaryotic cell, e.g., *E. coli*.

[00200] It may be desirable to decrease effector function. Exemplary Fc molecules having decreased effector function include those having the following substitutions:

N297A or N297Q (IgG1), L234A/L235A (IgG1), V234A/G237A (IgG2), L235A/G237A/E318A (IgG4), H268Q/V309L/A330S/A331S (IgG2), C220S/C226S/C229S/P238S (IgG1), C226S/C229S/E233P/L234V/L235A (IgG1), L234F/L235E/P331S (IgG1), S267E/L328F (IgG1)

[00201] Both the light and heavy chains are divided into regions of structural and functional homology. The terms "constant" and "variable" are used functionally. In this regard, it will be appreciated that the variable domains of both the light (VL) and heavy (VH) chain portions determine antigen recognition and specificity. Conversely, the constant domains of the light chain (CL) and the heavy chain (CH1, CH2 and CH3) confer important biological properties such as secretion, transplacental mobility, Fc receptor binding, complement binding, and the like. By convention, the numbering of the constant region domains in conventional antibodies increases as they become more distal from the antigen-binding site or amino-terminus of the antibody. In conventional antibodies, the N-terminal portion is a variable region and at the C-terminal portion is a constant region; the CH3 and CL domains comprise the carboxyterminus of the heavy and light chain, respectively.

[00202] As used herein, the term "heavy chain constant region" includes amino acid sequences derived from an immunoglobulin heavy chain. A polypeptide comprising a heavy chain constant region comprises at least one of: a CH1 domain, a hinge (e.g., upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, or a variant or fragment thereof. For example, an antigen-binding polypeptide for use in the disclosure may comprise a polypeptide chain comprising a CH1 domain; a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, and a CH2 domain; a polypeptide chain comprising a CH1 domain and a CH3 domain; a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, and a CH3 domain, or a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, a CH2 domain, and a CH3 domain. In some embodiments, a polypeptide of the disclosure comprises a polypeptide chain comprising a CH3 domain. Further, an antibody for use in the disclosure may lack at least a portion of a CH2 domain (e.g., all or part of a CH2 domain). It should be understood that the heavy chain constant region may be modified such that they vary in amino acid sequence from the naturally occurring immunoglobulin molecule.

[00203] The heavy chain constant region of an antibody disclosed herein may be derived from different immunoglobulin molecules. For example, a heavy chain constant region of a polypeptide may comprise a CH1 domain derived from an IgG1 molecule and a hinge region derived from an IgG3 molecule. In another example, a heavy chain constant region can comprise a hinge region derived, in part, from an IgG1 molecule and, in part, from an IgG3 molecule. In another example, a heavy chain portion can comprise a chimeric hinge derived, in part, from an IgG1 molecule and, in part, from an IgG4 molecule.

[00204] As used herein, the term "light chain constant region" includes amino acid sequences derived from antibody light chain. Preferably, the light chain constant region

comprises at least one of a constant kappa domain or constant lambda domain. A "light chain heavy chain pair" refers to the collection of a light chain and heavy chain that can form a dimer through a disulfide bond between the CL domain of the light chain and the CH1 domain of the heavy chain.

[00205] The subunit structures and three-dimensional configurations of the constant regions of the various immunoglobulin classes are well known. As used herein, the term "VH domain" includes the amino terminal variable domain of an immunoglobulin heavy chain and the term "CH1 domain" includes the first (most amino terminal) constant region domain of an immunoglobulin heavy chain. The CH1 domain is adjacent to the VH domain and is amino terminal to the hinge region of an immunoglobulin heavy chain molecule.

[00206] As used herein the term "CH2 domain" includes the portion of a heavy chain molecule that extends, e.g., from about residue 244 to residue 360 of an antibody using conventional numbering schemes (residues 244 to 360, Kabat numbering system; and residues 231-340, EU numbering system). The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed between the two CH2 domains of an intact native IgG molecule. The CH3 domain extends from the CH2 domain to the C-terminal of the IgG molecule and comprises approximately 108 residues.

[00207] As used herein, the term "hinge region" includes the portion of a heavy chain molecule that joins the CH1 domain to the CH2 domain. This hinge region comprises approximately 25 residues and is flexible, thus allowing the two N-terminal antigen-binding regions to move independently. Hinge regions can be subdivided into three distinct domains: upper, middle, and lower hinge domains.

[00208] The term "bi-specific monoclonal antibody" or "BSMAb" refers to an antibody that can simultaneously engage two different types of epitopes on the same target or on different targets. An advantage is their ability to redirect specific polyclonal immune cells (e.g. T cells and NK cells) to tumor cells to enhance tumor killing. These antibodies can be divided into two types: IgG like bispecific antibodies which carry an Fc region and therefore retain Fc-mediated effector functions and the non-IgG like formats which rely on their antigen binding capacity to exert their effects. Recombinant techniques have also led to the creation of small fragment molecules. Single chain variable fragments from two different monoclonal antibodies can be combined to form bivalent bispecific antibodies. Examples include bispecific T cell engagers (BiTEs), tandem single chain variable fragments (taFvs), diabodies (DBs), single chain diabodies (scDBs), and triple bodies. These scFv based antibody

fragments have high tumor specificity and tumor penetration due to their small size (ranging from 50 to 60 kDa).

[00209] The term “tri-specific monoclonal antibody” or “TSMAb” refers to an antibody that can simultaneously engage three different types of epitopes on the same target or on different targets.

[00210] The term “scFv” or “scFv fragment antibody” refers to a small molecular antibody, consisting of VH and VL domains, either in the configuration of VL-VH or VH-VL, with a linker region between them. The scFv fragment antibody can more easily penetrate blood vessel wall and the solid tumor, which makes it a preferred carrier of targeting drugs.

[00211] The term “scFvs” or “single-chain variable fragment” refers to divalent (or bivalent) single-chain variable fragments (di-scFvs, bi-scFvs) that can be engineered by linking two scFvs. This can be done by producing a single peptide chain with two VH and two VL regions, yielding tandem scFvs, also known as scFv-scFv molecules. Another possibility is the creation of scFvs with linker peptides that are too short for the two variable regions to fold together (about five amino acids), forcing scFvs to dimerize. This type is known as diabodies.

[00212] The term “humanized antibody” refers to an antibody from non-human species whose protein sequences have been modified to increase its similarity to antibody variants produced naturally in humans. The process of “humanization” is usually applied to monoclonal antibodies developed for administration to humans (e.g. antibodies developed as anti-cancer drugs). Humanization can be necessary when the process of developing a specific antibody involves generation in a non-human immune system (such as that in mice).

[00213] Bispecific antibodies can be generated by chemical cross-linking or by the hybrid hybridoma technology. Alternatively, bispecific antibody molecules can be produced by recombinant techniques, for example by linking 2 scFv molecules together with a short linker. For example, VH1-Linker1-VL1-Linker2-VH2-Linker3-VL2. With Linker1 and Linker3 having lengths between 15-30 amino acids and Linker2 being 5-10 amino acids in length. Linkers may be composed of a variety of amino acids, for example repeating units of GGGGS, GKPGS, GEPGS, and/or GGPGS. Dimerization across 2 scFv molecules can be promoted by reducing the length of the linker joining the VH and the VL domain from about 15 amino acids, routinely used to produce scFv fragments, to about 5 amino acids. These linkers favor intrachain assembly of the VH and VL domains, with the configuration VH1-linker1-VL2-Linker2-VH2-Linker 3VL1 and linkers 1 and 3 being 5 amino acids in length. Any

suitable short linker can be used. Thus, two fragments assemble into a dimeric molecule. Further reduction of the linker length to 0-2 amino acids can generate trimeric (triabodies) or tetrameric (tetrabodies) molecules.

[00214] A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

[00215] One of the challenges for efficiently producing bispecific antibody preparations concerns reducing the formation of homodimeric molecules in favor of heterodimeric molecules, when co-expressing chains of different binding specificities. A "heterodimeric antibody" can utilize the "knobs-into-holes" or "charge-pair" formats to preferentially promote correct association of the 2 molecules to form a heterodimer with 2 specificities. These formats are specific to the heavy chain Fc part of the constant region in antibodies. For the knob-into-holes format, the "knobs" part is engineered by replacing a small amino acid with a larger one. It fits into the "hole," which is engineered by replacing a large amino acid with a smaller one. Introduction of T366W mutations in the first Fc creates the "knob" and introduction of T366S, L368A, and Y407V mutations in the second Fc creates the "hole" (numbering of the residues according to the Kabat EU numbering system). For the charge pair format, heterodimerization is favored through stabilizing ionic interactions by introducing interfacing charge residues in the opposing Fc domains. For example, D356K, E357K, and D399K in a first Fc domain, and the mutations K370E, K409D, and K439E into a second Fc domain, or combination thereof. For example, K392D and K409D mutations in a first Fc chain, and D399K and D356K mutations in a second Fc chain, K409E in the first Fc and D399K in the Fc, K409E in the first Fc and D399R in the second Fc, K409D in the first Fc and D399K in the second Fc, K409D in the first Fc and D399R in the second Fc, K392E in the first Fc and D399K in the second Fc, K392D in the first Fc and D399R in the second Fc, K392D in the first Fc and D399K in the second Fc, K409D and K360D in the first Fc and D399K and D356K in the second Fc, K409D and K370D in the first Fc and D399K and E357K in the second Fc, K409D and K392D in the first Fc and D399K, D356K, and E357K in the second Fc, K409D and K392D in the first Fc and D399K in the second Fc, K409D and K392D in the first Fc and D399K and D356K in the second Fc, K409D and K392D in the first Fc and D399K and E357K in the

second Fc, K409D and K370D in the first Fc and D399K and D357K in the second Fc, D399K in the first Fc and K409D and K360D in the second Fc, and/or K409D and K439D in the first Fc and D399K and D356K in the second Fc, numbered according to the Kabat EU numbering system. Additionally, cysteines may be introduced to stabilize the pairing of heterodimers, for example S234C in the first Fc and Y349C in the second Fc or Y349C in the first Fc and S344C in the second Fc.

[00216] The phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein, often in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and more typically more than 10 to 100 times background. Specific binding to an antibody under such conditions requires an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the selected antigen and not with other proteins. This selection may be achieved by subtracting out antibodies that cross-react with other molecules. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (see, e.g., Harlow & Lane, *Using Antibodies, A Laboratory Manual* (1998) for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity).

[00217] An "immune response" refers to the action of a cell of the immune system (for example, T lymphocytes, B lymphocytes, natural killer (NK) cells, macrophages, eosinophils, mast cells, dendritic cells and neutrophils) and soluble macromolecules produced by any of these cells or the liver (including Abs, cytokines, and complement) that results in selective targeting, binding to, damage to, destruction of, and/or elimination from a vertebrate's body of invading pathogens, cells or tissues infected with pathogens, cancerous or other abnormal cells, or, in cases of autoimmunity, neurodegeneration or pathological inflammation, normal human cells or tissues.

[00218] An "immunoregulator" refers to a substance, an agent, a signaling pathway or a component thereof that regulates an immune response. "Regulating," "modifying" or "modulating" an immune response refers to any alteration in a cell of the immune system or in the activity of such cell. Such regulation includes stimulation or suppression of the immune system which may be manifested by an increase or decrease in the number of various cell

types, an increase or decrease in the activity of these cells, or any other changes which can occur within the immune system. Both inhibitory and stimulatory immunoregulators have been identified, some of which may have enhanced function in the cancer, infectious disease or neurodegenerative microenvironment.

[00219] A cytotoxic T cell (also known as TC, cytotoxic T lymphocyte, CTL, T-killer cell, cytolytic T cell, CD8+ T-cell or killer T cell) is a T lymphocyte (a type of white blood cell) that kills cancer cells, cells that are infected (particularly with viruses), or cells that are damaged in other ways.

[00220] The term "immunotherapy" refers to the treatment of a subject afflicted with, or at risk of contracting or suffering a recurrence of, a disease by a method comprising inducing, enhancing, suppressing or otherwise modifying an immune response. "Treatment" or "therapy" of a subject refers to any type of intervention or process performed on, or the administration of an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, slowing down or preventing the onset, progression, development, severity or recurrence of a symptom, complication, condition or biochemical indicia associated with a disease.

[00221] "Potentiating an endogenous immune response" means increasing the effectiveness or potency of an existing immune response in a subject. This increase in effectiveness and potency may be achieved, for example, by overcoming mechanisms that suppress the endogenous host immune response or by stimulating mechanisms that enhance the endogenous host immune response.

[00222] Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are near each other, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[00223] "Conservatively modified variants" applies to both amino acid and nucleic acid

sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence with respect to the expression product, but not with respect to actual probe sequences.

[00224] The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection. Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

[00225] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are

designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[00226] A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to the full length of the reference sequence, usually about 25 to 100, or 50 to about 150, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

[00227] A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are

halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

[00228] "Nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, and complements thereof. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

[00229] Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

[00230] A particular nucleic acid sequence also implicitly encompasses "splice variants." Similarly, a particular protein encoded by a nucleic acid implicitly encompasses any protein encoded by a splice variant of that nucleic acid. "Splice variants," as the name suggests, are products of alternative splicing of a gene. After transcription, an initial nucleic acid transcript may be spliced such that different (alternate) nucleic acid splice products encode different polypeptides. Mechanisms for the production of splice variants vary, but include alternate splicing of exons. Alternate polypeptides derived from the same nucleic acid by read-through transcription are also encompassed by this definition. Any products of a splicing reaction,

including recombinant forms of the splice products, are included in this definition. An example of potassium channel splice variants is discussed in Leicher *et al.*, *J. Biol. Chem.* 273(52):35095-35101 (1998).

[00231] The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

[00232] As used herein, the term "prevention" means all of the actions by which the occurrence of the disease is restrained or retarded.

[00233] As used herein, the term "treatment" means all of the actions by which the symptoms of the disease have been alleviated, improved or ameliorated. In the present specification, "treatment" means that the symptoms of cancer, neurodegeneration, or infectious disease are alleviated, improved or ameliorated by administration of the antibodies disclosed herein.

[00234] The term "administration" refers to the introduction of an amount of a predetermined substance into a patient by a certain suitable method. The composition disclosed herein may be administered via any of the common routes, as long as it is able to reach a desired tissue, for example, but is not limited to, intraperitoneal, intravenous, intramuscular, subcutaneous, intradermal, oral, topical, intranasal, intrapulmonary, or intrarectal administration. However, since peptides are digested upon oral administration, active ingredients of a composition for oral administration should be coated or formulated for protection against degradation in the stomach.

[00235] The term "subject" refers to those suspected of having or diagnosed with cancer, a neurodegenerative or an infectious disease. However, any subject to be treated with the pharmaceutical composition disclosed herein is included without limitation. The pharmaceutical composition including an anti-DLL3 antibody disclosed herein is administered to a subject suspected of having cancer, a neurodegenerative or an infectious disease.

[00236] Construction of suitable vectors containing the desired sequences and control

sequences employs standard ligation and restriction techniques, which are well understood in the art (see Maniatis *et al.*, in *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York (1982)). Isolated plasmids, DNA sequences, or synthesized oligonucleotides are cleaved, tailored, and re-ligated in the form desired.

[00237] For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96 (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). The genes encoding the heavy and light chains of an antibody of interest can be cloned from a cell, e.g., the genes encoding a monoclonal antibody can be cloned from a hybridoma and used to produce a recombinant monoclonal antibody. Gene libraries encoding heavy and light chains of monoclonal antibodies can also be made from hybridoma or plasma cells. Random combinations of the heavy and light chain gene products generate a large pool of antibodies with different antigenic specificity (see, e.g., Kuby, *Immunology* (3rd ed. 1997)). Techniques for the production of single chain antibodies or recombinant antibodies (U.S. Pat. No. 4,946,778, U.S. Pat. No. 4,816,567) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized or human antibodies (see, e.g., U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); and Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995)). Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990); Marks *et al.*, *Biotechnology* 10:779-783 (1992)). Antibodies can also be made bispecific, i.e., able to recognize two different antigens (see, e.g., WO 93/08829, Traunecker *et al.*, *EMBO J.* 10:3655-3659 (1991); and Suresh *et al.*, *Methods in Enzymology* 121:210 (1986)). Antibodies can also be heteroconjugates, e.g., two covalently joined antibodies, or immunotoxins (see, e.g., U.S. Pat. No. 4,676,980, WO 91/00360; and WO 92/200373).

[00238] Methods for humanizing antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import

residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers (see, e.g., Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988) and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[00239] The term "cancer" refers to human cancers and carcinomas, sarcomas, adenocarcinomas, etc., including solid tumors, kidney, breast, lung, kidney, bladder, urinary tract, urethra, penis, vulva, vagina, cervical, colon, ovarian, prostate, pancreas, stomach, brain, head and neck, skin, uterine, testicular, esophagus, and liver cancer. Additional cancers include, for example, Hodgkin's Disease, multiple myeloma, neuroblastoma, breast cancer, ovarian cancer, lung cancer, rhabdomyosarcoma, primary thrombocytosis, primary macroglobulinemia, small-cell lung tumors, primary brain tumors, stomach cancer, colon cancer, malignant pancreatic insulanoma, malignant carcinoid, premalignant skin lesions, testicular cancer, thyroid cancer, neuroblastoma, esophageal cancer, genitourinary tract cancer, malignant hypercalcemia, cervical cancer, endometrial cancer, and adrenal cortical cancer.

[00240] The term "checkpoint inhibitor" or "immune checkpoint inhibitor" refers to an agent such as a drug that inhibits/blocks the inhibitory checkpoint molecules. Some cancers can protect themselves from attack by stimulating immune checkpoint targets. Checkpoint therapy can block inhibitory checkpoints, restoring immune system function.

[00241] The term "immune checkpoint regulator" refers to receptors and their associated ligands, which together provide a means for inhibiting or stimulating signaling pathways that otherwise lead to T-cell activation. Immune checkpoint regulators include TIGIT and its CD155 ligand, PVR; PD-1 and its ligands, PD-L1 and PD-L2; CTLA-4 and its ligands, B7-1 and B7-2; TIM-3 and its ligand, Galectin-9; LAG-3 and its ligands, including liver sinusoidal endothelial cell lectin (LSEctin) and Galectin-3; CD122 and its CD122R ligands; CD70, B7H3, B and T lymphocyte attenuator (BTLA), and VISTA.

[00242] The term "checkpoint regulator antagonist," "immune checkpoint binding

antagonist" and "immune checkpoint antagonist" refer to a class of agents that interfere with (or inhibit) the activity of an immune checkpoint regulator so that, as a result of the binding to the checkpoint regulator or its ligand, signaling through the checkpoint regulator receptor is blocked or inhibited. By inhibiting this signaling, immune-suppression can be reversed so that T cell immunity against cancer cells can be re-established or enhanced. Immune checkpoint regulator antagonists include antibody fragments, peptide inhibitors, dominant negative peptides and small molecule drugs, either in isolated forms or as part of a fusion protein or conjugate. Example targets of checkpoint regulator antagonists include PD1, PDL1, CTLA4, LAG3, TIM-3, TIGIT, VISTA.

[00243] The term "immune checkpoint binding agonist" and "immune checkpoint agonist" refer to a class of agents that stimulate the activity of an immune checkpoint regulator so that, as a result of the binding to the checkpoint regulator or its ligand, signaling through the checkpoint regulator receptor is stimulated. By stimulating this signaling, T cell immunity against cancer cells can be re-established or enhanced. The targets of checkpoint regulator agonists include members of the tumor necrosis factor (TNF) receptor superfamily, such as CD27, CD40, OX40 (CD 134), glucocorticoid-induced TNFR family-related protein (GITR), and 4-1BB (CD137) and their ligands. Additional targets of checkpoint regulator agonists belong to the B7-CD28 superfamily, including CD28 and ICOS.

[00244] In any of the embodiments above, one or more cancer therapies, e.g., chemotherapy, radiation therapy, immunotherapy, surgery, or hormone therapy can be co-administered further with an antibody of the invention.

[00245] In one embodiment, the chemotherapeutic reagent is an alkylating agent: nitrogen mustards, nitrosoureas, tetrazines, aziridines, cisplatins and derivatives, and non-classical alkylating agents. Nitrogen mustards include mechlorethamine, cyclophosphamide, melphalan, chlorambucil, ifosfamide and busulfan. Nitrosoureas include N-Nitroso-N-methylurea (MNU), carmustine (BCNU), lomustine (CCNU) and semustine (MeCCNU), fotemustine and streptozotocin. Tetrazines include dacarbazine, mitozolomide and temozolomide. Aziridines include thiotepa, mytomyacin and diaziquone (AZQ). Cisplatin and derivatives include cisplatin, carboplatin and oxaliplatin. In one embodiment the chemotherapeutic reagent is an anti-metabolites: the anti-folates (e.g., methotrexate), fluoropyrimidines (e.g., fluorouracil and capecitabine), deoxynucleoside analogues and thiopurines. In another embodiment the chemotherapeutic reagent is an anti-microtubule agent such as vinca alkaloids (e.g., vincristine and vinblastine) and taxanes (e.g., paclitaxel and docetaxel). In another embodiment the chemotherapeutic reagent is a topoisomerase inhibitor or a cytotoxic antibiotic such as doxorubicin, mitoxantrone, bleomycin, actinomycin,

and mitomycin.

[00246] The contacting of the patient with the antibody or antibody fragment, can be by administering the antibody to the patient intravenously, intraperitoneally, intramuscularly, intratumorally, or intradermally. In some embodiments the antibody is co-administered with a cancer therapy agent.

[00247] The term “formulation” as used herein refers to the antibodies disclosed herein and excipients combined together which can be administered and has the ability to bind to the corresponding receptors and initiate a signal transduction pathway resulting in the desired activity. The formulation can optionally comprise other agents.

[00248] All numerical designations, e.g., pH, temperature, time, concentration, and molecular weight, including ranges, are to be understood as approximations in accordance with common practice in the art. When used herein, the term “about” may connote variation (+) or (-) 1%, 5% or 10% of the stated amount, as appropriate given the context. It is to be understood, although not always explicitly stated, that the reagents described herein are merely exemplary and that equivalents of such are known in the art.

[00249] Many known and useful compounds and the like can be found in Remington's Pharmaceutical Sciences (13th Ed), Mack Publishing Company, Easton, PA—a standard reference for various types of administration. As used herein, the term “formulation(s)” means a combination of at least one active ingredient with one or more other ingredient, also commonly referred to as excipients, which may be independently active or inactive. The term “formulation” may or may not refer to a pharmaceutically acceptable composition for administration to humans or animals and may include compositions that are useful intermediates for storage or research purposes.

[00250] As the patients and subjects of the invention method are, in addition to humans, veterinary subjects, formulations suitable for these subjects are also appropriate. Such subjects include livestock and pets as well as sports animals such as horses, greyhounds, and the like.

DETAILED DESCRIPTION

[00251] The DLL3 gene provides instructions for making a protein that helps control the Notch pathway, an important pathway in embryonic development. DLL3 is usually an intracellular protein but it is also expressed on the surface of cancer cells. DLL3 is expressed normally on the inside of cells and at low levels on normal tissues. However, lung

tumor cells overexpress the gene and cell surface DLL3 levels are increased. Recent studies have reported that DLL3 is also expressed in other tumor types of neuroendocrine origin, including melanoma, glioblastoma multiforme, small cell bladder cancer, metastatic castration-resistant prostate cancer, and neuroendocrine lung tumors.

[00252] CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137) CD3, CD28 and CD137 are receptors present on T cells. T cells can be activated by antigen-presenting cells via CD3, CD28 and CD137. Two parallel therapeutic strategies are pursued for activating or engaging T cells to kill tumor cells.

[00253] Embodiments of the invention include methods of diagnosing, prognosing, treating, monitoring and preventing cancer, including refractory cancer, using anti-DLL3 antibodies and antibody conjugates, pharmaceutical compositions thereof, and articles of manufacture. More specifically, the invention is directed to bispecific molecules that bind to DLL3 and activate CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137).

[00254] Embodiments of the invention also include methods of diagnosing, prognosing, treating, monitoring and preventing cancer, including refractory cancer, using anti-MUC17 antibodies and antibody conjugates, pharmaceutical compositions thereof, and articles of manufacture. More specifically, the invention is directed to bispecific molecules that bind to MUC17 and activate CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137).

[00255] Embodiments of the invention also include methods of diagnosing, prognosing, treating, monitoring and preventing cancer, including refractory cancer, using anti-CLDN18.2 antibodies and antibody conjugates, pharmaceutical compositions thereof, and articles of manufacture. More specifically, the invention is directed to bispecific molecules that bind to CLDN18.2 and activate CD (cluster of differentiation) molecules (e.g. CD3, CD28 and CD137).

DLL3 T-Cell Engagers

[00256] Embodiments of the invention include bispecific monoclonal antibodies (BSMAbs). The single chain variable fragment (scFv) of a first antibody can be joined with the antigen binding fragment (Fab) of a second antibody. For example, the scFv portion of an antibody against CD3 can be linked to a Fab portion of an antibody against DLL3. They can be joined with a linker, such as 4xGKPGS and 4xG4S linkers. The IgG1 Fc can be heterodimerized with charge pair or “knob into hole” mutations or charge pair mutations. The Fc effector function can be minimized through the introduction of N297A/G mutations or

LLP mutations. The combination can bring an effector cell (T-cell or NK cell) into the proximity of the tumor cell to enhance antitumor effect.

[00257] FIG. 1A – 1F and 2A – 2C depict several formats for bispecific molecules of the invention. The DLL3 x CD3 bispecific molecules can activate T cell cytotoxicity against DLL3 expressing CHO cells or NCI-H82 tumor cells. This is exemplified by the release of LDH upon cell death, as well as the upregulation of CD25 on the T cells. When combined with DLL3 x CD28 or DLL3 x CD137 bispecific molecules, the T cells are further activated, proliferate, and release IFN gamma and IL-2.

[00258] CD28 signaling is essential for the activity of anti-PD1 and anti-PDL1 antibodies, thus co-dosing the DLL3 x CD28 bispecific molecules with anti-PD1 and anti-PDL1 can improve the responses to the inhibition of the PD1/PDL1 pathway. CD137 is highly expressed on activated T cells, which cannot be stimulated by PD1/PDL1 stimulation alone. However, DLL3 x CD137 or DLL3 x CD28 x CD137 stimulation combined with PD-1 blockade results in robust antitumor immunity.

[00259] FIG. 1A – 1F depict several Scfv-Fc x Fab-Fc formats for bispecific molecules of the invention. Each is a Scfv-Fc fragment joined with a Fab-Fc fragment. FIG. 1A depicts an anti-CD3 Scfv paired with an anti-DLL3 Fab (CH1-VH + CK-VL). Similarly, FIG. 1B depicts an anti-CD28 Scfv paired with an anti-DLL3 Fab molecule (CH1-VH + CK-VL).

[00260] FIG. 1C depicts an anti-DLL3 Scfv-Fc paired with an anti-CD3 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 1D depicts an anti-DLL3 Scfv paired with an anti-CD28 Fab molecule (CH1-VH + CK-VL).

[00261] FIG. 1E depicts an anti-CD137 Scfv paired with an anti-DLL3 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 1F depicts an anti-DLL3 Scfv-Fc paired with an anti-CD137 Fab-Fc molecule (CH1-VH + CK-VL).

[00262] FIG. 2A – 2C depict Scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. Each is a Scfv-scfv-Fc fragment is joined with a Fc fragment.

[00263] FIG. 2A depicts an anti-DLL3, anti-CD3 Scfv-Fc x Fab-Fc molecule. FIG. 2B depicts an anti-DLL3, anti-CD28 Scfv-Fc x Fc molecule. FIG. 2C depicts an anti-DLL3, anti-CD137 Scfv-Fc x Fc molecule.

[00264] FIG. 2D – 2F depict combinations of DLL3 bi-specific T-Cell Engagers according to embodiments of the invention, specifically, Scfv-scfv-Fc x Fab-Fc molecules.

[00265] FIG. 2D depicts an anti-DLL3, anti-CD3, anti-DLL3 Scfv-scFv-Fc x Fab-Fc molecule. FIG. 2E depicts an anti-DLL3, anti-CD28, anti-DLL3 Scfv-scFv-Fc x Fab-Fc molecule. FIG. 2F depicts an anti-DLL3, anti-CD137, anti-DLL3 Scfv-scFv-Fc x Fab-Fc molecule.

DLL3 Bispecific Molecules with two CD137 Fragments

[00266] FIG. 20A to 20F depict bispecific molecules with two CD137 Fab fragments.

[00267] FIG. 20A depicts an anti-CD137, anti-DLL3 Fab molecule. Similarly, FIG. 20B depicts an anti-CD137, anti-DLL3, anti-CD3 Fab molecule. FIG. 20C depicts an alternative configuration of an anti-CD137, anti-DLL3, anti-CD3 Fab molecule.

[00268] FIG. 21A and 21B depict bispecific molecules with two CD137 scFv fragments. Similarly, FIG. 21A depicts an anti-DLL3, anti-CD3, anti-CD137 scFv molecule.

[00269] FIG. 21B depicts an alternative configuration of an anti-DLL3, anti-CD3, anti-CD137 scFv molecule. FIG. 21C depicts an alternative configuration of an anti-DLL3, anti-CD3, anti-CD137 scFv molecule. FIG. 21D depicts an alternative configuration of an anti-DLL3, anti-CD3, anti-CD137 scFv molecule. FIG. 21E depicts an alternative configuration of an anti-DLL3, anti-CD3, anti-CD137 scFv molecule. FIG. 21F depicts an alternative configuration of an anti-DLL3, anti-CD3, anti-CD137 scFv molecule.

[00270] In an embodiment, the bispecific molecule can be co-administered or combined with an antagonist such as PD1, PDL1, TIGIT, LAG3, TIM3, VISTA or CTLA4. Alternatively, the bispecific molecule can be co-administered or combined with a bispecific antagonist such as PD1 x TIGIT, LAG3 x TIGIT, PD1 x LAG3, PD1 x TIM3 or VEGF x TGFBR2. The bispecific molecule can also be co-administered or combined with an agonist such as CD40, GITR, CD27, OX40 or 4-1BB.

MUC17 T-Cell Engagers

[00271] Embodiments of the invention include bispecific monoclonal antibodies (BSMAbs). The single chain variable fragment (scFv) of a first antibody can be joined with the antigen binding fragment (Fab) of a second antibody. For example, the scFv portion of an antibody against CD3 can be linked to a Fab portion of an antibody against MUC17. They can be joined with a linker, such as 4xGKPGS and 4xG4S linkers. The IgG1 Fc can be heterodimerized with charge pair or “knob into hole” mutations or charge pair mutations. The Fc effector function can be minimized through the introduction of N297A/G mutations or LLP mutations. The combination can bring an effector cell (T-cell or NK cell) into the

proximity of the tumor cell to enhance antitumor effect.

[00272] FIG. 22A – 22F and 23A – 23F depict several formats for the bispecific molecules of the invention. The MUC17 x CD3 bispecific molecules can activate T cell cytotoxicity against MUC17 expressing CHO cells or ASPC1 tumor cells. This is exemplified by the release of LDH upon cell death, as well as the upregulation of CD25 on the T cells. When combined with MUC17 x CD28 or MUC17 x CD137 bispecific molecules, the T cells are further activated, proliferate, and release IFN gamma and IL-2.

[00273] CD28 signaling is essential for the activity of anti-PD1 and anti-PDL1 antibodies, thus co-dosing the MUC17 x CD28 bispecific molecules with anti-PD1 and anti-PDL1 can improve the responses to the inhibition of the PD1/PDL1 pathway. CD137 is highly expressed on activated T cells, which cannot be stimulated by PD1/PDL1 stimulation alone. However, MUC17 x CD137 or MUC17 x CD28 x CD137 stimulation combined with PD-1 blockade results in robust antitumor immunity.

[00274] FIG. 21A – 21F depict several Scfv-Fc x Fab-Fc formats for the bispecific molecules of the invention. Each is a Scfv-Fc fragment joined with a Fab-Fc fragment. FIG. 21A depicts an anti-CD3 Scfv paired with an anti-MUC17 Fab (CH1-VH + CK-VL). Similarly, FIG. 21B depicts an anti-CD28 Scfv paired with an anti-MUC17 Fab molecule (CH1-VH + CK-VL).

[00275] FIG. 21C depicts an anti-MUC17 Scfv-Fc paired with an anti-CD3 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 21D depicts an anti-MUC17 Scfv paired with an anti-CD28 Fab molecule (CH1-VH + CK-VL).

[00276] FIG. 21E depicts an anti-CD137 Scfv paired with an anti-MUC17 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 21F depicts an anti-MUC17 Scfv-Fc paired with an anti-CD137 Fab-Fc molecule (CH1-VH + CK-VL).

[00277] FIG. 22A – 22C depict Scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. Each is a Scfv-scfv-Fc fragment is joined with a Fc fragment.

[00278] FIG. 22A depicts an anti-MUC17, anti-CD3 Scfv-scfv-Fc x -Fc molecule. FIG. 23B depicts an anti-MUC17, anti-CD28 Scfv-scfv-Fc x Fc molecule. FIG. 22C depicts an anti-MUC17, anti-CD137 Scfv-scfv-Fc x Fc molecule.

[00279] FIG. 22D – 22F depict combinations of MUC17 bi-specific T-Cell Engagers

according to embodiments of the invention, specifically, Scfv-scFv-Fc x Fab-Fc molecules.

[00280] FIG. 22D depicts an anti-MUC17, anti-CD3, anti-MUC17 Scfv-scFv-Fc x Fab-Fc molecule. FIG. 22E depicts an anti-MUC17, anti-CD28, anti-MUC17 Scfv-scFv-Fc x Fab-Fc molecule. FIG. 22F depicts an anti-MUC17, anti-CD137, anti-MUC17 Scfv-scFv-Fc x Fab-Fc molecule.

Muc17x CD137 and DLL3 x CD137 molecules

[00281] FIG. 38A and 38B depict Muc17x CD137 and DLL3 x CD137 molecules. FIG. 38A depicts an anti-Muc17 + BBK-4 Scfv-scFv-Fc x Fab-Fc molecule. Similarly, FIG. 38B depicts a BBK-4 + BBK-4 + anti-Muc17 Scfv-scFv-Fc x Fab-Fc molecule.

[00282] FIG. 39A and 39B depict bispecific Muc17 x CD137 molecules. FIG. 39A depicts an alternative configuration of a urelumab antibody with anti-Muc17scfv fused to the C-terminus of the heavy chain. FIG. 39B depicts a BBK-4 antibody with anti-Muc17scfv fused to the C-terminus of the heavy chain.

[00283] In an embodiment, the bispecific molecule can be co-administered or combined with an antagonist such as PD1, PDL1, TIGIT, LAG3, TIM3, VISTA or CTLA4. Alternatively, the bispecific molecule can be co-administered or combined with a bispecific antagonist such as PD1 x TIGIT, LAG3 x TIGIT, PD1 x LAG3, PD1 x TIM3 or VEGF x TGFBR2. The bispecific molecule can also be co-administered or combined with an agonist such as CD40, GITR, CD27, OX40 or 4-1BB.

CLDN 18.2 T-Cell Engagers

[00284] Embodiments of the invention include bispecific monoclonal antibodies (BSMAbs). The single chain variable fragment (scFv) of a first antibody can be joined with the antigen binding fragment (Fab) of a second antibody. For example, the scFv portion of an antibody against CD3 can be linked to a Fab portion of an antibody against CLDN18.2. They can be joined with a linker such as 4xGKPGS and 4xG4S linkers. The IgG1 Fc can be heterodimerized with charge pair or “knob into hole” mutations or charge pair mutations. The Fc effector function can be minimized through the introduction of N297A/G mutations or LLP mutations. The combination can bring an effector cell (T-cell or NK cell) into the proximity of the tumor cell to enhance antitumor effect.

[00285] FIG. 40A – 40D and 41A – 41F depict several formats for the bispecific molecules of the invention. The CLDN18.2 x CD3 bispecific molecules CLDN18.2 x CD28 x CD3 and CLDN18.2 x CD137 x CD3 can activate T cell cytotoxicity against huCLDN18.2 expressing CHO cells or SNU-601 tumor cells. This is exemplified by the release of LDH upon cell death, as well as the upregulation of CD25 on the T cells. When combined with CLDN18.2 x CD28 or CLDN18.2 x CD137 bispecific molecules, the T cells are further activated, proliferate, and release IFN gamma and IL-2.

[00286] CD28 signaling is essential for the activity of anti-PD1 and anti-PDL1 antibodies, thus co-dosing the CLDN18.2 x CD28 bispecific molecules with anti-PD1 and anti-PDL1 can improve the responses to the inhibition of the PD1/PDL1 pathway. CD137 is highly expressed on activated T cells, which cannot be stimulated by PD1/PDL1 stimulation alone. However, CLDN18.2 x CD137 or CLDN18.2 x CD28 x CD137 stimulation combined with PD-1 blockade results in robust antitumor immunity.

[00287] FIG. 40A – 40D and 41A – 41F depict several Scfv-Fc x Fab-Fc formats for the bispecific molecules of the invention. Each is a Scfv-Fc fragment joined with a Fab-Fc fragment. FIG. 40A depicts an anti-CD3 Scfv paired with an anti-CLDN18.2 Fab (CH1-VH + CK-VL). Similarly, FIG. 40B depicts an anti-CD28 Scfv paired with an anti-CLDN18.2 Fab molecule (CH1-VH + CK-VL).

[00288] FIG. 40C depicts an anti-CLDN18.2 Scfv-Fc paired with an anti-CD3 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 40D depicts an anti-CLDN18.2 Scfv paired with an anti-CD28 Fab molecule (CH1-VH + CK-VL).

[00289] FIG. 40E depicts an anti-CD137 Scfv paired with an anti-CLDN18.2 Fab molecule (CH1-VH + CK-VL). Similarly, FIG. 40F depicts an anti-CLDN18.2 Scfv-Fc paired with an anti-CD137 Fab-Fc molecule (CH1-VH + CK-VL).

[00290] FIG. 41A – 41C depict Scfv-scfv-Fc x Fc formats for the bispecific molecules of the invention. Each is a Scfv-scfv-Fc fragment is joined with a Fc fragment.

[00291] FIG. 41A depicts an anti-CLDN18.2, anti-CD3 Scfv-Scfv-Fc x -Fc molecule. FIG. 41B depicts an anti-CLDN18.2, anti-CD28 Scfv-Scfv-Fc x Fc molecule. FIG. 41C depicts an anti-CLDN18.2, anti-CD137 Scfv-Scfv-Fc x Fc molecule.

[00292] FIG. 41D – 41F depict combinations of CLDN18.2 bi-specific T-Cell Engagers

according to embodiments of the invention, specifically, Scfv-scfv-Fc x Fab-Fc molecules.

[00293] FIG. 41D depicts an anti-CLDN18.2, anti-CD3, anti-CLDN18.2 Scfv-scfv-Fc x Fab-Fc molecule. FIG. 41E depicts an anti-CLDN18.2, anti-CD28, anti-CLDN18.2 Scfv-scfv-Fc x Fab-Fc molecule. FIG. 41F depicts an anti-CLDN18.2, anti-CD137, anti-CLDN18.2 Scfv-scfv-Fc x Fab-Fc molecule.

[00294] In an embodiment, the bispecific molecule can be co-administered or combined with an antagonist such as PD1, PDL1, TIGIT, LAG3, TIM3, VISTA or CTLA4. Alternatively, the bispecific molecule can be co-administered or combined with a bispecific antagonist such as PD1 x TIGIT, LAG3 x TIGIT, PD1 x LAG3, PD1 x TIM3 or VEGF x TGFBR2. The bispecific molecule can also be co-administered or combined with an agonist such as CD40, GITR, CD27, OX40 or 4-1BB.

Methods from Producing Bispecific T-Cell Engagers

[00295] Another aspect relates to a method for producing a bispecific antibody comprising culturing a cell transiently or stably expressing one or more constructs encoding one or more polypeptide chains in the bispecific antibody; and purifying the bispecific antibody from the cultured cells. Any cell capable of producing a functional bispecific antibody can be used. In preferred embodiments, the bispecific antibody-expressing cell is of eukaryotic or mammalian origin, preferably a human cell or Chinese hamster cell. Cells from various tissue cell types may be used to express the bispecific antibodies. In other embodiments, the cell is a yeast cell, an insect cell or a bacterial cell. Preferably, the bispecific antibody-producing cell is stably transformed with a vector expressing the bispecific antibody.

[00296] One or more expression vectors encoding the antibody heavy or light chains can be introduced into a cell by any conventional method, such as by naked DNA technique, cationic lipid-mediated transfection, polymer-mediated transfection, peptide-mediated transfection, virus-mediated infection, physical or chemical agents or treatments, electroporation, etc. In addition, cells may be transfected with one or more expression vectors for expressing the bispecific antibody along with a selectable marker facilitating selection of stably transformed clones expressing the bispecific antibody. The antibodies produced by such cells may be collected and/or purified according to techniques known in the art, such as by centrifugation, chromatography, etc.

[00297] Examples of suitable selectable markers for mammalian cells include

dihydrofolate reductase (DHFR), thymidine kinase, neomycin, neomycin analog G418, hygromycin, zeocin, blasticidin, and puromycin. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow independent of a supplemented media. Two examples are CHO DHFR cells and mouse LTK cells. These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented media. An alternative to supplementing the media is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the DHFR or TK gene will not be capable of survival in non-supplemented media.

[00298] The second category is dominant selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would survive the selection. Examples of such dominant selection use the drugs neomycin, mycophenolic acid, or hygromycin. The three examples employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid) or hygromycin, respectively. Others include the neomycin analog G418 and puromycin.

[00299] Exemplary bispecific antibody-expressing cells include human Jurkat, human embryonic kidney (HEK) 293, Chinese hamster ovary (CHO) cells, mouse WEHI fibrosarcoma cells, as well as unicellular protozoan species, such as *Leishmania tarentolae*. In addition, stably transformed, antibody producing cell lines may be produced using primary cells immortalized with c-myc or other immortalizing agents.

[00300] In some embodiments, the cell lines express at least 1 mg, at least 2 mg, at least 5 mg, at least 10 mg, at least 20 mg, at least 50 mg, at least 100 mg, at least 500 mg, at least 1 gram, at least 2 grams, at least 4 grams, or at least 10 grams of the bispecific antibody/liter of culture. Bispecific antibodies can be isolated from bispecific antibody expressing cells following culture and maintenance in any appropriate culture medium, such as RPMI, DMEM, and AIM V®. The bispecific antibodies can be purified using conventional protein purification methodologies (e.g., affinity purification, chromatography, etc.), including the use of Protein-A or Protein-G immunoaffinity purification. In some embodiments,

bispecific antibodies are engineered for secretion into culture supernatants for isolation therefrom.

Methods of Treatment

[00301] Another aspect of the present application relates to a method for treating a cell proliferative disorder. The method comprises administering to a subject in need thereof an effective amount of a bispecific antibody according to the present disclosure. In another aspect, a method for treating a cell proliferative disorder comprises administering to a subject in need thereof an effective amount of one or more expression vectors expressing a bispecific antibody according to the present disclosure.

[00302] Any suitable route or mode of administration can be employed for providing the patient with a therapeutically or prophylactically effective dose of the bispecific antibody. Exemplary routes or modes of administration include parenteral {e.g., intravenous, intraarterial, intramuscular, subcutaneous, intratumoral}, oral, topical (nasal, transdermal, intradermal or intraocular), mucosal {e.g., nasal, sublingual, buccal, rectal, vaginal}, inhalation, intralymphatic, intraspinal, intracranial, intraperitoneal, intratracheal, intravesical, intrathecal, enteral, intrapulmonary, intralymphatic, intracavitary, intraorbital, intracapsular and transurethral, as well as local delivery by catheter or stent.

[00303] A pharmaceutical composition comprising a bispecific antibody in accordance with the present disclosure can be formulated in any pharmaceutically acceptable carrier(s) or excipient(s). As used herein, the term "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Pharmaceutical compositions can include suitable solid or gel phase carriers or excipients. Exemplary carriers or excipients include calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Exemplary pharmaceutically acceptable carriers include one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. In many cases it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Pharmaceutically acceptable carriers can further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the therapeutic agents.

[00304] The bispecific antibody can be incorporated into a pharmaceutical composition

suitable for parenteral administration. Suitable buffers include but are not limited to, sodium succinate, sodium citrate, sodium phosphate or potassium phosphate. Sodium chloride can be used to modify the toxicity of the solution at a concentration of 0-300 mM (optimally 150 mM for a liquid dosage form). Cryoprotectants can be included for a lyophilized dosage form, principally 0-10% sucrose (optimally 0.5-1.0%). Other suitable cryoprotectants include trehalose and lactose. Bulking agents can be included for a lyophilized dosage form, principally 1- 10% mannitol (optimally 2-4%). Stabilizers can be used in both liquid and lyophilized dosage forms, principally 1-50 mM L-Methionine (optimally 5-10 mM). Other suitable bulking agents include glycine, arginine, can be included as 0-0.05% polysorbate-80 (optimally 0.005-0.0 1%). Additional surfactants include but are not limited to polysorbate 20 and BRIJ surfactants.

[00305] Therapeutic bispecific antibody preparations can be lyophilized and stored as sterile powders, preferably under vacuum, and then reconstituted in bacteriostatic water (containing, for example, benzyl alcohol preservative) or in sterile water prior to injection. Pharmaceutical compositions can be formulated for parenteral administration by injection e.g., by bolus injection or continuous infusion.

[00306] The therapeutic agents in the pharmaceutical compositions may be formulated in a "therapeutically effective amount" or a "prophylactically effective amount". A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount of the recombinant vector may vary depending on the condition to be treated, the severity and course of the condition, the mode of administration, whether the antibody or agent is administered for preventive or therapeutic purposes, the bioavailability of the particular agent(s), the ability of the bispecific antibody to elicit a desired response in the individual, previous therapy, the age, weight and sex of the patient, the patient's clinical history and response to the antibody, the type of the bispecific antibody used, discretion of the attending physician, etc. A therapeutically effective amount is also one in which any toxic or detrimental effects of the recombinant vector is outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result.

[00307] Preferably, the polypeptide domains in the bispecific antibody are derived from the same host in which they are to be administered in order to reduce inflammatory responses against the administered therapeutic agents.

[00308] The bispecific antibody is suitably administered to the patient at one time or over

a series of treatments and may be administered to the patient at any time from diagnosis onwards. The bispecific antibody may be administered as the sole treatment or in conjunction with other drugs or therapies useful in treating the condition in question.

[00309] As a general proposition, a therapeutically effective amount or prophylactically effective amount of the bispecific antibody will be administered in a range from about 1 ng/kg body weight/day to about 100 mg/kg body weight/day whether by one or more administrations. In a particular embodiment, each bispecific antibody is administered in the range of from about 1 ng/kg body weight/day to about 10 mg/kg body weight/day, about 1 ng/kg body weight/day to about 1 mg/kg body weight/day, about 1 ng/kg body weight/day to about 100 g/kg body weight/day, about 1 ng/kg body weight/day to about 10 g/kg body weight/day, about 1 ng/kg body weight/day to about 1 g/kg body weight/day, about 1 ng/kg body weight/day to about 100 ng/kg body weight/day, about 1 ng/kg body weight/day to about 10 ng/kg body weight/day, about 10 ng/kg body weight/day to about 100 mg/kg body weight/day, about 10 ng/kg body weight/day to about 10 mg/kg body weight/day, about 10 ng/kg body weight/day to about 1 mg/kg body weight/day, about 10 ng/kg body weight/day to about 100 g/kg body weight/day, about 10 ng/kg body weight/day to about 10 mg/kg body weight/day, about 10 ng/kg body weight/day to about 1 mg/kg body weight/day, 10 ng/kg body weight/day to about 100 ng/kg body weight/day, about 100 ng/kg body weight/day to about 100 mg/kg body weight/day, about 100 ng/kg body weight/day to about 10 mg/kg body weight/day, about 100 ng/kg body weight/day to about 1 mg/kg body weight/day, about 100 ng/kg body weight/day to about 100 mg/kg body weight/day, about 100 ng/kg body weight/day to about 10 mg/kg body weight/day, about 100 ng/kg body weight/day to about 1 mg/kg body weight/day, about 1 mg/kg body weight/day to about 100 mg/kg body weight/day, about 1 mg/kg body weight/day to about 10 mg/kg body weight/day, about 1 mg/kg body weight/day to about 100 mg/kg body weight/day, about 1 mg/kg body weight/day to about 10 mg/kg body weight/day, about 10 mg/kg body weight/day to about 100 mg/kg body weight/day, about 10 mg/kg body weight/day to about 10 mg/kg body weight/day, about 10 mg/kg body weight/day to about 1 mg/kg body weight/day, about 10 mg/kg body weight/day to about 100 mg/kg body weight/day, about 100 mg/kg body weight/day to about 100 mg/kg body weight/day, about 100 mg/kg body weight/day to about 10 mg/kg body weight/day, about 100 mg/kg body weight/day to about 1 mg/kg body weight/day, about 1 mg/kg body weight/day to about 100 mg/kg body weight/day, about 1 mg/kg body weight/day to about 10 mg/kg body weight/day, about 10 mg/kg body weight/day to about 100 mg/kg body weight/day.

[00310] In other embodiments, the bispecific antibody is administered at a dose of 500 g to 20 g every three days, or 25 mg/kg body weight every three days.

[00311] In other embodiments, each bispecific antibody is administered in the range of about 10 ng to about 100 ng per individual administration, about 10 ng to about 1 g per individual administration, about 10 ng to about 10 g per individual administration, about 10 ng to about 100 mg per individual administration, about 10 ng to about 1mg per individual administration, about 10 ng to about 10 mg per individual administration, about 10 ng to about 100 mg per individual administration, about 10 ng to about 1000 mg per injection, about 10 ng to about 10,000 mg per individual administration, about 100 ng to about 1 mg per individual administration, about 100 ng to about 10 mg per individual administration, about 100 ng to about 100 mg per individual administration, about 100 ng to about 1mg per individual administration, about 100 ng to about 10 mg per individual administration, about 100 ng to about 100 mg per individual administration, about 100 ng to about 1000 mg per injection, about 100 ng to about 10,000 mg per individual administration, about 1 mg to about 10 mg per individual administration, about 1 mg to about 100 mg per individual administration, about 1 mg to about 1 mg per individual administration, about 1 mg to about 10 mg per individual administration, about 1 mg to about 100 mg per individual administration, about 1 mg to about 1000 mg per injection, about 1 mg to about 10,000 mg per individual administration, about 10 mg to about 100 mg per individual administration, about 10 mg to about 1mg per individual administration, about 10 mg to about 10 mg per individual administration, about 10 mg to about 100 mg per individual administration, about 10 mg to about 1000 mg per injection, about 10 mg to about 10,000 mg per individual administration, about 100 mg to about 1mg per individual administration, about 100 mg to about 10 mg per individual administration, about 100 mg to about 100 mg per individual administration, about 100 mg to about 1000 mg per injection, about 100 mg to about 10,000 mg per individual administration, about 1mg to about 10 mg per individual administration, about 1 mg to about 100 mg per individual administration, about 1mg to about 1000 mg per injection, about 1mg to about 10,000 mg per individual administration, about 10 mg to about 100 mg per individual administration, about 10 mg to about 1000 mg per injection, about 10 mg to about 10,000 mg per individual administration, about 100 mg to about 1000 mg per injection, about 100 mg to about 10,000 mg per individual administration and about 1000 mg to about 10,000 mg per individual administration. The bispecific antibody may be administered daily, every 2, 3, 4, 5, 6 or 7 days, or every 1, 2, 3 or 4 weeks.

[00312] In other particular embodiments, the amount of the bispecific antibody may be administered at a dose of about 0.0006 mg/day, 0.001 mg/day, 0.003 mg/day, 0.006 mg/day,

0.01 mg/day, 0.03 mg/day, 0.06 mg/day, 0.1 mg/day, 0.3 mg/day, 0.6 mg/day, 1 mg/day, 3 mg/day, 6 mg/day, 10 mg/day, 30 mg/day, 60 mg/day, 100 mg/day, 300 mg/day, 600 mg/day, 1000 mg/day, 2000 mg/day, 5000 mg/day or 10,000 mg/day. As expected, the dosage will be dependent on the condition, size, age and condition of the patient.

[00313] In certain embodiments, the coding sequences for a bispecific antibody are incorporated into a suitable expression vector (e.g., viral or non-viral vector) for expressing an effective amount of the bispecific antibody in patient with a cell proliferative disorder. In certain embodiments comprising administration of e.g., one or more recombinant AAV (rAAV) viruses, the pharmaceutical composition may comprise the rAAVs in an amount comprising at least 10^{10} , at least 10^{11} , at least 10^{12} , at least 10^{13} , or at least 10^{14} genome copies (GC) or recombinant viral particles per kg, or any range thereof. In certain embodiments, the pharmaceutical composition comprises an effective amount of the recombinant virus, such as rAAV, in an amount comprising at least 10^{10} , at least 10^{11} , at least 10^{12} , at least 10^{13} , at least 10^{14} , at least 10^{15} genome copies or recombinant viral particles genome copies per subject, or any range thereof.

[00314] Dosages can be tested in several art-accepted animal models suitable for any particular cell proliferative disorder.

[00315] Delivery methodologies may also include the use of polycationic condensed DNA linked or unlinked to killed viruses, ligand linked DNA, liposomes, eukaryotic cell delivery vehicles cells, deposition of photopolymerized hydrogel materials, use of a handheld gene transfer particle gun, ionizing radiation, nucleic charge neutralization or fusion with cell membranes, particle mediated gene transfer and the like.

[00316] In other aspects of this embodiment, a pharmaceutical composition compound disclosed herein reduces the size of a tumor by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%. In yet other aspects of this embodiment, a pharmaceutical composition disclosed herein reduces the size of a tumor from, e.g., about 5% to about 100%, about 10% to about 100%, about 20% to about 100%, about 30% to about 100%, about 40% to about 100%, about 50% to about 100%, about 60% to about 100%, about 70% to about 100%, about 80% to about 100%, about 10% to about 90%, about 20% to about 90%, about 30% to about 90%, about 40% to about 90%, about 50% to about 90%, about 60% to about 90%, about 70% to about 90%, about 10% to about 80%, about 20% to about 80%, about 30% to about 80%, about 40% to about 80%, about 50% to about 80%, or about

60% to about 80%, about 10% to about 70%, about 20% to about 70%, about 30% to about 70%, about 40% to about 70%, or about 50% to about 70%.

[00317] A pharmaceutical composition disclosed herein is in an amount sufficient to allow customary administration to an individual. In aspects of this embodiment, a pharmaceutical composition disclosed herein may be, e.g., at least 5 mg, at least 10 mg, at least 15 mg, at least 20 mg, at least 25 mg, at least 30 mg, at least 35 mg, at least 40 mg, at least 45 mg, at least 50 mg, at least 55 mg, at least 60 mg, at least 65 mg, at least 70 mg, at least 75 mg, at least 80 mg, at least 85 mg, at least 90 mg, at least 95 mg, or at least 100 mg of a pharmaceutical composition. In other aspects of this embodiment, a pharmaceutical composition disclosed herein may be, e.g., at least 5 mg, at least 10 mg, at least 20 mg, at least 25 mg, at least 50 mg, at least 75 mg, at least 100 mg, at least 200 mg, at least 300 mg, at least 400 mg, at least 500 mg, at least 600 mg, at least 700 mg, at least 800 mg, at least 900 mg, at least 1,000 mg, at least 1,100 mg, at least 1,200 mg, at least 1,300 mg, at least 1,400 mg, or at least 1,500 mg of a pharmaceutical composition. In yet other aspects of this embodiment, a pharmaceutical composition disclosed herein may be in the range of, e.g., about 5 mg to about 100 mg, about 10 mg to about 100 mg, about 50 mg to about 150 mg, about 100 mg to about 250 mg, about 150 mg to about 350 mg, about 250 mg to about 500 mg, about 350 mg to about 600 mg, about 500 mg to about 750 mg, about 600 mg to about 900 mg, about 750 mg to about 1,000 mg, about 850 mg to about 1,200 mg, or about 1,000 mg to about 1,500 mg. In still other aspects of this embodiment, a pharmaceutical composition disclosed herein may be in the range of, e.g., about 10 mg to about 250 mg, about 10 mg to about 500 mg, about 10 mg to about 750 mg, about 10 mg to about 1,000 mg, about 10 mg to about 1,500 mg, about 50 mg to about 250 mg, about 50 mg to about 500 mg, about 50 mg to about 750 mg, about 50 mg to about 1,000 mg, about 50 mg to about 1,500 mg, about 100 mg to about 250 mg, about 100 mg to about 500 mg, about 100 mg to about 750 mg, about 100 mg to about 1,000 mg, about 100 mg to about 1,500 mg, about 200 mg to about 500 mg, about 200 mg to about 750 mg, about 200 mg to about 1,000 mg, about 200 mg to about 1,500 mg, about 5 mg to about 1,500 mg, about 5 mg to about 1,000 mg, or about 5 mg to about 250 mg.

[00318] A pharmaceutical composition disclosed herein may comprise a solvent, emulsion or other diluent in an amount sufficient to dissolve a pharmaceutical composition disclosed herein. In other aspects of this embodiment, a pharmaceutical composition disclosed herein may comprise a solvent, emulsion or a diluent in an amount of, e.g., less than about 90% (v/v), less than about 80% (v/v), less than about 70% (v/v), less than about 65% (v/v), less than about 60% (v/v), less than about 55% (v/v), less than about 50% (v/v),

less than about 45% (v/v), less than about 40% (v/v), less than about 35% (v/v), less than about 30% (v/v), less than about 25% (v/v), less than about 20% (v/v), less than about 15% (v/v), less than about 10% (v/v), less than about 5% (v/v), or less than about 1% (v/v). In other aspects of this embodiment, a pharmaceutical composition disclosed herein may comprise a solvent, emulsion or other diluent in an amount in a range of, e.g., about 1% (v/v) to 90% (v/v), about 1% (v/v) to 70% (v/v), about 1% (v/v) to 60% (v/v), about 1% (v/v) to 50% (v/v), about 1% (v/v) to 40% (v/v), about 1% (v/v) to 30% (v/v), about 1% (v/v) to 20% (v/v), about 1% (v/v) to 10% (v/v), about 2% (v/v) to 50% (v/v), about 2% (v/v) to 40% (v/v), about 2% (v/v) to 30% (v/v), about 2% (v/v) to 20% (v/v), about 2% (v/v) to 10% (v/v), about 4% (v/v) to 50% (v/v), about 4% (v/v) to 40% (v/v), about 4% (v/v) to 30% (v/v), about 4% (v/v) to 20% (v/v), about 4% (v/v) to 10% (v/v), about 6% (v/v) to 50% (v/v), about 6% (v/v) to 40% (v/v), about 6% (v/v) to 30% (v/v), about 6% (v/v) to 20% (v/v), about 6% (v/v) to 10% (v/v), about 8% (v/v) to 50% (v/v), about 8% (v/v) to 40% (v/v), about 8% (v/v) to 30% (v/v), about 8% (v/v) to 20% (v/v), about 8% (v/v) to 15% (v/v), or about 8% (v/v) to 12% (v/v).

[00319] The final concentration of a pharmaceutical composition disclosed herein in a pharmaceutical composition disclosed herein may be of any concentration desired. In an aspect of this embodiment, the final concentration of a pharmaceutical composition in a pharmaceutical composition may be a therapeutically effective amount. In other aspects of this embodiment, the final concentration of a pharmaceutical composition in a pharmaceutical composition may be, e.g., at least 0.00001 mg/mL, at least 0.0001 mg/mL, at least 0.001 mg/mL, at least 0.01 mg/mL, at least 0.1 mg/mL, at least 1 mg/mL, at least 10 mg/mL, at least 25 mg/mL, at least 50 mg/mL, at least 100 mg/mL, at least 200 mg/mL or at least 500 mg/mL. In other aspects of this embodiment, the final concentration of a pharmaceutical composition in a pharmaceutical composition may be in a range of, e.g., about 0.00001 mg/mL to about 3,000 mg/mL, about 0.0001 mg/mL to about 3,000 mg/mL, about 0.01 mg/mL to about 3,000 mg/mL, about 0.1 mg/mL to about 3,000 mg/mL, about 1 mg/mL to about 3,000 mg/mL, about 250 mg/mL to about 3,000 mg/mL, about 500 mg/mL to about 3,000 mg/mL, about 750 mg/mL to about 3,000 mg/mL, about 1,000 mg/mL to about 3,000 mg/mL, about 100 mg/mL to about 2,000 mg/mL, about 250 mg/mL to about 2,000 mg/mL, about 500 mg/mL to about 2,000 mg/mL, about 750 mg/mL to about 2,000 mg/mL, about 1,000 mg/mL to about 2,000 mg/mL, about 100 mg/mL to about 1,500 mg/mL, about 250 mg/mL to about 1,500 mg/mL, about 500 mg/mL to about 1,500 mg/mL, about 750 mg/mL to about 1,500 mg/mL, about 1,000 mg/mL to about 1,500 mg/mL, about 100 mg/mL to about 1,200 mg/mL, about 250 mg/mL to about 1,200 mg/mL, about 500 mg/mL to about 1,200 mg/mL, about 750 mg/mL to about 1,200 mg/mL, about 1,000 mg/mL to about 1,200 mg/mL, about 100 mg/mL to about 1,000 mg/mL, about 250 mg/mL to about 1,000 mg/mL,

about 500 mg/mL to about 1,000 mg/mL, about 750 mg/mL to about 1,000 mg/mL, about 100 mg/mL to about 750 mg/mL, about 250 mg/mL to about 750 mg/mL, about 500 mg/mL to about 750 mg/mL, about 100 mg/mL to about 500 mg/mL, about 250 mg/mL to about 500 mg/mL, about 0.00001 mg/mL to about 0.0001 mg/mL, about 0.00001 mg/mL to about 0.001 mg/mL, about 0.00001 mg/mL to about 0.01 mg/mL, about 0.00001 mg/mL to about 0.1 mg/mL, about 0.00001 mg/mL to about 1 mg/mL, about 0.001 mg/mL to about 0.01 mg/mL, about 0.001 mg/mL to about 0.1 mg/mL, about 0.001 mg/mL to about 1 mg/mL, about 0.001 mg/mL to about 10 mg/mL, or about 0.001 mg/mL to about 100 mg/mL.

[00320] Aspects of the present specification disclose, in part, treating an individual suffering from cancer. As used herein, the term "treating," refers to reducing or eliminating in an individual a clinical symptom of cancer; or delaying or preventing in an individual the onset of a clinical symptom of cancer. For example, the term "treating" can mean reducing a symptom of a condition characterized by a cancer, including, but not limited to, tumor size, by, e.g., at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% at least 95%, or at least 100%. The actual symptoms associated with cancer are well known and can be determined by a person of ordinary skill in the art by taking into account factors, including, without limitation, the location of the cancer, the cause of the cancer, the severity of the cancer, and/or the tissue or organ affected by the cancer. Those of skill in the art will know the appropriate symptoms or indicators associated with a specific type of cancer and will know how to determine if an individual is a candidate for treatment as disclosed herein.

[00321] In another aspect, a pharmaceutical composition disclosed herein reduces the severity of a symptom of a disorder associated with a cancer. In aspects of this embodiment, a pharmaceutical composition disclosed herein reduces the severity of a symptom of a disorder associated with a cancer by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%. In other aspects of this embodiment, a pharmaceutical composition disclosed herein reduces the severity of a symptom of a disorder associated with a cancer by, e.g., about 10% to about 100%, about 20% to about 100%, about 30% to about 100%, about 40% to about 100%, about 50% to about 100%, about 60% to about 100%, about 70% to about 100%, about 80% to about 100%, about 10% to about 90%, about 20% to about 90%, about 30% to about 90%, about 40% to about 90%, about 50% to about 90%, about 60% to about 90%, about 70% to about 90%, about 10% to about 80%,

about 20% to about 80%, about 30% to about 80%, about 40% to about 80%, about 50% to about 80%, or about 60% to about 80%, about 10% to about 70%, about 20% to about 70%, about 30% to about 70%, about 40% to about 70%, or about 50% to about 70%.

[00322] In aspects of this embodiment, a therapeutically effective amount of a pharmaceutical composition disclosed herein reduces a symptom associated with cancer by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 100%. In other aspects of this embodiment, a therapeutically effective amount of a pharmaceutical composition disclosed herein reduces a symptom associated with cancer by, e.g., at most 10%, at most 15%, at most 20%, at most 25%, at most 30%, at most 35%, at most 40%, at most 45%, at most 50%, at most 55%, at most 60%, at most 65%, at most 70%, at most 75%, at most 80%, at most 85%, at most 90%, at most 95% or at most 100%. In yet other aspects of this embodiment, a therapeutically effective amount of a pharmaceutical composition disclosed herein reduces a symptom associated with cancer by, e.g., about 10% to about 100%, about 10% to about 90%, about 10% to about 80%, about 10% to about 70%, about 10% to about 60%, about 10% to about 50%, about 10% to about 40%, about 20% to about 100%, about 20% to about 90%, about 20% to about 80%, about 20% to about 70%, about 20% to about 60%, about 20% to about 50%, about 20% to about 40%, about 30% to about 100%, about 30% to about 90%, about 30% to about 80%, about 30% to about 70%, about 30% to about 60%, or about 30% to about 50%.

[00323] In yet other aspects of this embodiment, a therapeutically effective amount of a pharmaceutical composition disclosed herein generally is in the range of about 0.001 mg/kg to about 100 mg/kg and administered, for example, every 3, 5, 7, 10 or 14 days. In aspects of this embodiment, an effective amount of a pharmaceutical composition disclosed herein may be, e.g., at least 0.001 mg/kg, at least 0.01 mg/kg, at least 0.1 mg/kg, at least 1.0 mg/kg, at least 5.0 mg/kg, at least 10 mg/kg, at least 15 mg/kg, at least 20 mg/kg, at least 25 mg/kg, at least 30 mg/kg, at least 35 mg/kg, at least 40 mg/kg, at least 45 mg/kg, or at least 50 mg/kg and administered, for example, every 3, 5, 7, 10 or 14 days. In other aspects of this embodiment, an effective amount of a pharmaceutical composition disclosed herein may be in the range of, e.g., about 0.001 mg/kg to about 10 mg/kg, about 0.001 mg/kg/day to about 15 mg/kg, about 0.001 mg/kg to about 20 mg/kg, about 0.001 mg/kg to about 25 mg/kg, about 0.001 mg/kg to about 30 mg/kg, about 0.001 mg/kg to about 35 mg/kg, about 0.001 mg/kg to about 40 mg/kg, about 0.001 mg/kg to about 45 mg/kg, about 0.001 mg/kg to about 50 mg/kg, about 0.001 mg/kg to about 75 mg/kg, or about 0.001 mg/kg to about 100

mg/kg and administered, for example, every 3, 5, 7, 10 or 14 days. In yet other aspects of this embodiment, an effective amount of a pharmaceutical composition disclosed herein may be in the range of, e.g., about 0.01 mg/kg to about 10 mg/kg, about 0.01 mg/kg to about 15 mg/kg, about 0.01 mg/kg to about 20 mg/kg, about 0.01 mg/kg to about 25 mg/kg, about 0.01 mg/kg to about 30 mg/kg, about 0.01 mg/kg to about 35 mg/kg, about 0.01 mg/kg to about 40 mg/kg, about 0.01 mg/kg to about 45 mg/kg, about 0.01 mg/kg to about 50 mg/kg, about 0.01 mg/kg to about 75 mg/kg, or about 0.01 mg/kg to about 100 mg/kg and administered, for example, every 3, 5, 7, 10 or 14 days. In still other aspects of this embodiment, an effective amount of a pharmaceutical composition disclosed herein may be in the range of, e.g., about 0.1 mg/kg to about 10 mg/kg, about 0.1 mg/kg to about 15 mg/kg, about 0.1 mg/kg to about 20 mg/kg, about 0.1 mg/kg to about 25 mg/kg, about 0.1 mg/kg to about 30 mg/kg, about 0.1 mg/kg to about 35 mg/kg, about 0.1 mg/kg to about 40 mg/kg, about 0.1 mg/kg to about 45 mg/kg, about 0.1 mg/kg to about 50 mg/kg, about 0.1 mg/kg to about 75 mg/kg, or about 0.1 mg/kg to about 100 mg/kg and administered, for example, every 3, 5, 7, 10 or 14 days.

[00324] Dosing can be single dosage or cumulative (serial dosing), and can be readily determined by one skilled in the art. For instance, treatment of a cancer may comprise a one-time administration of an effective dose of a pharmaceutical composition disclosed herein. Alternatively, treatment of a cancer may comprise multiple administrations of an effective dose of a pharmaceutical composition carried out over a range of time periods, such as, e.g., once daily, twice daily, trice daily, once every few days, or once weekly. The timing of administration can vary from individual to individual, depending upon such factors as the severity of an individual's symptoms. For example, an effective dose of a pharmaceutical composition disclosed herein can be administered to an individual once daily for an indefinite period of time, or until the individual no longer requires therapy. A person of ordinary skill in the art will recognize that the condition of the individual can be monitored throughout the course of treatment and that the effective amount of a pharmaceutical composition disclosed herein that is administered can be adjusted accordingly.

[00325] In one embodiment, a cancer therapeutic disclosed herein is capable of reducing the number of cancer cells or tumor size in an individual suffering from a cancer by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95% as compared to a patient not receiving the same treatment. In other aspects of this embodiment, a cancer therapeutic is capable of reducing the number of cancer cells or tumor size in an individual

suffering from a cancer by, e.g., about 10% to about 100%, about 20% to about 100%, about 30% to about 100%, about 40% to about 100%, about 50% to about 100%, about 60% to about 100%, about 70% to about 100%, about 80% to about 100%, about 10% to about 90%, about 20% to about 90%, about 30% to about 90%, about 40% to about 90%, about 50% to about 90%, about 60% to about 90%, about 70% to about 90%, about 10% to about 80%, about 20% to about 80%, about 30% to about 80%, about 40% to about 80%, about 50% to about 80%, or about 60% to about 80%, about 10% to about 70%, about 20% to about 70%, about 30% to about 70%, about 40% to about 70%, or about 50% to about 70% as compared to a patient not receiving the same treatment.

[00326] In a further embodiment, a cancer therapeutic and its derivatives have half-lives of 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, one month, two months, three months, four months or more.

[00327] In an embodiment, the period of administration of a cancer therapeutic is for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, or more. In a further embodiment, a period of during which administration is stopped is for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, or more.

[00328] In aspects of this embodiment, a therapeutically effective amount of a cancer therapeutic disclosed herein reduces or maintains a cancer cell population and/or tumor cell size in an individual by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 100%. In other aspects of this embodiment, a therapeutically effective amount of a cancer therapeutic disclosed herein reduces or maintains a cancer cell population and/or tumor cell size in an individual by, e.g., at most 10%, at most 15%, at most 20%, at most 25%, at most 30%, at most 35%, at most 40%, at most 45%, at most 50%, at most 55%, at most 60%, at most 65%, at most 70%, at most 75%, at most 80%, at most 85%, at most 90%, at most 95% or at most 100%. In yet other aspects of this embodiment, a

therapeutically effective amount of a cancer therapeutic disclosed herein reduces or maintains a cancer cell population and/or tumor cell size in an individual by, e.g., about 10% to about 100%, about 10% to about 90%, about 10% to about 80%, about 10% to about 70%, about 10% to about 60%, about 10% to about 50%, about 10% to about 40%, about 20% to about 100%, about 20% to about 90%, about 20% to about 80%, about 20% to about 70%, about 20% to about 60%, about 20% to about 50%, about 20% to about 40%, about 30% to about 100%, about 30% to about 90%, about 30% to about 80%, about 30% to about 70%, about 30% to about 60%, or about 30% to about 50%.

[00329] A pharmaceutical composition or cancer therapeutic is administered to an individual. An individual is typically a human being, but can be an animal, including, but not limited to, dogs, cats, birds, cattle, horses, sheep, goats, reptiles and other animals, whether domesticated or not. Typically, any individual who is a candidate for treatment is a candidate with some form of cancer, whether the cancer is benign or malignant, a tumor, solid or otherwise, a cancer call not located in a tumor or some other form of cancer. Among the most common types of cancer include, but are not limited to, bladder cancer, breast cancer, colon and rectal cancer, endometrial cancer, kidney cancer, renal cancer, leukemia, lung cancer, melanoma, non-Hodgkins lymphoma, pancreatic cancer, prostate cancer, stomach cancer and thyroid cancer. Pre-operative evaluation typically includes routine history and physical examination in addition to thorough informed consent disclosing all relevant risks and benefits of the procedure.

[00330] In one aspect, a pharmaceutical composition disclosed herein reduces a symptom of a disorder associated with a cancer. In aspects of this embodiment, a pharmaceutical composition disclosed herein reduces a symptom of a disorder associated with a cancer by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%. In other aspects of this embodiment, a pharmaceutical composition disclosed herein reduces a symptom of a disorder associated with a cancer by, e.g., about 10% to about 100%, about 20% to about 100%, about 30% to about 100%, about 40% to about 100%, about 50% to about 100%, about 60% to about 100%, about 70% to about 100%, about 80% to about 100%, about 10% to about 90%, about 20% to about 90%, about 30% to about 90%, about 40% to about 90%, about 50% to about 90%, about 60% to about 90%, about 70% to about 90%, about 10% to about 80%, about 20% to about 80%, about 30% to about 80%, about 40% to about 80%, about 50% to about 80%, or about 60% to about 80%, about 10% to about 70%, about 20% to about 70%, about 30% to about 70%, about 40% to about 70%, or

about 50% to about 70%.

[00331] In another aspect, a pharmaceutical composition disclosed herein reduces the frequency of a symptom of a disorder associated with a cancer incurred over a given time period. In aspects of this embodiment, a pharmaceutical composition disclosed herein reduces the frequency of a symptom of a disorder associated with a cancer incurred over a given time period by, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%. In other aspects of this embodiment, a pharmaceutical composition disclosed herein reduces the frequency of a symptom of a disorder associated with a cancer incurred over a given time period by, e.g., about 10% to about 100%, about 20% to about 100%, about 30% to about 100%, about 40% to about 100%, about 50% to about 100%, about 60% to about 100%, about 70% to about 100%, about 80% to about 100%, about 10% to about 90%, about 20% to about 90%, about 30% to about 90%, about 40% to about 90%, about 50% to about 90%, about 60% to about 90%, about 70% to about 90%, about 10% to about 80%, about 20% to about 80%, about 30% to about 80%, about 40% to about 80%, about 50% to about 80%, or about 60% to about 80%, about 10% to about 70%, about 20% to about 70%, about 30% to about 70%, about 40% to about 70%, or about 50% to about 70%.

Table 1 – DLL3 HC and LC Pairs

Full ab name	VH Seq ID	VL seq ID	HCDR1 Seq ID	HCDR2 Seq ID	HCDR3 Seq ID	LCDR1 Seq ID	LCDR2 Seq ID	LCDR3 SeqID
DLL3.3	72	76	7	14	27	31	40	47
DLL3.4	73	77	1	11	22	32	39	54
DLL3.26	58	78	6	16	24	33	43	49
DLL3.27	65	78	5	16	24	33	43	49
DLL3.1	71	79	2	10	22	32	46	55
DLL3.2	73	79	1	11	22	32	46	55
DLL3.8	67	80	4	12	23	36	44	48
DLL3.9	64	81	3	13	28	32	46	54
DLL3.22	57	82	6	15	25	33	43	51
DLL3.23	59	82	6	16	25	33	43	51

DLL3.24	61	82	6	18	25	33	43	51
DLL3.25	63	82	6	16	25	33	43	51
DLL3.15	56	83	6	15	24	34	43	49
DLL3.5	58	83	6	16	24	34	43	49
DLL3.16	60	83	6	18	24	34	43	49
DLL3.17	62	83	6	16	24	34	43	49
DLL3.18	57	84	6	15	25	37	42	51
DLL3.19	59	84	6	16	25	37	42	51
DLL3.20	61	84	6	18	25	37	42	51
DLL3.21	63	84	6	16	25	37	42	51
DLL3.11	56	85	7	15	24	38	42	49
DLL3.12	58	85	6	16	24	38	42	49
DLL3.13	60	85	6	18	24	38	42	49
DLL3.14	62	85	6	16	24	38	42	49
DLL3.32	70	86	5	16	25	33	43	51
DLL3.33	70	86	5	16	25	33	43	51
DLL3.10	69	87	5	16	24	34	43	49
DLL3.31	69	87	5	16	24	34	43	49
DLL3.29	68	88	5	17	26	34	43	50
DLL3.30	68	88	5	17	26	34	43	50
DLL3.36	68	88	5	17	26	34	43	50
DLL3.34	74	89	8	19	23	35	45	52
DLL3.28	66	90	9	21	29	32	39	54

Table 2 – DLL3–CD3

format	Molecule Name	Seq ID chain1	seq ID chain2	seq ID chain3
DLL3-scFvxCD3-scFv	3D34C	341	239	-
DLL3-scFvxCD3-scFv	3D35C	342	239	-
DLL3-scFvxCD3-scFv	3D36C	346	239	-
DLL3-scFvxCD3-scFv	3D36D	343	239	-
DLL3-	3D36I	347	239	-

scFvxCD3-scFv				
DLL3-scFvxCD3-scFv	3D36K	348	239	-
DLL3-scFvxCD3-scFv	3D37C	345	239	-
DLL3-scFvxCD3-scFv	3D44I	344	239	-
DLL3-Fab/CD3-scFv	3D1	273	290	298
DLL3-Fab/CD3-scFv	3D10	273	292	296
DLL3-Fab/CD3-scFv	3D10B	262	292	296
DLL3-Fab/CD3-scFv	3D10C	263	292	296
DLL3-Fab/CD3-scFv	3D11B	262	286	310
DLL3-Fab/CD3-scFv	3D11C	263	286	310
DLL3-Fab/CD3-scFv	3D12B	262	288	308
DLL3-Fab/CD3-scFv	3D12C	263	288	308
DLL3-Fab/CD3-scFv	3D13B	262	289	306
DLL3-scFvxCD3-scFv/DLL3-Fab	3D34-22C	341	276	302
DLL3-scFvxCD3-scFv/DLL3-Fab	3D35-22C	342	276	302
DLL3-scFvxCD3-scFv/DLL3-Fab	3D36-22C	346	276	302
DLL3-scFvxCD3-scFv/DLL3-Fab	3D37-22C	345	276	302
DLL3-Fab/CD3-scFv	3D13C	263	289	306
DLL3-scFvxCD3-scFv/DLL3-Fab	3D45I	347	276	297
DLL3-Fab/CD3-scFv	3D14B	262	284	312
DLL3-	3D14C	263	284	312

Fab/CD3-scFv				
DLL3-Fab/CD3-scFv	3D15C	263	287	309
DLL3-Fab/CD3-scFv	3D16C	263	288	307
DLL3-Fab/CD3-scFv	3D17C	263	289	305
DLL3-Fab/CD3-scFv	3D18C	263	276	304
DLL3-Fab/CD3-scFv	3D19C	263	274	304
DLL3-Fab/CD3-scFv	3D1B	262	290	298
DLL3-Fab/CD3-scFv	3D1C	263	290	298
DLL3-Fab/CD3-scFv	3D1I	269	290	298
DLL3-Fab/CD3-scFv	3D20C	263	278	304
DLL3-Fab/CD3-scFv	3D21C	263	280	304
DLL3-scFvxCD3-scFv-Fc-Fc	3DBM	Benchmark CD3xDLL3		
DLL3-Fab/CD3-scFv	3D22C	263	276	302
DLL3-Fab/CD3-scFv	3D22D	264	276	302
DLL3-Fab/CD3-scFv	3D22I	269	276	302
DLL3-Fab/CD3-scFv	3D22K	271	276	302
DLL3-Fab/CD3-scFv	3D23C	263	274	302
DLL3-Fab/CD3-scFv	3D24C	263	278	302
DLL3-Fab/CD3-scFv	3D25C	263	280	302
DLL3-Fab/CD3-scFv	3D26C	263	277	303
DLL3-Fab/CD3-scFv	3D27C	263	275	303
DLL3-scFvxCD3-scFv/DLL3-Fab	3D34-16C	341	288	307
DLL3-scFvxCD3-scFv/DLL3-Fab	3D35-16C	342	288	307
DLL3-scFvxCD3-scFv/DLL3-Fab	3D36-16C	346	288	307

DLL3-scFvxCD3-scFv/DLL3-Fab	3D37-16C	345	288	307
DLL3-Fab/CD3-scFv	3D28C	263	279	303
DLL3-Fab/CD3-scFv	3D29C	263	281	303
DLL3-Fab/CD3-scFv	3D30C	263	277	301
DLL3-Fab/CD3-scFv	3D31C	263	275	301
DLL3-Fab/CD3-scFv	3D32C	263	279	301
DLL3-Fab/CD3-scFv	3D33C	263	281	301
DLL3-Fab/CD3-scFv	3D38I	269	283	297
DLL3-scFvxCD3-scFv/DLL3-Fab	3D34-1C	341	290	298
DLL3-scFvxCD3-scFv/DLL3-Fab	3D35-1C	342	290	298
DLL3-scFvxCD3-scFv/DLL3-Fab	3D36-1C	346	290	298
DLL3-scFvxCD3-scFv/DLL3-Fab	3D37-1C	345	290	298
DLL3-Fab/CD3-scFv	3D39I	269	276	297
DLL3-Fab/CD3-scFv	3D4	273	291	295
DLL3-Fab/CD3-scFv	3D40I	269	285	299
DLL3-Fab/CD3-scFv	3D41I	269	282	300
DLL3-Fab/CD3-scFv	3D42I	269	294	313
DLL3-Fab/CD3-scFv	3D43I	269	293	311
DLL3-Fab/CD3-scFv	3D4B	262	291	295
DLL3-Fab/CD3-scFv	3D4C	263	291	295
DLL3-Fab/CD3-scFv	3D4D	264	291	295
DLL3-Fab/CD3-scFv	3D4E	265	291	295

DLL3-Fab/CD3-scFv	3D4F	266	291	295
DLL3-Fab/CD3-scFv	3D4G	267	291	295
DLL3-scFvxCD3-scFv/DLL3-Fab	3D34-4C	341	291	295
DLL3-scFvxCD3-scFv/DLL3-Fab	3D35-4C	342	291	295
DLL3-scFvxCD3-scFv/DLL3-Fab	3D36-4C	346	291	295
DLL3-scFvxCD3-scFv/DLL3-Fab	3D37-4C	345	291	295
DLL3-Fab/CD3-scFv	3D4H	268	291	295
DLL3-Fab/CD3-scFv	3D4I	269	291	295
DLL3-Fab/CD3-scFv	3D4J	270	291	295
DLL3-Fab/CD3-scFv	3D4K	271	291	295
DLL3-Fab/CD3-scFv	3D4L	272	291	295
DLL3-Fab/CD3-scFv	3D7	273	292	298
DLL3-scFvxCD3-scFv/DLL3-Fab	3D34-7C	341	292	298

Table 3 – DLL3–CD28

format	Molecule Name	Seq ID chain 1	Seq Id chain 2	seq id chain 3
CD28-Fab/DLL3-scFv	28D1	425	426	431
CD28-Fab/DLL3-scFv	28D2	425	426	434
CD28-Fab/DLL3-scFv	28D3	425	426	432

CD28-Fab/DLL3-scFv	28D4	425	426	433
CD28-scFv/DLL3-Fab	28D9	427	290	298
CD28-scFv/DLL3-Fab	28D10	427	291	295
CD28-scFv/DLL3-Fab	28D11	427	292	298
CD28-scFv/DLL3-Fab	28D12	427	292	296
CD28-scFv/DLL3-Fab	28D13	428	291	295
CD28-scFv/DLL3-Fab	28D14	429	291	295
CD28-scFv/DLL3-Fab	28D15	430	291	295
CD28-scFv/DLL3-Fab	28D16	430	292	296
CD28-scFv/DLL3-Fab	28D17	430	276	302
CD28-scFv/DLL3-Fab	28D18	430	290	298
CD28-scFv/DLL3-Fab	28D19	430	276	297

Table 4 – DLL4-41BB

format	Molecule Name	Seq ID chain1	seq ID chain2	seq Id chain3
4-1BB-Fab/DLL3-scFv	4D1	437	438	431
4-1BB-Fab/DLL3-scFv	4D2	437	438	434
4-1BB-Fab/DLL3-scFv	4D3	437	438	432
4-1BB-Fab/DLL3-scFv	4D4	437	438	433

4-1BB-scFv/DLL3-Fab	4D5	441	291	295
4-1BB-scFv/DLL3-Fab	4D6	442	291	295
4-1BB-scFv/DLL3-Fab	4D7	445	291	295
4-1BB-Fab/DLL3-scFv	4D8	437	438	466
4-1BB-Fab/DLL3-scFv	4D9	437	438	467
4-1BB-scFv/DLL3-Fab	4D10	446	291	295
4-1BB-scFv/DLL3-Fab	4D11	447	291	295
4-1BB-scFv/DLL3-Fab	4D12	448	291	295
4-1BB-scFv/DLL3-Fab	4D13	444	291	295
4-1BB-scFv/DLL3-Fab	4D14	443	290	298
DLL3-scFv/4-1BB-Fab	4D15	432	439	440
DLL3scFv-41BBscFv-fc x 41BBFab-fc	4D16	468	439	440
4-1BBscFv-41BBscFv-Fc x DLL3Fab-Fc	4D17	469	291	295
41BBFab-Fc-DLL3scFv	4D18	470	472	440
41BBFab-Fc-DLL3scFv	4D19	471	473	298

Table 5 – MUC17 VH and VL pairs

AB Name	VH Seq	VL Seq	HCDR1 Seq ID	HCDR2 Seq ID	HCDR3 Seq ID	LCDR1 Seq ID	LCDR2 Seq ID	LCDR3 Seq ID

	ID	ID						
Muc17.7	146	149	92	106	111	118	121	124
Muc17.21	146	148	92	106	111	118	121	124
Muc17.22	146	150	92	106	111	118	121	124
Muc17.23	146	169	92	106	111	118	121	124
Muc17.24	146	147	92	106	111	118	121	126
Muc17.2	139	154	93	105	108	116	119	123
Muc17.1	127	166	94	103	108	116	119	122
Muc17.10	127	164	94	103	108	116	119	122
Muc17.11	127	162	94	103	108	116	119	122
muc17.12	127	165	94	103	108	116	119	122
Muc17.13	127	161	94	103	108	116	119	122
Muc17.14	127	160	94	103	108	116	119	122
Muc17.25	140	163	94	103	108	116	119	122
Muc17.26	140	160	94	103	108	116	119	122
Muc17.27	140	153	94	103	108	116	119	122
Muc17.28	140	155	94	103	108	116	119	122
Muc17.29	129	163	94	103	108	116	119	122
Muc17.30	129	160	94	103	108	116	119	122
Muc17.31	129	153	94	103	108	116	119	122
Muc17.8	127	153	94	107	108	116	119	122
Muc17.9	127	163	94	103	108	116	119	122
Muc17.3	141	156	95	104	112	117	120	123
Muc17.15	145	159	97	101	109	115	119	125
Muc17.16	145	152	97	101	109	115	119	125
Muc17.17	128	152	96	99	109	115	119	125
Muc17.18	145	151	97	101	109	114	119	125
Muc17.19	145	167	97	101	109	114	119	125
Muc17.31	136	168	98	101	109	115	119	125
Muc17.32	135	168	97	101	109	115	119	125
Muc17.33	135	159	97	101	109	115	119	125
Muc17.34	135	152	97	101	109	115	119	125
Muc17.35	133	168	97	101	109	115	119	125
Muc17.20	131	157	97	100	110	115	119	125
Muc17.36	134	168	97	101	109	115	119	125
Muc17.37	132	168	97	101	109	115	119	125
Muc17.38	137	168	97	101	109	115	119	125
Muc17.39	144	152	97	99	109	115	119	125
Muc17.4	145	168	97	101	109	115	119	125
Muc17.40	144	168	97	99	109	115	119	125
Muc17.41	144	167	97	99	109	114	119	125
Muc17.42	143	152	96	101	109	115	119	125
Muc17.43	143	168	96	101	109	115	119	125
Muc17.44	143	167	96	101	109	114	119	125
Muc17.45	130	159	97	101	109	115	119	125
Muc17.46	142	167	96	99	109	114	119	125
Muc17.47	142	168	96	99	109	115	119	125
Muc17.48	136	159	97	101	109	115	119	125
Muc17.5	131	159	97	100	110	115	119	125
Muc17.49	136	152	97	101	109	115	119	125

Table 6 – MUC17 VH x CD3

format	Molecule Name	SEQ ID Chain1	SEQ ID Chain2	SEQ ID Chain3
Muc17-Fab/CD3-scFv	3M23C	263	379	387
Muc17-Fab/CD3-scFv	3M24C	263	379	388
Muc17-Fab/CD3-scFv	3M25C	263	372	390
Muc17-Fab/CD3-scFv	3M26C	263	372	389
Muc17-Fab/CD3-scFv	3M27C	263	377	390
Muc17-Fab/CD3-scFv	3M28C	263	371	390
Muc17-Fab/CD3-scFv	3M29C	263	368	382
Muc17-scFvxCD3-scFv-scfc	3M2C2	352		
Muc17-Fab/CD3-scFv	3M30C	263	368	383
Muc17-Fab/CD3-scFv	3M31C	263	368	385
Muc17-Fab/CD3-scFv	3M32C	263	368	384
Muc17-Fab/CD3-scFv	3M33C	263	368	381
Muc17-Fab/CD3-scFv	3M34C	263	370	394
Muc17-Fab/CD3-scFv	3M35C	263	370	391
Muc17-Fab/CD3-scFv	3M36C	263	370	387
Muc17-Fab/CD3-scFv	3M37C	263	369	394
Muc17-Fab/CD3-scFv	3M38C	263	369	391
Muc17-Fab/CD3-scFv	3M39C	263	369	387
Muc17-Fab/CD3-scFv	3M40C	263	379	394
Muc17-Fab/CD3-scFv	3M41C	263	379	391
Muc17-Fab/CD3-scFv	3M42C	263	379	387
Muc17-Fab/CD3-scFv	3M43C	263	376	399
Muc17-Fab/CD3-scFv	3M44C	263	376	386
Muc17-Fab/CD3-scFv	3M45C	263	376	390
Muc17-Fab/CD3-scFv	3M46C	263	380	399
Muc17-Fab/CD3-	3M47C	263	380	386

scFv				
Muc17-Fab/CD3-scFv	3M48C	263	380	390
Muc17-Fab/CD3-scFv	3M49C	263	377	399
Muc17-Fab/CD3-scFv	3M50C	263	377	386
Muc17-Fab/CD3-scFv	3M51C	263	377	390
Muc17-Fab/CD3-scFv	3M52C	263	369	397
Muc17-Fab/CD3-scFv	3M53C	263	369	392
Muc17-Fab/CD3-scFv	3M54C	263	369	396
Muc17-Fab/CD3-scFv	3M55C	263	369	398
Muc17-scFv/CD3-Fab	3M55D	264	369	400
Muc17-scFv/CD3-Fab	3M55I	269	369	400
Muc17-scFv/CD3-Fab	3M55K	271	369	400
Muc17-Fab/CD3-scFv	3M56C	263	374	399
Muc17-Fab/CD3-scFv	3M57C	263	375	399
Muc17-Fab/CD3-scFv	3M58C	263	373	399
Muc17-Fab/CD3-scFv	3M59C	263	378	399
Muc17-Fab/CD3-scFv	3M60C	263	369	393
Muc17-scFvxCD3-scFv	3M61C	350	239	
Muc17-scFvxCD3-scFv	3M62C	363	239	
Muc17-scFvxCD3-scFv	3M62D	362	239	
Muc17-scFvxCD3-scFv	3M62I	364	239	
Muc17-scFvxCD3-scFv	3M62K	365	239	
Muc17-scFvxCD3-scFv/Muc17-Fab	3M63C	350	380	399
Muc17-scFvxCD3-scFv/Muc17-Fab	3M64C	363	369	398
Muc17-scFv/CD3-Fab	3M65C	366	263	400
Muc17-scFv/CD3-Fab	3M66C	367	263	400
Muc17-scFvxCD3-scFv	3M67I	349	239	
Muc17-scFvxCD3-	3M68I	354	239	

scFv				
Muc17-scFvxCD3-scFv-scfc	3M8B7	351		
1MU32scFv – CD3scFv – Fc		361	239	
1MU8AscFv – CD3scFv – Fc		353	239	
1MU32scFv(Y32F) – CD3scFv – Fc		360	239	
1MU32scFv(M34L) – CD3scFv – Fc		357	239	
1MU32scFv(T58S) – CD3scFv – Fc		359	239	

Table 7 – MUC17 x CD28

format	Molecule Name	SeqID Chain1	SeqID Chain2	SeqID Chain3
Muc17-Fab/CD28-scFv	28M1	427	368	384
Muc17-Fab/CD28-scFv	28M2	427	380	399
Muc17-Fab/CD28-scFv	28M3	427	369	398
Muc17-Fab/CD28-scFv	28M4	430	368	384
Muc17-Fab/CD28-scFv	28M5	430	380	399
Muc17-Fab/CD28-scFv	28M6	430	369	398

Table 8 – MUC17 x 41BB

format	Molecule Name	Seq ID chain1	seq ID chain2	seq Id chain3
Muc17-scfv/4-1BB-Fab	4M1	366	437	438
Muc17-scfv/4-1BB-Fab	4M2	367	437	438
Muc17-scfv/4-1BB-Fab	4M3	474	437	438
4-1BB-scfv/Muc17-Fab	4M4	451	369	398
4-1BB-	4M5	545	369	398

scFv/Muc17-Fab				
4-1BB-scFv/Muc17-Fab	4M6	450	369	398
4-1BB-scFv/Muc17-Fab	4M7	451	380	399
4-1BB-scFv/Muc17-Fab	4M8	452	380	399
4-1BB-scFv/Muc17-Fab	4M9	453	369	398
4-1BB-scFv/Muc17-Fab	4M10	447	369	398
4-1BB-scFv/Muc17-Fab	4M11	448	369	398
4-1BB-scFv/Muc17-Fab	4M12	444	369	398
4-1BB-scFv/Muc17-Fab	4M13	443	369	398
4-1BB-scFv/Muc17-Fab	4M14	452	380	399
4-1BB-scFv/Muc17-Fab	4M15	453	380	399

Table 9 – CLDN VH and HL pairs

AB Name	VH SeqID	VL SeqID	HCDR1 Seq ID	HCDR2 Seq ID	HCDR3 SeqID	LCDR1 Seq ID	LCDR2 Seq ID	LCDR3 SeqID
CLDN182.1	203	208	175	180	186	188	191	195
CLDN182.2	202	207	174	179	187	188	191	194
CLDN182.3	198	209	170	181	185	188	191	196
CLDN182.7	198	207	170	181	185	188	191	196
cldn18.2.4	201	212	173	176	182	190	191	193
CLDN18.8	201	211	173	176	182	190	191	193
CLDN182.5	204	210	171	177	184	189	191	192
CLDN182.6	206	206	172	178	183	188	191	192
CLDN182.9	206	213	172	178	183	188	191	192
CLDN182.10	200	212	173	176	182	190	191	193
CLDN182.11	200	211	173	176	182	190	191	193
CLDN182.12	197	209	170	181	185	188	191	196
CLDN182.13	197	207	170	181	185	188	191	196
CLDN182.14	199	207	174	179	187	188	191	194
CLDN182.15	205	206	172	178	183	188	191	192
CLDN182.16	205	213	172	178	183	188	191	192

Table 10 – CLDN x CD3

format	Molecule Name	SEQID Chain 1	SEQID Chain 2	SEQID Chain 3
Cldn-Fab/CD3-scFv	3C17C	263	407	414
Cldn-Fab/CD3-scFv	3C18C	263	405	418
Cldn-Fab/CD3-scFv	3C19C	263	405	417
Cldn-Fab/CD3-scFv	3C20C	263	404	418
Cldn-Fab/CD3-scFv	3C21C	263	404	417
Cldn-Fab/CD3-scFv	3C22C	263	402	415
Cldn-Fab/CD3-scFv	3C23C	263	402	411
Cldn-Fab/CD3-scFv	3C24C	263	401	415
Cldn-Fab/CD3-scFv	3C25C	263	401	411
Cldn-Fab/CD3-scFv	3C26C	263	408	416
Cldn-Fab/CD3-scFv	3C27C	263	406	413
Cldn-Fab/CD3-scFv	3C28C	263	403	413
Cldn-Fab/CD3-scFv	3C29C	263	410	412
Cldn-Fab/CD3-scFv	3C30C	263	410	419
Cldn-Fab/CD3-scFv	3C31C	263	409	412
Cldn-Fab/CD3-scFv	3C32C	263	409	419
Cldn-	3C18D	264	405	418

Fab/CD3-scFv				
Cldn-Fab/CD3-scFv	3C18I	269	405	418
Cldn-Fab/CD3-scFv	3C18K	271	405	418
Cldn-Fab/CD3-scFv	3C22D	264	402	415
Cldn-Fab/CD3-scFv	3C22I	269	402	415
Cldn-Fab/CD3-scFv	3C22K	271	402	415
Cldn-Fab/CD3-scFv	3C26D	264	408	416
Cldn-Fab/CD3-scFv	3C26I	269	408	416
Cldn-Fab/CD3-scFv	3C26K	271	408	416
Cldn-Fab/CD3-scFv	3C27D	264	406	413
Cldn-Fab/CD3-scFv	3C27I	269	406	413
Cldn-Fab/CD3-scFv	3C27K	271	406	413
CLDN-scFvxCD3-scFv-scfc	3CBM			

Table 11 – CLDN x CD28

format	Molecule Name	SeqID Chain1	SeqID Chain2	SeqID Chain3
Cldn-Fab/CD28-scFv	28C1	427	405	418
Cldn-Fab/CD28-scFv	28C2	427	402	415
Cldn-Fab/CD28-scFv	28C3	427	408	416
Cldn-Fab/CD28-	28C4	427	406	413

scFv				
Cldn-Fab/CD28-scFv	28C5	430	405	418
Cldn-Fab/CD28-scFv	28C6	430	402	415
Cldn-Fab/CD28-scFv	28C7	430	408	416
Cldn-Fab/CD28-scFv	28C8	430	406	413
Cldn-Fab/CD28-scFv	28C9	435	408	416
Cldn-Fab/CD28-scFv	28C10	436	408	416

Table 12 – CLDN x 41BB

format	Molecule Name	SeqID chain 1	SeqID chain 2	SeqID chain 3
Cldn-scfv/4-1BB-Fab	4C1	475	437	438
Cldn-scfv/4-1BB-Fab	4C2	476	437	438
Cldn-scfv/4-1BB-Fab	4C3	477	437	438
Cldn-scfv/4-1BB-Fab	4C4	478	437	438
Cldn-Fab/4-1BB-scFv	4C5	451	405	418
Cldn-Fab/4-1BB-scFv	4C6	454	405	418
Cldn-Fab/4-1BB-scFv	4C7	451	408	416
Cldn-Fab/4-1BB-scFv	4C8	459	408	416
Cldn-Fab/4-1BB-scFv	4C9	479	408	416
Cldn-Fab/4-1BB-scFv	4C10	464	408	416

Cldn-Fab/4-1BB-scFv	4C11	460	408	416
Cldn-Fab/4-1BB-scFv	4C12	463	408	416
Cldn-Fab/4-1BB-scFv	4C13	465	408	416
Cldn-Fab/4-1BB-scFv	4C14	461	408	416
Cldn-Fab/4-1BB-scFv	4C15	454	408	416
Cldn-Fab/4-1BB-scFv	4C16	457	408	416
Cldn-Fab/4-1BB-scFv	4C17	455	408	416
Cldn-Fab/4-1BB-scFv	4C18	458	408	416
Cldn-Fab/4-1BB-scFv	4C19	456	408	416

EXAMPLES

[00332] The compositions and methods described herein will be further understood by reference to the following examples, which are intended to be purely exemplary. The compositions and methods described herein are not limited in scope by the exemplified embodiments, which are intended as illustrations of single aspects only. Any methods that are functionally equivalent are within the scope of the invention. Various modifications of the compositions and methods described herein in addition to those expressly described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications fall within the scope of the invention.

EXAMPLE 1

Humanized anti-DLL3 antibodies binding to human and cynomolgus DLL3 expressing CHO cells

[00333] To evaluate the ability of anti-DLL3 antibodies to bind, human serial dilutions of the anti-DLL3 antibodies were added to CHO-K1 cells (20,000 cells/well) over-expressing human or cyno DLL3. The mixtures were incubated at 4°C for 20 minutes, washed 3 times, and stained with the secondary antibody, PE labeled F(ab')₂-Goat anti-human IgG Fc (Thermo H10104) at 4°C for 20 minutes. Cells were washed and resuspended in 7-Amino-Actinomycin D (7-AAD) solution and fixed in 10% neutral buffered formalin solution for 15 minutes before analysis with the iQue Intellicyt system. FIG. 3A is a graph of the concentration (nM) versus the mean fluorescence intensity.

[00334] Four humanized antibodies were used in this example (DLL3.1, DLL3.2, DLL3.3, DLL3.4). The experiment was repeated with cyno DLL3 expressing CHO cells. FIG. 3B is also a graph of the concentration (nM) versus the mean fluorescence intensity.

EXAMPLE 2

Anti-DLL3scfv-Fc binding to huDLL3 expressing CHO cells

[00335] The experiment was repeated to evaluate the ability of anti-DLL3scfv-Fc antibody fragment to bind human DLL3. FIG. 4 is a graph of the concentration (nM) of the molecules versus the mean fluorescence intensity for binding to the cells. Six antibody fragments were used in this example (DLL3.1 VH-VL, DLL3.2 VH-VL, DLL3.3 VH-VL, DLL3.4 VH-VL, DLL3.1 VL-VH and DLL3.4 VL-VH). All of the molecules bind DLL3 expressing cells in the scfv-Fc format.

EXAMPLE 3

DLL3Fab-Fc x CD3scfv-Fc mediated killing of DLL3 expressing CHO cells by human PBMC cells

[00336] Cell death or cytotoxicity was evaluated by the quantification by plasma membrane damage by measuring lactate dehydrogenase (LDH) released from damaged cells. Cells were collected (adherent and suspension) and re-suspended with assay medium (e.g., medium containing 10% serum). Peripheral blood mononuclear cells (PBMCs) and target cells, in an effector to target ratio of 10:1, were applied to a 96-well plate and cultured in 200µl assay medium containing the antibody formulation in triplicate wells. The cells were placed in an incubator (5 % CO₂, 90 % humidity, 37°C). The cells were then centrifuged at 250 x g for 10 min. 100µl supernatant plus 100µl LDH assay reagent were transferred into corresponding wells of an optically clear 96-well plate and incubated for up to 30 min at room

temperature. The absorbance of all samples was measured at 490-500 nm using a microtiter plate reader.

[00337] Cytotoxicity of CHO cells expressing DLL3 was measured by the release of lactate dehydrogenase (LDH). FIG. 5 is a graph of the concentration (nM) of the molecules versus the percent of maximum killing of the DLL3-CHO cells by the PBMCs. It demonstrates the DLL3 x CD3 bispecific molecules 3D1C, 3D4C, 3D7C, 3D22C and 3D32C are able to stimulate the killing of the DLL3-CHO cells by human PBMC cells.

EXAMPLE 4

DLL3 Fab-Fc x CD3scfv-Fc mediated activation of human T-cells in the presence of DLL3 expressing CHO cells

[00338] T cell activation in the presence of CHO cells expressing DLL3 or NCI-H82 tumor cells and the DLL3 x CD3 bispecific molecules was measured by the increase in cell surface CD25. Cells were collected from the cultures described in Example 3, washed 1x with PBS buffer containing BSA, and co-stained with anti-CD3 and anti-CD25 antibodies for 30 minutes. Cells were then washed 1x with PBS-BSA buffer and analyzed using a flow cytometer. FIG. 6 is a graph of the concentration (nM) versus the CD25 Mean Fluorescence Intensity (MFI) of the CD3 positive population showing DLL3 x CD3 bispecific molecules 3D1C, 3D4C, 3D7C, 3D22C and 3D32C activate T cells when in the presence of CHO cells expressing DLL3.

EXAMPLE 5

DLL3scfv-CD3scfv-Fc x Fc mediated killing of DLL3 expressing CHO cells by human T cells

[00339] Cytotoxicity of CHO cells expressing DLL3 was measured by the release of lactate dehydrogenase (LDH), as described in Example 3. FIG. 7 is a graph of the concentration (nM) of the molecules versus the percent of maximum killing of the DLL3-CHO cells, showing bispecific molecules 3D34C, 3D36C, 3D35C and 3D37C stimulate PBMC killing of CHO cells expressing DLL3.

EXAMPLE 6

DLL3scfv-CD3scfv-Fc x Fc mediated activation of human T-cells in the presence of DLL3 expressing CHO cells

[00340] T cell activation in the presence of CHO cells expressing DLL3 and the DLL3 x CD3 bispecific molecules was measured by the increase in cell surface CD25, as described in Example 4. FIG. 8 is a graph of the concentration (nM) of the molecules versus the CD25 MFI showing bispecific molecules 3D34C, 3D36C, 3D35C and 3D37C stimulate T cells in the presence of CHO cells expressing DLL3

EXAMPLE 7

DLL3Fab-Fc x DLL3scfv-CD3scfv-Fc mediated killing of DLL3 expressing NCI-H82 cells by human T cells

[00341] Cytotoxicity of NCI-H82 cells expressing DLL3 was measured by the release of lactate dehydrogenase (LDH), as described in Example 3. FIG. 9A – 9C are graphs of the concentration (nM) of the molecules versus the percent of maximum killing of the NCI-H82 cells by PBMCs. FIG. 9A shows bispecific molecules 3D36-1C, 3D36-4C, 3D36-7C and 3D36-10C stimulate killing of NCI-H82 cells by PBMCs. FIG. 9B shows bispecific molecules 3D34-1C, 3D34-4C, 3D34-7C and 3D34-10C stimulate killing of NCI-H82 cells by PBMCs. FIG. 9C shows bispecific molecules 3D37-1C, 3D37-4C, 3D37-7C and 3D37-10C stimulate killing of NCI-H82 cells by PBMCs.

EXAMPLE 8

Killing of DLL3 expressing NCI-H82 cell with human PBMC cells and anti-CD3 variant molecules of DLL3Fab-Fc x CD3scfv-Fc and DLL3scfv-CD3scfv-Fc

[00342] Cytotoxicity of NCI-H82 cells expressing DLL3 was measured by the release of lactate dehydrogenase (LDH), as described in Example 3. FIG. 10A and 10B are graphs of the concentration (nM) of the molecules versus the percent of maximum killing of the NCI-H82 cells by PBMCs. FIG. 10A shows CD3 variants C, D, I and K in the 3D22 molecule configuration have similar activities. FIG. 10B shows CD3 variants C, D, I and K in the 3D36 molecule configuration have similar activities.

EXAMPLE 9

DLL3scfv-Fc x CD28Fab-Fc in combination with DLL3scfv-CD3scfv-scFc; activation of PBMC cells to express IL-2 when cultured with DLL3 expressing NCI-H82 cells

[00343] Human PBMC were cultured together with NCI-H82 cells and stimulated with 10pM of DLL3 x CD3 bispecific molecules and DLL3 x CD28 bispecific molecules, 28D1-28D8. After 48 hours of culture, T cell activation was measured as an increase in IL-2

secreted into the medium and an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA. The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50uL of mouse anti-human IL-2 capture antibody at a concentration of 2µg/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200uL PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50uL of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50uL of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5µg/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). FIG. 11A – 11F are graphs showing the concentration (nM) of the CD28 x DLL3 bispecific molecules versus the level of secreted IL-2, as absorbance at 650nm from the IL-2 ELISA. FIG. 11A shows the scDLL3-CD3-Fc (aka 3DBM) bispecific does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D1, 28D2, 28D3, or 28D4, are also present. FIG. 11B shows the scDLL3-CD3-Fc bispecific does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D5, 28D6, 28D7, or 28D8, are also present. FIG. 11C shows the DLL3-CD3 bispecific 3D36C does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D1, 28D2, 28D3, or 28D4, are also present. FIG. 11D shows the DLL3-CD3 bispecific 3D36C does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D5, 28D6, 28D7, or 28D8, are also present. FIG. 11E shows the DLL3-CD3 bispecific 3D22C does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D1, 28D2, 28D3, or 28D4, are also present. FIG. 11F shows the DLL3-CD3 bispecific 3D22C does not stimulate T cells to secrete IL-2 unless the DLL3 x CD28 bispecific molecules, 28D5, 28D6, 28D7, or 28D8, are also present.

EXAMPLE 10

HPLC-size exclusion chromatography analysis of HEK293 transiently expressed and Protein A purified bispecific molecules using various CD3 affinity variants

[00344] FIG. 12 is a table showing the size exclusion data from the analysis of DLL3 x CD3 bispecific molecules of the Scfv-fc x Fab-Fc configuration utilizing affinity variants of the CD3 scfv. All of the variants exhibit high percentages of the desired main peak and low levels of high molecular weight (HMW) material and low molecular weight material (LMW).

EXAMPLE 11

Killing of NCI-H82 tumor cells of PBMCs with variants of 3D22I

[00345] Cytotoxicity of NCI-H82 cells expressing DLL3 was measured by the release of lactate dehydrogenase (LDH), as described in Example 3. FIG. 13 is a graph of the concentration (nM) of the molecules versus the percent of maximum killing of the NCI-H82 cells by PBMCs. The bispecific molecule 3D22I and its variants, 3D38I, 3D39I, 3D40I and 3D41I, have varying levels of killing, with 3D38I and 3D39I retaining similar abilities to stimulate the killing of NCI-H82 cells by PBMCs.

EXAMPLE 12**Expression of CD25 by PBMCs when stimulated with variants of 3D22I in the presence of NCI-H82 tumor cells**

[00346] The expression of CD25 by PBMCs when stimulated in the presence of NCI-H82 tumor cells was measured with variants of 3D22I. FIG. 14 is a graph of the concentration (nM) of the molecules versus the CD25 MFI on CD3+ T cells from the PBMCs. 3D22I and its variants, 3D38I, 3D39I, 3D40I and 3D41I have varying levels of T cell activation as exemplified by increased CD25 MFI, with 3D38I and 3D39I retaining similar abilities to stimulate the killing of NCI-H82 cells by PBMCs.

EXAMPLE 13**DLL3 scfv x CD3scfv x DLL3 Fab variant 3D45I more potently stimulates killing of NCI-H82 cells by PBMCs than 3D39I**

[00347] FIG. 15 demonstrates the variant 3D45I potently stimulates killing of NCI-H82 cells by PBMCs. Similarly, FIG. 16 demonstrates the variant 3D45I stimulates expression of CD25 by CD3+ T cells in the presence of NCI-H82 cells.

EXAMPLE 14**CD28scfv-Fc x DLL3Fab-Fc PBMC cells to secrete IL-2 better than 3DBM alone**

[00348] Bispecific molecules (CD28scfv-Fc x DLL3Fab-Fc), 28D9, 28D10, 28D11, and 28D12, in combination with 50M of CD3-DLL3 benchmark, 3DBM, were shown to activate PBMC cells to secrete IL-2. 3DBM alone does not stimulate the secretion of IL-2. FIG. 17 is a graph of the concentration (nM) of the bispecific DLL3 x CD28 molecules and IL-2 levels

as determined by ELISA and shown as absorbance 650nm from the IL-2 ELISA.

EXAMPLE 15

CD28-Scfv-Fc (C50S) x DLL3-Fab-Fc variants 28D13 and 28D15, with the free cysteine in the anti-CD28 Scfv engineered out, induce IL-2 secretion by PBMCs similarly to the parental molecule, 28D10, when combined with 50pM benchmark, 3DBM in the presence of NCI-H82 cells

[00349] Bispecific molecules, 28D13 (C50G), 28D14 (C50A) and 28D15 (C50S), with the free cysteine in the anti-CD28 Scfv engineered out, induce IL-2 secretion by PBMCs similarly to the parental molecule, 28D10, when combined with 50pM benchmark, 3DBM in the presence of NCI-H82 cells. FIG. 18 is a graph of the concentration (nM) of the molecules versus the Absorbance at 650nm from the IL-2 ELISA.

EXAMPLE 16

4-1BB Fab-Fc x DLL3scfv-Fc bispecific 4D3 increases IFNgamma secretion as well as Urelumab when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule

[00350] Bispecific molecule 4D3 (4-1BB Fab-Fc x DLL3scfv-Fc) was shown to increase IFNgamma secretion when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule. FIG. 19A is a graph of concentration (nM) of Urelumab versus Absorbance at 650 nm from the ELISA to measure IFNgamma levels over time in culture. FIG. 19B demonstrates bispecific molecule 4D3 stimulates the secretion of IFNgamma to similar levels over time as compared to Urelumab.

EXAMPLE 17

MUC17xCD3 Bispecific Molecules bind Muc17-CHOK1 and ASPC1 cells

[00351] Seven humanized antibodies, 1MU11A, 1MU32A, 1MU36A, 1MU16A, 1MU37A, 1MU43A, and 1MU47A, were assessed for the ability to bind to CHO-K1 cells expressing the membrane proximal fragment of MUC17.

[00352] To evaluate the ability of anti-MUC17 antibodies to bind cell expressed MUC17, serial dilutions of the anti-MUC17 antibodies were added to the MUC17 expressing CHO-K1

cells at a concentration of 20,000 cells/well. The antibody:cell mixtures were incubated at 4°C for 20 minutes, washed 3 times, and stained with the secondary antibody, PE labeled F(ab')₂-Goat anti-human IgG Fc (Thermo H10104) at 4°C for 20 minutes. Cells were washed and resuspended in 7-Amino-Actinomycin D (7-AAD) solution and fixed in 10% neutral buffered formalin solution for 15 minutes before analysis with the iQue Intellicyt system. FIG. 23 is a graph of the concentration (nM) versus the mean fluorescence intensity (MFI) of binding to MUC17-CHO cells.

[00353] The experiment was repeated with APSC1 cells, which endogenously express full length human MUC17. FIG. 24 shows a graph of the concentration (nM) versus the mean fluorescence intensity (MFI) for the antibodies binding to the ASPC1 cells.

EXAMPLE 18

MUC17xCD3 bispecific molecules 3M55C, 3M46C, and 3M32C Kill Muc17 expressing CHO cells with human PBMCs

[00354] The experiment was conducted to evaluate the ability of human peripheral mononuclear (PBMCs) effector cells to kill Muc17 expressing CHO target cells when stimulated by MUC17xCD3 bispecific molecules. Cell cytotoxicity was determined as the amount of lactate dehydrogenase (LDH) released from damaged cells as a percent of the total LDH release with 1% Triton-X (Max Killing) added to the cell mixtures at time 0. For the cytotoxicity assays, target (MUC17-CHO or ASPC1) and effector cells (human PBMCs) were suspended in 200ul of medium containing 10% serum at an effector to target ratio of 10:1, in a 96-well plate. Dilutions of the bispecific molecules were added to the cultures in triplicate. The 96-well plates were cultured at 37°C for 48 hours. The cells were then centrifuged at 250 x g for 10 min, and 100ul of the supernatant plus were transferred into corresponding wells of an optically clear 96-well plate containing 100ul LDH assay reagent per well. The plates were then incubated for up to 30 min at room temperature. The absorbance of all samples was measured at 490-500 nm using a microtiter plate reader.

[00355] FIG. 25 is a graph of the concentration (nM) of bispecific molecules 3M32C, 3M46C, 3M55C versus the percent of maximal killing of the MUC17-CHO cells (% Max Killing) by PBMCs, showing various potencies for killing.

EXAMPLE 19

PBMC killing of ASPC1 cells with MUC17xCD3 bispecific molecules of various formats of antibody 1MU32A

[00356] MUC17xCD3 bispecific molecules derived from anti-MUC17 antibody 1MU32A were assessed for their ability to stimulate PBMC cells to become activated and to kill ASPC1 cells. The three formats assessed were scfv-Fc + Fab-Fc (3M46C and 3M66C), scfv-scfv-Fc + Fab-Fc (3M64C), and scfv-scfv-Fc (3M62C). Cell killing was assessed as described in Example 18. Assessment of CD25 expression on CD3+ T cells within PBMC effector cell population was performed on the remaining cells from the cultures assessed for LDH release. The cells were collected, washed one time with PBS buffer containing 1% BSA, and stained with anti-CD3 and anti-CD25 antibodies for 30 minutes. Cells were then washed one time with PBS-BSA buffer and analyzed using a flow cytometer.

[00357] FIG. 26A is a graph of the concentration (nM) versus the percent maximum killing showing varying levels of killing by the molecules. FIG. 26B is a graph of the concentration (nM) versus the CD25 mean fluorescence intensity (MFI), showing similar levels of T cell activation by the molecules of the various formats.

[00358] FIG. 26C – 26F depict constructs of the bispecific molecules. FIG. 26C depicts construct 3M46C (anti-CD3 + 1MU32A). FIG. 26D depicts construct 3M64C (anti-MUC17 + anti-CD3 + 1MU11A). FIG. 26E depicts construct 3M42C (anti-MUC17 + anti-CD3). FIG. 26F depicts construct 3M66C (anti-MUC17 + anti-CD3).

EXAMPLE 20

PBMC killing of ASPC1 cells with MUC17xCD3 bispecific molecules of various formats of antibody 1MU11A

[00359] MUC17xCD3 bispecific molecules derived from anti-MUC17 antibody 1MU11A in three formats, scfv-Fc + Fab-Fc (3M55C and 3M65C), scfv-scfv-Fc + Fab-Fc (3M63C), and scfv-scfv-Fc (3M61C), were assessed for their ability to stimulate PBMC cells to become activated and to kill ASPC1 cells as described in the above examples.

[00360] FIG. 27A is a graph of the concentration (nM) versus the percent maximum killing, showing the various formats are all able to stimulate PBMCs to kill ASPC1 cells. FIG. 27B is a graph of the concentration (nM) of the molecules versus the CD25 mean fluorescence intensity (MFI) on CD3+ T cells, showing similar trends for T cell activation by the various molecules, as compared to killing.

[00361] FIG. 27C – 27F depict constructs of the bispecific molecules. FIG. 27C depicts

construct 3M55C (anti-CD3 + 1MU11A). FIG. 27D depicts construct 3M63C (anti-MUC17 + anti-CD3 + 1MU32A). FIG. 27E depicts construct 3M61C (anti-MUC17 + anti-CD3). FIG. 27F depicts construct 3M65C (anti-MUC17 + anti-CD3).

EXAMPLE 21

CD28xMuc17 bispecific in combination with 10pM of MUC17xCD3 bispecific molecule 3M62C activates T-cells to express IL-2 and CD25

[00362] Human PBMC were cultured together with ASPC1 cells and stimulated with 10pM of MUC17 x CD3 bispecific 3M62C. Additionally, MUC17 x CD28 bispecific molecules 28M1, 28M2, and 28M3 were added to the cultures. After 48 hours of culture, T cell activation was measured as an increase in IL-2 secreted into the medium and an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA. The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50uL of mouse anti-human IL-2 capture antibody at a concentration of 2µg/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200uL PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50uL of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50uL of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5µg/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). CD25 expression levels were measured as described in Example 3.

[00363] FIG. 28A shows IL-2 secretion as a function of the concentration (nM) of the molecules versus absorbance from the IL-2 ELISA. 3M82C weakly stimulates the secretion of IL-2 but when added to the CD28 x Muc17 bispecific molecules IL-2 secretion is significantly increased. FIG. 28B shows CD25 Expression as the concentration (nM) versus the CD25 MFI. Similarly, the combination of CD28 x Muc17 and CD3 x Muc17 bispecific molecules activates T cells to a greater degree than the CD3 x Muc17 bispecific alone.

[00364] FIG. 28C – 28F depict constructs of the bispecific molecules. FIG. 28C depicts construct 28M1 (anti-CD28 + 1MU37A). FIG. 28D depicts construct 28M2 (anti- CD28 + 1MU32A). FIG. 28E depicts construct 28M3 (anti-CD28 + 1MU11A). FIG. 28F depicts construct 3M62C (1MU32A + anti-CD3).

EXAMPLE 22

CD28xMuc17 bispecific molecule in combination with 20pM of MUC17xCD3 (3M55C) bispecific molecule activates T-cells to express IL-2 and CD25

[00365] Human PBMC were cultured together with ASPC1 cells and stimulated with 20pM of MUC17 x CD3 bispecific 3M55C. Additionally, MUC17 x CD28 bispecific molecules 28M1, 28M2, and 28M3 were also added to the cultures. Activation was measured by the increase IL-2 secretion and the increase of in cell surface CD25 on CD3+ T cells, as described above in the Example 21.

[00366] FIG. 29A shows IL-2 secretion as a function of the concentration (nM) of the CD28xMuc17 bispecific molecules versus absorbance from the IL-2 ELISA. 3M55C alone does not stimulate the secretion of IL-2 but when the CD28 x Muc7 bispecific molecules, 28M1, 28M2, 28M3, are added to the culture, IL-2 levels are significantly increased. FIG. 29B shows the combination of CD3 x MUC17 and CD28 x Muc17 bispecific molecules increase CD25 expression to a greater degree than the CD3 x Muc17 alone, as indicated in the graph as the concentration (nM) of the CD28xMUC17 bispecific molecules versus the CD25 MFI on CD3+ T cells.

[00367] FIG. 29C – 29F depict constructs of the bispecific molecules. FIG. 29C depicts construct 28M1 (anti-CD28 + 1MU37A). FIG. 28D depicts construct 28M2 (anti- CD28 + 1MU32A). FIG. 28E depicts construct 28M3 (anti-CD28 + 1MU11A). FIG. 28F depicts construct 3M55C (anti-CD3 + 1MU11A).

EXAMPLE 23

CD28xMuc17 bispecific molecules alone do not PBMC cells

[00368] The experiment was repeated to demonstrate that CD28xMuc17 bispecific molecules alone do not activate PBMC cells. Human PBMC cells, ASPC1 cells and MUC17 x CD28 bispecific molecules 28M1, 28M2, and 28M3, were cultured for 48 hours as described above, and assessed as described in the Example 5. FIG. 30A shows IL-2 secretion as a function of the concentration (nM) of the CD28xMUC17 bispecific molecules versus absorbance from the IL-2 ELISA. FIG. 30B shows CD25 expression as the concentration (nM) of the CD28xMUC17 bispecific molecules versus the CD25 MFI on CD3+ T cells. 28M1, 28M2, and 28M3 do not activate T cells without CD3 stimulation by the MUC17xCD3 bispecific molecule.

EXAMPLE 24

Bioactivity of multiple CD3 affinity variants: PBMC killing of ASPC1 cells expressing Muc17

[00369] FIG. 31 shows concentration versus percent maximum killing. The bispecific constructs 3M16B, 3M16C, 3M16D, 3M16E, 3M16F, 3M16G, 3M16I, 3M16K and 3M16L show varying abilities to stimulate PBMCs to kill ASPC1 cells.

EXAMPLE 25**Binding of MUC17scfv-Fc x CD3Fab-Fc constructs as compared to Muc17Fab-Fc x CD3scfv-Fc**

[00370] FIG. 32 shows binding of anti-Muc17 bispecific molecules as scfv and Fab formats to Muc17 expressing cells as a graph of concentration of the bispecific molecules versus Absorbance at 650 nm. 1MU11A and 1MU32A retain activities in the scfv format.

EXAMPLE 26**CD137 Fab x Muc17 Scfv bispecific molecules 4M1 increases IFNgamma secretion by PBMC when combined with 2pM CD3xMUC17 benchmark molecule 3M8B7 and in the presence of ASPC1 cells**

[00371] FIG. 33 shows concentration of 4M1 versus the level of secreted IFNgamma (absorbance at 650 nm) indicating increasing concentrations of 4M1 in combination with 2pM of the CD3 x Muc17 molecule 3M8B7 increase the levels of IFNgamma that are secreted over time in culture.

EXAMPLE 27**CD137 Fab x Muc17 Scfv bispecific molecule 4M2 increase IFNgamma secretion by PBMC when combined with 2pM of 3M8B7 benchmark and in the presence of ASPC1 cells**

[00372] FIG. 34 shows concentration of 4M2 versus IFNgamma (absorbance at 650 nm) indicating increasing concentrations of 4M2 in combination with 2pM of the CD3 x Muc17 molecule 3M8B7 increase the levels of IFNgamma that are secreted over time in culture.

EXAMPLE 28

Muc17xCD137 bispecific 4M2 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of CHO cells expressing Muc17

[00373] FIG. 35 shows concentration of 4M2 versus IFN γ (absorbance at 650 nm) indicating increasing concentrations of 4M2 in combination with 2pM of 10pM of the CD3 x Muc17 molecule 3M8B7 increase the levels of IFN γ that are secreted over time in culture. 4M2 alone does not stimulate the secretion of IFN γ

EXAMPLE 29

Muc17xCD137 bispecific 4M7 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of CHO cells expressing Muc17

[00374] FIG. 36 shows concentration of 4M7 versus the level of secreted IFN γ (absorbance at 650 nm), indicating increasing concentrations of 4M7 in combination with 2pM and 10pM of the CD3 x Muc17 molecule 3M8B7 increase the levels of IFN γ that are secreted over time in culture. 4M7 alone does not stimulate the secretion of IFN γ

EXAMPLE 29

Muc17xCD137 bispecific 4M8 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFN γ in the presence of CHO cells expressing Muc17

[00375] FIG. 37 shows concentration versus IFN γ (absorbance at 650 nm) indicating increasing concentrations of 4M8 in combination with 2pM and 10pM of the CD3 x Muc17 molecule 3M8B7 increase the levels of IFN γ that are secreted over time in culture. 4M8 alone does not stimulate the secretion of IFN γ .

EXAMPLE 30

CLDN18.2xCD3 Bispecific molecules bind to CHO cells expressing huCLND18.2

[00376] Six humanized antibodies, formatted as CD3 x CLDN18.2 bispecific molecules, 3C17C, 3C18C, 3C22C, 3C26C, 3C27C, 3C29C, were assessed for the ability to bind to CHO-K1 cells that were stably transfected with human CLDN18.2.

[00377] To evaluate the ability of anti-CLDN18.2 bispecific molecules to bind cell-expressed CLDN18.2, serial dilutions of the anti-CLDN18.2 bispecific molecules were added to the CLDN18.2 expressing CHO-K1 cells at a concentration of 20,000 cells/well. The bispecific molecules:cell mixtures were incubated at 4°C for 20 minutes, washed 3 times, and stained with the secondary antibody, PE labeled F(ab')₂-Goat anti-human IgG Fc (Thermo H10104) at 4°C for 20 minutes. Cells were washed and resuspended in 7-Amino-Actinomycin D (7-AAD) solution and fixed in 10% neutral buffered formalin solution for 15 minutes before analysis with the iQue Intellicyt system. FIG. 42 is a graph of the concentration (nM) of the bispecific molecules versus the mean fluorescence intensity (MFI) of binding to CLDN18.2-CHO cells, showing all of the bispecific molecules bind human CLDN18.2.

EXAMPLE 31

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules in the presence of CLDN18.2 expressing CHO cells

[00378] The experiment was conducted to evaluate the ability of CLDN18.2x CD3 bispecific molecules to activate and upregulate CD25 on T-cells.

[00379] Target and effector cells were suspended in 200µl of medium containing 10% serum at an effector to target ratio of 10:1, in a 96-well plate. Dilutions of the bispecific molecules were added to the cultures in triplicate. The 96-well plates were cultured at 37°C for 48 hours. The cells were collected, washed one time with PBS buffer containing 1% BSA, and stained with anti-CD3 and anti-CD25 antibodies for 30 minutes. Cells were then washed one time with PBS-BSA buffer and analyzed using a flow cytometer. FIG. 43A is a graph of the concentration (nM) of bispecific molecules 3C18C, 3C22C, 3C26C and 3C27C versus the CD25 mean fluorescence intensity (MFI), showing all of the CD3 x CDLN18.2 bispecific molecules can activate T cells to increase the expression of CD25.

EXAMPLE 32

PBMC killing of CHO cells with CLDN18.2xCD3 bispecific molecules

[00380] CLDN18.2xCD3 bispecific molecules were assessed for their ability to stimulate PBMC cells to kill CLDN18.2 expressing CHO cells. The molecules tested were 3C18C, 3C22C, 3C26C and 3C27C. Cell cytotoxicity was determined as the amount of lactate dehydrogenase (LDH) released from damaged cells as a percent of the total LDH release with 1% Triton-X (Max Killing) added to the cell mixtures at time 0. For the cytotoxicity

assays, target (CLDN-CHO) and effector cells (human PBMCs) were suspended in 200µl of medium containing 10% serum at an effector to target ratio of 10:1, in a 96-well plate. Dilutions of the bispecific molecules were added to the cultures in triplicate. The 96-well plates were cultured at 37°C for 48 hours. The cells were then centrifuged at 250 x g for 10 min, and 100µl of the supernatant plus were transferred into corresponding wells of an optically clear 96-well plate containing 100µl LDH assay reagent per well. The plates were then incubated for up to 30 min at room temperature. The absorbance of all samples was measured at 490-500 nm using a microtiter plate reader. FIG. 43B is a graph of the concentration (nM) of the bispecific molecules versus the percent maximum killing, showing all of the CLDN18.2 x CD3 bispecific molecules can stimulate PBMCs to kill CHO cells expressing CLDN18.2.

EXAMPLE 33

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 affinity variant in the presence of CLDN18.2 expressing SNU-601 cells

[00381] The experiment was conducted to evaluate the ability of CLDN18.2x CD3 bispecific molecules to activate and upregulate T-cells. Assessment of CD25 expression on CD3+ T cells within PBMC effector cell population was performed on the remaining cells from the cultures assessed for LDH release for Example 3. The cells were collected, washed one time with PBS buffer containing 1% BSA, and stained with anti-CD3 and anti-CD25 antibodies for 30 minutes. Cells were then washed one time with PBS-BSA buffer and analyzed using a flow cytometer. FIG. 44A is a graph of the concentration (nM) of bispecific molecules 3C18C, 3C18D, 3C18I and 3C18K versus the CD25 mean fluorescence intensity (MFI), showing all four 3D18 variants exhibit similar abilities to stimulate T cells to increase expression of CD25.

EXAMPLE 34

Killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules with CD3 affinity variants

[00382] CLDN18.2xCD3 bispecific molecules were assessed for their ability to stimulate PBMC cells to become activated and to kill SNU-601 tumor cells. The molecules tested were 3C18C, 3C18D, 3C18I and 3C18K.

[00383] Cell cytotoxicity was determined as the amount of lactate dehydrogenase (LDH) released from damaged cells as a percent of the total LDH release with 1% Triton-X (Max

Killing) added to the cell mixtures at time 0, as described in Example 3. FIG. 44B is a graph of the concentration (nM) of the bispecific molecule variants versus the percent maximum killing, showing all four 3D18 variants exhibit similar abilities to stimulate PBMCs to kill SNU-601 cells.

EXAMPLE 35

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 affinity variants in the presence of CLDN18.2 expressing SNU-601 cells

[00384] The experiment was conducted to evaluate the ability of CLDN18.2x CD3 bispecific molecules to activate and upregulate CD25 on T-cells. The laboratory method is that described in the Example 4. FIG. 45A shows CD25 expression as the concentration (nM) of the bispecific molecule variants versus the CD25 MFI on CD3+ T cells, showing all four of the 3D22 variants are similarly able to stimulate T cells to increase expression of CD25.

EXAMPLE 36

Killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecule with CD3 affinity variants

[00385] CLDN18.2xCD3 bispecific molecules were assessed for their ability to stimulate PBMC cells to become activated and to kill SNU-601 tumor cells. The molecules tested were 3C22C, 3C22D, 3C22I and 3C22K.

[00386] Cell cytotoxicity was determined as the amount of lactate dehydrogenase (LDH) released from damaged cells as a percent of the total LDH release with 1% Triton-X (Max Killing) added to the cell mixtures at time 0 as described in Example 32. FIG. 45B is a graph of the concentration (nM) of the bispecific molecule variants versus the percent maximum killing, showing all four of the 3C22 variants have similar abilities to stimulate PBMCs to kill SNU-601 cells.

EXAMPLE 37

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecific molecules with CD3 affinity variants in the presence of CLDN18.2 expressing SNU-601 cells

[00387] The experiment was conducted to evaluate the ability of CLDN18.2x CD3 bispecifics to activate and upregulate CD25 on T-cells. The molecules tested were 3C26C,

3C26D, 3C26I and 3C26K. The laboratory method is that described in the Example 33. FIG. 46A shows CD25 expression as the concentration (nM) of the bispecific molecule variants versus the CD25 MFI, showing all four 3C26 variants have similar abilities to stimulate T cells to express CD25.

EXAMPLE 38

Killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecific molecules with CD3 affinity variants

[00388] CLDN18.2xCD3 bispecific molecules were assessed for their ability to stimulate PBMC cells to become activated and to kill SNU-601 tumor cells. The molecules tested were 3C26C, 3C26D, 3C26I and 3C26K.

[00389] Cell cytotoxicity was determined as the amount of lactate dehydrogenase (LDH) released from damaged cells as a percent of the total LDH release with 1% Triton-X (Max Killing) added to the cell mixtures at time 0 as described in Example 32. FIG. 46B is a graph of the concentration (nM) bispecific molecule variants versus the percent maximum killing, showing all four 3C26 variants are similarly able to stimulate PBMCs to kill SNU-601 cells.

EXAMPLE 39

CD3xCldn18.2 binding to Cldn18.2-CHO cells

[00390] CD3xCLDN18.2 bispecific molecules were assessed for their ability to bind to CHO cells expressing Cldn18.2. The molecules tested were 3C17C, 3C18C, 3C22C, 3C26C, 3C27C and 3C29C.

[00391] FIG. 47 is a graph of the concentration (nM) of the CD3cDLND18.2 bispecific molecules versus mean fluorescence intensity (MFI) of binding, showing all six bispecific molecules are able to bind CHO cells expressing CLDN18.2.

EXAMPLE 40

CD28xCLND18.2 bispecific molecules in combination with 10pM of CLND18.2xCD3 bispecific molecule 3C18C activate T-cells to express IL-2 and CD25

[00392] Human PBMC were cultured together with SNU-601 cells and stimulated with 10pM of CLND18.2 x CD3 bispecific 3C18C. Additionally, CLDN18.2 x CD28 bispecifics, 28C5, 28C6, 28C7, and 28C8, were added to the cultures. After 48 hours of culture, T cell activation was measured as an increase in IL-2 secreted into the medium and an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA.

The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50 μ L of mouse anti-human IL-2 capture antibody at a concentration of 2 μ g/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200 μ L PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50 μ L of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50 μ L of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5 μ g/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). CD25 expression levels were measured as described in Example 33. FIG. 48A shows CD25 MFI as a function of the concentration (nM) versus absorbance, indicating the addition of the CD28 x CLDN18.2 bispecific molecule to 3C18C increased T cells activity and the expression of CD25. Similarly, FIG. 48B shows the amount of IL-2 secreted into the culture as the concentration (nM) with increasing concentrations of the CD28 x CLDN18.2 bispecific molecules, indicating the addition of the CD28 x CLDN18.2 bispecific molecules to 3C18C increased the secretion of IL-2.

EXAMPLE 41

CD28xCLND18.2 bispecific molecules in combination with 10pM of CLND18.2xCD3 bispecific molecule 3C22C activate T-cells to express IL-2 and CD25

[00393] Human PBMC were cultured together with SNU-601 cells and stimulated with 10pM of CLND18.2 x CD3 bispecific 3C22C. Additionally, CLDN18.2 x CD28 bispecifics, 28C5, 28C6, 28C7, and 28C8, were added to the cultures. After 48 hours of culture, T cell activation was measured as an increase in IL-2 secreted into the medium and an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA. The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50 μ L of mouse anti-human IL-2 capture antibody at a concentration of 2 μ g/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200 μ L PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50 μ L of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50 μ L of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5 μ g/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). CD25 expression levels were measured as described in Example 33. FIG. 49A shows CD25 Expression as the concentration (nM), indicating the addition of the CD28 x CLDN18.2 bispecific molecules to 3C22C stimulated T cells to express CD25. FIG. 49B shows IL-2 secretion as a function of the concentration

(nM) of the CD28xCLND18.2 bispecific molecules versus absorbance from the IL-2 ELISA, showing the addition of the CD28 x CLDN18.2 bispecific molecules to 3C22C stimulated PBMCs to secrete IL-2.

EXAMPLE 42

CD28xCLND18.2 bispecific molecules in combination with 20pM of CLND18.2xCD3 bispecific molecule 3C26C activates T-cells to express IL-2 and CD25

[00394] Human PBMC were cultured together with SNU-601 cells and stimulated with 20pM of CLND18.2 x CD3 bispecific 3C26C. Additionally, CLDN18.2 x CD28 bispecifics, 28C5, 28C6, 28C7, and 28C8, were added to the cultures. After 48 hours of culture, T cell activation was measured as an increase in IL-2 secreted into the medium and an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA. The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50µL of mouse anti-human IL-2 capture antibody at a concentration of 2ug/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200µL PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50µL of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50µL of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5µg/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). CD25 expression levels were measured as described in Example 33. FIG. 50A shows CD25 Expression as the concentration (nM) versus the CD25 MFI, indicating the addition of the CD28 x CLDN18.2 bispecific molecules to 3C26C increased T cell activation and the expression of CD25. FIG. 50B shows the levels of IL-2 secreted, as determined by absorbance readings from the IL-2 ELISA, versus the concentration (nM) of the CD28xCLDN18.2 bispecific molecules, indicating the addition of the CD28xCLDN18.2 bispecific molecules to 3C26C increases the secretion of IL-2 by PBMCs.

EXAMPLE 43

CD28xCLND18.2 bispecific in combination with 2pM of CLND18.2xCD3 bispecific molecule 3C27C activates T-cells to express IL-2 and CD25

[00395] Human PBMC were cultured together with SNU-601 cells and stimulated with 2pM of CLND18.2 x CD3 bispecific 3C27C. Additionally, CLDN18.2 x CD28 bispecific molecules, 28C5, 28C6, 28C7, and 28C8, were added to the cultures. After 48 hours of culture, T cell activation was measured as an increase in IL-2 secreted into the medium and

an increase of in cell surface CD25 on CD3+ T cells. IL-2 secretion was measured using an IL-2 ELISA. The ELISA utilized high protein-binding 96-well plates that were coated overnight with 50µL of mouse anti-human IL-2 capture antibody at a concentration of 2ug/ml. Plates were washed with PBS+0.05% Tween-20 (PBST) and blocked with 200µL PBS with 1% BSA. After washing, the coated plates were incubated for 120 minutes with 50µL of the supernatant from the PBMC:Target cell cultures stimulated with bispecific molecules. Plates were washed, and then incubated for 60 minutes with 50µL of biotinylated mouse anti-human IL-2 detection antibody at a concentration of 0.5µg/ml. Plates were washed and incubated with streptavidin-HRP for 20 minutes. After washing, captured IL-2 was quantified using 3,3',5,5'-tetramethylbenzidine (TMB). CD25 expression levels were measured as described in Example 33. FIG. 51A shows CD25 expression as the concentration (nM) of the CD28xCLDN18.2 bispecific versus the CD25 MFI on CD3+ T cells, indicating the addition of the CD28xCLDN18.2 bispecific molecules to 3C27C increases T cell activation and the expression of CD25. FIG. 51B shows the levels of IL-2 secreted, as determined by absorbance readings from the IL-2 ELISA, versus the concentration (nM) of the molecules of the CD28xCLDN18.2 bispecific molecules, indicating the addition of the CD28 x CLDN18.2 bispecific molecules to 3C27C stimulates PBMCs to secrete IL-2.

EXAMPLE 44

CD28xCLDN18.2 bispecific molecules alone do not activate T-cells

[00396] The experiment was repeated to demonstrate that CD28xCLDN18.2 bispecific molecules alone do not activate T-cells. Human PBMC cells, SNU-601 cells and CLDN18.2 x CD28 bispecific molecules 28C5, 28C6, 28C7, and 28C8, were cultured for 48 hours as described above, and assessed as described in the Example 40. FIG. 52A shows CD25 expression as the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus the CD25 MFI on CD3+ T cells, indicating the CD28 x CLDN18.2 bispecific molecules do not activate T cells without the CD3 x CLDN18.2 molecules being present. FIG. 52B shows the levels of IL-2 secreted, as determined by absorbance readings from the IL-2 ELISA, versus the concentration (nM) of the CD28xCLDN18.2 bispecific molecules, indicating the CD28 x CLDN18.2 bispecific molecules do not stimulate PBMCs to secrete IL-2 without the CD3 x CLDN18.2 molecules being present.

EXAMPLE 45

CD3xCldn18.2 bites alone activate PBMCs to express CD25 but to secrete only low levels of IL-2

[00397] FIG. 53A is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus mean CD25 fluorescence intensity (MFI) on CD3+ T cells for the four CD3 x CLDN18.2 bispecific molecules, showing they stimulate the expression of CD25 by T cells. FIG. 53B is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus CD25 mean fluorescence intensity (MFI) on CD3+ T cells, showing that in the absence of the CD28 x CLDN18.2 bispecific molecules, the four CD3 x CLDN18.2 bispecific molecules only stimulate low levels of IL-2 secretion.

EXAMPLE 46

CD3xCldn18.2 bispecific 3C22C stimulates PBMC mediated killing of GSU cells more potently than 3 lots of the benchmark CD3 x CLDN18.2 molecule, 3CBM

[00398] FIG. 54 is a graph of the concentration (nM) of the CD3xCLDN18.2 bispecific molecules versus percent maximum killing of the GSU target cells by the PBMCs.

EXAMPLE 47

CD3xCldn18.2 bispecific 3C22C stimulates PBMC to express CD25 in the presence of GSU cells more potently than 3 lots of the benchmark, 3CBM

[00399] FIG. 55 is a graph of the concentration (nM) of the CD3xCLDN18.2 bispecific molecules versus CD25 mean fluorescence intensity (MFI) on CD3+ T cells.

EXAMPLE 48

3C27I is more potent at killing SNU-601 cells than 3C18I, 3C22I, or 3C26I

[00400] FIG. 56 is a graph of the concentration (nM) of the CD3xCLDN18.2 bispecific molecules versus percent killing of SNU-601 target cells by the PBMCs.

EXAMPLE 49

CD28scFvxCldn18.2Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 bispecific, 3C18C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells

[00401] FIG. 57 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus absorbance at 650 nm from the IL-2 ELISA, showing the addition of the CD28 x CLDN18.2 bispecific molecules to 3C18C increases the secretion of IL-2 by PBMCs.

EXAMPLE 50

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 bispecific, 3C22C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells

[00402] FIG. 58 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus absorbance at 650 nm from the IL-2 ELISA, showing the addition of the CD28 x CLDN18.2 bispecific molecules to 3C22C increases the secretion of IL-2 by PBMCs.

EXAMPLE 51

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 Bispecific, 3C26C, activate PBMCs to produce IL-2 when co-cultured with SNU-601

[00403] FIG. 59 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus absorbance at 650 nm from the IL-2 ELISA, showing the addition of the CD28 x CLDN18.2 bispecific molecules to 3C26C increases the secretion of IL-2 by PBMCs.

EXAMPLE 52

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 alone do not activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells

[00404] FIG. 60 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus CD25 mean fluorescence intensity (MFI) on CD3+ T cells.

EXAMPLE 53

Cldn18.2xCD28 bispecific molecules 28C7 and 28C10 in combination with 5pM of the CD3 x CLDN18.2 bispecific 3C22I activates T-cells to secrete IL-2

[00405] FIG. 61 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus the concentration of secreted IL-2 (pg/mL), as determined by the IL-2 ELISA.

EXAMPLE 54

CLDIN18.2 x CD28 bispecific molecules 28C5, 28C6, 28C7 and 28C8 in combination with a CLND18.3 x CD3 bispecific molecule induced IL-2 secretion by PBMCs when in

the presence of CHO cells expressing CLDN18.2 but not with parental CHO cells

[00406] FIG. 62 is a graph of the concentration (nM) of the CD28xCLDN18.2 bispecific molecules versus concentration of secreted IL-2 (pg/mL), as determined by the IL-2 ELISA.

EXAMPLE 55

CD137 x Cldn18.2 bispecific molecule 4C1 in combination with 10pM of the CD3 x CLDN18.2 bispecific molecule 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells

[00407] FIG. 63 is a graph of the fold increase in IFNgamma over unstimulated versus the concentration of the CD137 x CLDN18.2 specific molecules over time.

EXAMPLE 56

CD137 x Cldn18.2 bispecific molecule 4C2 in combination with 10pM of the CD3 x CLDN18.2 bispecific 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells

[00408] FIG. 64 is a graph of the fold increase in IFNgamma over unstimulated versus the concentration of the CD137 x CLDN18.2 specific molecules over time.

EXAMPLE 57

CD137xCldn18.2 bispecific molecule 4C6 in combination with 3C22I activate T-cells to secrete IFNgamma

[00409] FIG. 65 is a graph of fold increase in IFNgamma over unstimulated versus the concentration of the CD137 x CLDN18.2 specific molecules over time.

EXAMPLE 58

CD137xCldn18.2 bispecific molecule 4C5 in combination with 3C22I activate T-cells to secrete IFNgamma

[00410] FIG. 66 is a graph of the fold increase in IFNgamma over unstimulated versus the concentration of the CD137 x CLDN18.2 specific molecules over time.

EXAMPLE 59

CD137xCldn18.2 bispecific molecules 4C1 and 4C5 in combination with 80pM 3C27I increase the number of CD8 cells in the presence of mitomycin treated CHO cells expressing CLND18.2

[00411] FIG. 66 is a graph of the CD8+ cell counts as a fold increase over the number of CD8+ cells when stimulated with 3C27I alone versus the concentration of the CD137 x CDLN18.2 bispecific molecules.

[00412] The therapeutic method of the present specification may include the step of administering the composition including the antibody at a pharmaceutically effective amount. The total daily dose should be determined through appropriate medical judgment by a physician, and administered once or several times. The specific therapeutically effective dose level for any particular patient may vary depending on various factors well known in the medical art, including the kind and degree of the response to be achieved, concrete compositions according to whether other agents are used therewith or not, the patient's age, body weight, health condition, gender, and diet, the time and route of administration, the secretion rate of the composition, the time period of therapy, other drugs used in combination or coincident with the composition disclosed herein, and like factors well known in the medical arts.

[00413] In still another aspect, the present specification provides a use of the therapeutic protein or the pharmaceutical composition including the same in the preparation of drugs for the prevention or treatment of cancer, a neurodegenerative or an infectious disease.

[00414] In one embodiment, the dose of the composition may be administered daily, semi-weekly, weekly, bi-weekly, or monthly. The period of treatment may be for a week, two weeks, a month, two months, four months, six months, eight months, a year, or longer. The initial dose may be larger than a sustaining dose. In one embodiment, the dose ranges from a weekly dose of at least 0.01 mg/kg, at least 0.25 mg/kg, at least 0.3 mg/kg, at least 0.5 mg/kg, at least 0.75 mg/kg, at least 1 mg/kg, at least 2 mg/kg, at least 3 mg/kg, at least 4 mg/kg, at least 5 mg/kg, at least 6 mg/kg, at least 7 mg/kg, at least 8 mg/kg, at least 9 mg/kg, at least 10 mg/kg, at least 15 mg/kg, at least 20 mg/kg, at least 25 mg/kg, or at least 30 mg/kg. In one embodiment, a weekly dose may be at most 1.5 mg/kg, at most 2 mg/kg, at most 2.5 mg/kg, at most 3 mg/kg, at most 4 mg/kg, at most 5 mg/kg, at most 6 mg/kg, at most 7 mg/kg, at most 8 mg/kg, at most 9 mg/kg, at most 10 mg/kg, at most 15 mg/kg, at

most 20 mg/kg, at most 25 mg/kg, or at most 30 mg/kg. In a particular aspect, the weekly dose may range from 5 mg/kg to 20 mg/kg. In an alternative aspect, the weekly dose may range from 10 mg/kg to 15 mg/kg.

[00415] The present specification also provides a pharmaceutical composition for the administration to a subject. The pharmaceutical composition disclosed herein may further include a pharmaceutically acceptable carrier, excipient, or diluent. As used herein, the term "pharmaceutically acceptable" means that the composition is sufficient to achieve the therapeutic effects without deleterious side effects, and may be readily determined depending on the type of the diseases, the patient's age, body weight, health conditions, gender, and drug sensitivity, administration route, administration mode, administration frequency, duration of treatment, drugs used in combination or coincident with the composition disclosed herein, and other factors known in medicine.

[00416] The pharmaceutical composition including the antibody disclosed herein may further include a pharmaceutically acceptable carrier. For oral administration, the carrier may include, but is not limited to, a binder, a lubricant, a disintegrant, an excipient, a solubilizer, a dispersing agent, a stabilizer, a suspending agent, a colorant, and a flavorant. For injectable preparations, the carrier may include a buffering agent, a preserving agent, an analgesic, a solubilizer, an isotonic agent, and a stabilizer. For preparations for topical administration, the carrier may include a base, an excipient, a lubricant, and a preserving agent.

[00417] The disclosed compositions may be formulated into a variety of dosage forms in combination with the aforementioned pharmaceutically acceptable carriers. For example, for oral administration, the pharmaceutical composition may be formulated into tablets, troches, capsules, elixirs, suspensions, syrups or wafers. For injectable preparations, the pharmaceutical composition may be formulated into an ampule as a single dosage form or a multidose container. The pharmaceutical composition may also be formulated into solutions, suspensions, tablets, pills, capsules and long-acting preparations.

[00418] On the other hand, examples of the carrier, the excipient, and the diluent suitable for the pharmaceutical formulations include, without limitation, lactose, dextrose, sucrose, sorbitol, mannitol, xylitol, erythritol, maltitol, starch, acacia rubber, alginate, gelatin, calcium phosphate, calcium silicate, cellulose, methylcellulose, microcrystalline cellulose, polyvinylpyrrolidone, water, methylhydroxybenzoate, propylhydroxybenzoate, talc, magnesium stearate and mineral oils. In addition, the pharmaceutical formulations may further include fillers, anti-coagulating agents, lubricants, humectants, flavorants, and antiseptics.

[00419] Further, the pharmaceutical composition disclosed herein may have any formulation selected from the group consisting of tablets, pills, powders, granules, capsules, suspensions, liquids for internal use, emulsions, syrups, sterile aqueous solutions, non-aqueous solvents, lyophilized formulations and suppositories.

[00420] The composition may be formulated into a single dosage form suitable for the patient's body, and preferably is formulated into a preparation useful for peptide drugs according to the typical method in the pharmaceutical field so as to be administered by an oral or parenteral route such as through skin, intravenous, intramuscular, intra-arterial, intramedullary, intramedullary, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, intracolonic, topical, sublingual, vaginal, or rectal administration, but is not limited thereto.

[00421] The composition may be used by blending with a variety of pharmaceutically acceptable carriers such as physiological saline or organic solvents. In order to increase the stability or absorptivity, carbohydrates such as glucose, sucrose or dextrans, antioxidants such as ascorbic acid or glutathione, chelating agents, low molecular weight proteins or other stabilizers may be used.

[00422] The administration dose and frequency of the pharmaceutical composition disclosed herein are determined by the type of active ingredient, together with various factors such as the disease to be treated, administration route, patient's age, gender, and body weight, and disease severity.

[00423] The total effective dose of the compositions disclosed herein may be administered to a patient in a single dose, or may be administered for a long period of time in multiple doses according to a fractionated treatment protocol. In the pharmaceutical composition disclosed herein, the content of active ingredient may vary depending on the disease severity. Preferably, the total daily dose of the peptide disclosed herein may be approximately 0.0001 μ g to 500 mg per 1 kg of body weight of a patient. However, the effective dose of the peptide is determined considering various factors including patient's age, body weight, health conditions, gender, disease severity, diet, and secretion rate, in addition to administration route and treatment frequency of the pharmaceutical composition. In view of this, those skilled in the art may easily determine an effective dose suitable for the particular use of the pharmaceutical composition disclosed herein. The pharmaceutical composition disclosed herein is not particularly limited to the formulation, and administration route and mode, as long as it shows suitable effects. Moreover, the pharmaceutical

composition may be administered alone or in combination or coincident with other pharmaceutical formulations showing prophylactic or therapeutic efficacy.

[00424] In still another aspect, the present specification provides a method for preventing or treating of cancer, infectious diseases or neurodegenerative diseases comprising the step of administering to a subject the chimeric protein or the pharmaceutical composition including the same.

[00425] Given the teachings and guidance provided herein, those skilled in the art will understand that a formulation described herein can be equally applicable to many types of biopharmaceuticals, including those exemplified, as well as others known in the art. Given the teachings and guidance provided herein, those skilled in the art also will understand that the selection of, for example, type(s) or and/or amount(s) of one or more excipients, surfactants and/or optional components can be made based on the chemical and functional compatibility with the biopharmaceutical to be formulated and/or the mode of administration as well as other chemical, functional, physiological and/or medical factors well known in the art. For example, non-reducing sugars exhibit favorable excipient properties when used with polypeptide biopharmaceuticals compared to reducing sugars. Accordingly, exemplary formulations are exemplified further herein with reference to polypeptide biopharmaceuticals. However, the range of applicability, chemical and physical properties, considerations and methodology applied to polypeptide biopharmaceutical can be similarly applicable to biopharmaceuticals other than polypeptide biopharmaceuticals.

[00426] In various embodiments, a formulation can include, without limitation, combinations of bioactive agents (such as viruses, proteins, antibodies, peptides and the like as described herein) in the formulation. For example, a formulation as described herein can include a single bioactive agent for treatment of one or more conditions, including without limitation, disease. A formulation as described herein also can include, in an embodiment, without limitation, two or more different bioactive agents for a single or multiple conditions. Use of multiple bioactive agents in a formulation can be directed to, for example, the same or different indications. Similarly, in another embodiment, multiple bioactive agents can be used in a formulation to treat, for example, both a pathological condition and one or more side effects caused by the primary treatment. In a further embodiment, multiple bioactive agents also can be included, without limitation, in a formulation as described herein to accomplish different medical purposes including, for example, simultaneous treatment and monitoring of the progression of the pathological condition. In an additional embodiment, multiple, concurrent therapies such as those exemplified herein as well as other combinations well known in the art are particularly useful for patient compliance because a

single formulation can be sufficient for some or all suggested treatments and/or diagnosis. Those skilled in the art will know those bioactive agents that can be admixed for a wide range of combination therapies. Similarly, in various embodiments, a formulation can be used with a small molecule drug and combinations of one or more bioactive agents together with one or more small molecule pharmaceuticals. Therefore, in various embodiments a formulation is provided containing 1, 2, 3, 4, 5 or 6 or more different bioactive agents, as well as, for one or more bioactive agents combined with one or more small molecule pharmaceuticals.

[00427] In various embodiments, a formulation can include, one or more preservatives and/or additives known in the art. Similarly, a formulation can further be formulated, without limitation, into any of various known delivery formulations. For example, in an embodiment, a formulation can include, surfactants, adjuvant, biodegradable polymers, hydrogels, etc., such optional components, their chemical and functional characteristics are known in the art. Similarly known in the art are formulations that facilitate rapid, sustained or delayed release of the bioactive agents after administration. A formulation as described can be produced to include these or other formulation components known in the art.

[00428] The composition can therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion via an implantation device or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. Appropriate dosages may be ascertained through use of appropriate dose-response data. In various embodiments, the bioactive agents in formulations described herein can, without limitation, be administered to patients throughout an extended time period, such as chronic administration for a chronic condition. The composition can be a solid, a semi-solid or an aerosol and a pharmaceutical composition is formulated as a tablet, geltab, lozenge, orally dissolved strip, capsule, syrup, oral suspension, emulsion, granule, sprinkle or pellet.

[00429] In an embodiment, for oral, rectal, vaginal, parenteral, pulmonary, sublingual and/or intranasal delivery formulations, tablets can be made by compression or molding, optionally with one or more accessory ingredients or additives. In an embodiment, compressed tablets are prepared, for example, by compressing in a suitable tableting machine, the active ingredients in a free-flowing form such as a powder or granules, optionally mixed with a binder (for example, without limitation, povidone, gelatin, hydroxypropylmethyl cellulose), lubricant, inert diluent, preservative, disintegrant (for example, without limitation, sodium starch glycolate, cross-linked povidone, cross-linked

sodium carboxymethyl cellulose) and/or surface-active or dispersing agent.

[00430] In an embodiment, molded tablets are made, for example, without limitation, by molding in a suitable tableting machine, a mixture of powdered compounds moistened with an inert liquid diluent. In an embodiment, the tablets may optionally be coated or scored, and may be formulated so as to provide slow or controlled release of the active ingredients, using, for example, without limitation, hydroxypropylmethyl cellulose in varying proportions to provide the desired release profile. In an embodiment, tablets may optionally be provided with a coating, without limitation, such as a thin film, sugar coating, or an enteric coating to provide release in parts of the gut other than the stomach. In an embodiment, processes, equipment, and toll manufacturers for tablet and capsule making are well-known in the art.

[00431] In an embodiment, capsule formulations can utilize either hard or soft capsules, including, without limitation, gelatin capsules or vegetarian capsules such as those made out of hydroxymethylpropylcellulose (HMPC). In an embodiment, a type of capsule is a gelatin capsule. In an embodiment, capsules may be filled using a capsule filling machine such as, without limitation, those available from commercial suppliers such as Miranda International or employing capsule manufacturing techniques well-known in the industry, as described in detail in *Pharmaceutical Capules*, 2nd Ed., F. Podczek and B. Jones, 2004. In an embodiment, capsule formulations may be prepared, without limitation, using a toll manufacturing center such as the Chao Center for Industrial Pharmacy & Contract Manufacturing, located at Purdue Research Park.

[00432] Packaging and instruments for administration may be determined by a variety of considerations, such as, without limitation, the volume of material to be administered, the conditions for storage, whether skilled healthcare practitioners will administer or patient self-compliance, the dosage regime, the geopolitical environment (e.g., exposure to extreme conditions of temperature for developing nations), and other practical considerations.

[00433] Injection devices include pen injectors, auto injectors, safety syringes, injection pumps, infusion pumps, glass prefilled syringes, plastic prefilled syringes and needle free injectors syringes may be prefilled with liquid, or may be dual chambered, for example, for use with lyophilized material. An example of a syringe for such use is the Lyo-Ject™, a dual-chamber pre-filled lyosyringe available from Vetter GmbH, Ravensburg, Germany. Another example is the LyoTip which is a prefilled syringe designed to conveniently deliver lyophilized formulations available from LyoTip, Inc., Camarillo, California, U.S.A. Administration by injection may be, without limitation intravenous, intramuscular, intraperitoneal, or subcutaneous, as appropriate. Administrations by non-injection route may

be, without limitation, nasal, oral, ocular, dermal, or pulmonary, as appropriate.

[00434] In certain embodiments, kits can comprise, without limitation, one or more single or multi-chambered syringes (e.g., liquid syringes and lyosyringes) for administering one or more formulations described herein. In various embodiments, the kit can comprise formulation components for parenteral, subcutaneous, intramuscular or IV administration, sealed in a vial under partial vacuum in a form ready for loading into a syringe and administration to a subject. In this regard, the composition can be disposed therein under partial vacuum. In all of these embodiments and others, the kits can contain one or more vials in accordance with any of the foregoing, wherein each vial contains a single unit dose for administration to a subject.

[00435] The kits can comprise lyophilates, disposed as herein, that upon reconstitution provide compositions in accordance therewith. In various embodiments the kits can contain a lyophilate and a sterile diluent for reconstituting the lyophilate.

[00436] Also described herein, are methods for treating a subject in need of therapy, comprising administering to the subject an effective amount of a formulation as described herein. The therapeutically effective amount or dose of a formulation will depend on the disease or condition of the subject and actual clinical setting.

[00437] In an embodiment, a formulation as described herein can be administered by any suitable route, specifically by parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. It will also be appreciated that the preferred route will vary with the condition and age of the recipient, and the disease being treated. Methods of determining the most effective means and dosage of administration are known to those of skill in the art and will vary, without limitation, with the composition used for therapy, the purpose of the therapy, and the subject being treated. Single or multiple administrations can be carried out, without limitation, the dose level and pattern being selected by the treating physician. Suitable dosage formulations and methods of administering the agents are known in the art.

[00438] The formulations as described herein can be used in the manufacture of medicaments and for the treatment of humans and other animals by administration in accordance with conventional procedures.

[00439] Also provided herein are combinatorial methods for developing suitable virus formulations using combinations of amino acids. These methods are effective for developing stable liquid or lyophilized formulations, and particularly pharmaceutical virus formulations.

[00440] Compositions in accordance with embodiments described herein have desirable properties, such as desirable solubility, viscosity, syringeability and stability. Lyophilates in accordance with embodiments described herein have desirable properties, as well, such as desirable recovery, stability and reconstitution.

[00441] In an embodiment, the pH of the pharmaceutical formulation is at least about 3.5, 3.75, 4, 4.25, 4.5, 4.75, 5, 5.25, 5.5, 5.75, 6, 6.25, 6.5, 6.75, 7, 7.25, 7.5, 7.75, 8, 8.25, 8.5, 8.75, or 9.

[00442] In an embodiment, the pH of the pharmaceutical formulation is from about 3 to about 9, about 4 to about 9, about 5 to about 9, about 6 to about 8, about 6 to about 7, about 6 to about 9, about 5 to about 6, about 5 to about 7, about 5 to about 8, about 4 to about 9, about 4 to about 8, about 4 to about 7, about 4 to about 6, about 4 to about 5, about 3 to about 8, about 3 to about 7, about 3 to about 6, about 3 to about 5, about 3 to about 4, about 7 to about 8, about 7 to about 9, about 7 to about 10.

[00443] In summary, embodiments include an antibody which binds to DLL3, Muc17 or Claudin 18.2 paired with an agonist antibody that activates CD3, CD28 or CD137. The antibody can be one of (1) an antibody with a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 7, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 14, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 27, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 31, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 40, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 47; or (2) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 1, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 11, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 22, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 39, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 54; or (3) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1

[illegible]

[illegible]

[illegible]

[illegible]

least the amino acid sequence as set forth in SEQ ID NO: 45, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 52.

(28) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 9, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 21, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 29, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 39, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 54.

[00444] Certain embodiments of the present invention are described herein, including the best mode known to the inventors for carrying out the invention. Of course, variations on these described embodiments will become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventor expects skilled artisans to employ such variations as appropriate, and the inventors intend for the present invention to be practiced otherwise than specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described embodiments in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[00445] Groupings of alternative embodiments, elements, or steps of the present invention are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other group members disclosed herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[00446] Unless otherwise indicated, all numbers expressing a characteristic, item, quantity, parameter, property, term, and so forth used in the present specification and claims are to be understood as being modified in all instances by the term "about." As used herein, the term "about" means that the characteristic, item, quantity, parameter, property, or term so qualified encompasses a range of plus or minus ten percent above and below the value of the stated characteristic, item, quantity, parameter, property, or term. Accordingly, unless indicated to the contrary, the numerical parameters set forth in the specification and attached

claims are approximations that may vary. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical indication should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques. Notwithstanding that the numerical ranges and values setting forth the broad scope of the invention are approximations, the numerical ranges and values set forth in the specific examples are reported as precisely as possible. Any numerical range or value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements. Recitation of numerical ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate numerical value falling within the range. Unless otherwise indicated herein, each individual value of a numerical range is incorporated into the present specification as if it were individually recited herein.

[00447] The terms “a,” “an,” “the” and similar referents used in the context of describing the present invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., “such as”) provided herein is intended merely to better illuminate the present invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the present specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[00448] Specific embodiments disclosed herein may be further limited in the claims using consisting of or consisting essentially of language. When used in the claims, whether as filed or added per amendment, the transition term “consisting of” excludes any element, step, or ingredient not specified in the claims. The transition term “consisting essentially of” limits the scope of a claim to the specified materials or steps and those that do not materially affect the basic and novel characteristic(s). Embodiments of the present invention so claimed are inherently or expressly described and enabled herein.

[00449] Groupings of alternative embodiments, elements, or steps of the present invention are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other group members disclosed herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written

description of all Markush groups used in the appended claims.

[00450] All patents, patent publications, and other publications referenced and identified in the present specification are individually and expressly incorporated herein by reference in their entirety for the purpose of describing and disclosing, for example, the compositions and methodologies described in such publications that might be used in connection with the present invention. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicants and does not constitute any admission as to the correctness of the dates or contents of these documents.

[00451] In closing, it is to be understood that although aspects of the present specification are highlighted by referring to specific embodiments, one skilled in the art will readily appreciate that these disclosed embodiments are only illustrative of the principles of the subject matter disclosed herein. Therefore, it should be understood that the disclosed subject matter is in no way limited to a particular methodology, protocol, and/or reagent, etc., described herein. As such, various modifications or changes to or alternative configurations of the disclosed subject matter can be made in accordance with the teachings herein without departing from the spirit of the present specification. Lastly, the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims. Accordingly, the present invention is not limited to that precisely as shown and described.

Table 13 – SEQUENCES

Seq ID	sequence	name
1	DYIFSNNYYIE	HCDR1; DLL3.2, DLL3.4
2	DYTFSNNYYIE	HCDR1; DLL3.1
3	DYYMN	HCDR1; DLL3.9
4	DYYVN	HCDR1; DLL3.8
5	GFTFSNYGMH	HCDR1; DLL3.10, DLL3.27, DLL3.29,

		DLL3.30, DLL3.31, DLL3.32, DLL3.33, DLL3.36
6	GFTFSSYGMH	HCDR1: DLL3.5, DLL3.12, DLL3.13, DLL3.14, DLL3.15, DLL3.16, DLL3.17, DLL3.18, DLL3.19, DLL3.20, DLL3.21, DLL3.22, DLL3.23, DLL3.24, DLL3.25, DLL3.26
7	GFTFSSYGMH	HCDR1: DLL3.3, DLL3.11
8	SAYYWN	HCDR1: DLL23.34, DLL3.35
9	SYAWS	HCDR1: DDL3.28
10	EILPGNGNTVYNEKFKD	HCDR2; DLL3.1
11	EILPGTGNTVYNEKFKD	HCDR2: DLL3.2, DLL3.4
12	IISPNDGGTNYNQKFKG	HCDR2; DLL3.8
13	VINPDNGITTYNQKFKG	HCDR2; DLL3.9
14	VINPYNDITIYNQKFQG	HCDR2: DLL3.3
15	VISGSGSSKYYADSVKG	HCDR2; DLL3.11, DLL3.15, DLL3.18, DLL3.22
16	VISHHGSSKYYADSVKG	HCDR2: DLL3.5, DLL3.10, DLL3.12, DLL3.14, DLL3.17, DLL3.19, DLL3.21,

		DLL3.23, DLL3.25, DLL3.26, DLL3.27, DLL3.31, DLL3.32, DLL3.33
17	VISHHGSSKYYARSVKG	HCDR2; DLL3.29, DLL3.30, DLL3.36
18	VISYDGSSKYYADSVKG	HCDR2; DLL3.13, DLL3.16, DLL3.20, DLL3.24
19	YISDVGHNYYNPSLKN	HCDR2; DLL3.34
20	YISDVGSNNYNPSLKN	HCDR2; DLL3.35
21	YVYYSGTTNYPNPSLKS	HCDR2; DLL3.28
22	WGDYALFAN	HCDR3:DL L3.1, DLL3.2, DLL3.4
23	DQVFAY	HCDR3; DLL3.8, DLL3.34, DLL3.35
24	DWFFYLFDY	HCDR3; DLL3.5, DLL3.10, DLL3.11, DLL3.12, DLL3.13, DLL3.14, DLL3.15, DLL3.16, DLL3.17, DLL3.26, DLL3.27, DLL3.31
25	DWFYFIFDY	HCDR3; DLL3.18, DLL3.19, DLL3.20, DLL3.21, DLL3.22, DLL3.23, DLL3.24, DLL3.25, DLL3.32, DLL3.33

26	DWWELVFDY	HCDR3; DLL3.29, DLL3.20, DLL3.36
27	EGVLYDGYEGAY	HCDR3; DLL3.3
28	GVWNYERSFDY	HCDR3; DLL3.9
29	SIAVTGFYFDY	HCDR3; DLL3.28
30	SASSSVSYMH	LCDR1; DLL3.35
31	KASQNVGIAVA	LCDR1; DLL3.3
32	KASQNVGTNVA	LCDR1: DLL3.1, DLL3.2, DLL3.4, DLL3.9, DLL3.28
33	KSSQSLLHSDAKTFLY	LCDR1; DLL3.22, DLL3.23, DLL3.24, DLL3.25, DLL3.26, DLL3.27, DLL3.32, DLL3.33
34	KSSQSLLHSDGKTFLY	LDCR1: DLL3.5, DLL3.10, DLL3.15, DLL3.16, DLL3.17, DLL3.29, DLL3.30, DLL3.32, DLL3.36
35	RASESVHSYGNSLIH	LDCR1; DLL3.34
36	RSSKSLLHSNGITYLY	LCDR1; DLL3.8
37	RSSQSLLHSDAKTFLD	LCDR1; DLL3.18, DLL3.19, DLL3.20, DLL3.21,
38	RSSQSLLHSDGKTFLD	LCDR1: DLL3.11, DLL3.12, DLL3.13, DLL3.14
39	SASYRYS	LCDR2:

		DLL3.4, DLL3.28
40	AASNRYT	LCDR2: DLL3.3
41	DTSKLAS	LCDR2; DLL3.35
42	EVSNRAS	LCDR2; DLL3.11, DLL3.12, DLL3.13, DLL3.14, DLL3.18, DLL3.19, DLL3.20, DLL3.21
43	EVSNRFS	LCDR2: DLL3.5, DLL3.10, DLL3.15, DLL3.16, DLL3.17, DLL3.22, DLL3.23, DLL3.14, DLL3.25, DLL3.26, DLL3.27, DLL3.29, DLL3.30, DLL3.31, DLL3.32, DLL3.33, DLL3.36
44	QMSNLAS	LCDR2; DLL3.8
45	RASNLES	LCDR2;DLL 3.34
46	SASYRYS	LCDR2; DLL3.1, DLL3.2, DLL3.9
47	QQYSTYPYT	LCDR3: DLL3.3
48	AQNLELP	LCDR3: DLL3.8
49	LQGERLPFT	LCDR3;DLL 3.5, DLL3.10, DLL3.11, DLL3.12, DLL3.13, DLL3.14, DLL3.15, DLL3.16,

		DLL3.17, DLL3.26, DLL3.27, DLL3.31
50	LQGIHLPFT	LCDR3; DLL3.29, DLL3.30, DLL3.36
51	LQGRELPFT	LCDR3; DLL3.18, DLL3.19, DLL3.20, DLL3.21, DLL3.22, DLL3.23, DLL3.24, DLL3.25, DLL3.32, DLL3.33
52	QQTNEP	LCDR3; DLL3.34
53	QQWSSNPLT	LCDR3; DLL3.35
54	QQYNNYPLT	LCDR3; DLL3.4, DLL3.9, DLL3.28
55	QQYNSYPFT	LCDR3; DLL3.1, DLL3.2
56	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISGSGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.11, DLL3.15
57	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISGSGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.18, DLL3.22
58	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.5, DLL3.12, DLL3.26
59	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.19, DLL3.23
60	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISYDGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.13, DLL3.16,
61	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWAVISYDGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFDYWGQGTLVTVSS	VH; DLL3.20, DLL3.24
62	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWSVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAKD WFFYLFDYWGQGTLVTVSS	VH; DLL3.14, DLL3.17
63	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWWSVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAKD WFFYLFDYWGQGTLVTVSS	VH; DLL3.21, DLL3.25

64	EVQLQQSGPVLVKPGASVKMSCKASGFTFTDYYMNWVKQSHGK SLEWIGVINPDNGITTYNQKFKGKATLTVDKSSSTAYMELNGLTSE DSAVYYCARGVWNYERSFDYWGQGTTTLTVSS	VH; DLL3.9
65	EVQLVESGGGLVQPGLSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWVAVISHHGSSKYYADSVKGRYTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFYDYWGQGTTLTVSS	VH; DLL3.27
66	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGL EWIGYVYYSGTTNYPNPSLKSRTISVDTSKNQFSLKLSSVTAADTA VYYCASIATGIFYDYWGQGTTLTVSS	VH; DLL3.28
67	QVQLQQSGPVLVKPGASVKMSCKASGYSTFDYYVNWVKQSHGK SLEWIGIISPNDGGTNYNQKFKGKATLTVDKSSSTAYMEVNSLTSE DSAVYYCARDDDL GWYFDVWGTGTTVTVSS	VH; DLL3.8
68	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWVAVISHHGSSKYYARSVKGRFTISRDN SKNTLYLEMNSLRA EDTAVYYCARDWWELVFDYWGQGTTLTVSS	VH; DLL3.29, DLL3.30, DLL3.36
69	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWVAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFYDYWGQGTTLTVSS	VH DLL3.10, DLL3.31
70	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWVAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFYFIFYDYWGQGTTLTVSS	VH; DLL3.32, DLL3.33
71	QVQLVQSGAEVKKPGASVKVSKASDYTFSNYYIEWVRQAPGQG LEWMGEILPGNGNTVYNEKFKDRVTMTVD TSTSTAYMELRSLRSD DTAVYYCARWGDYALFANWGQGTTLTVSS	VH; DLL3.1
72	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYFMNWVRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVD RSTSTVYMELSSLRS EDTAVYYCAREGVLYDGYEGAYWGQGTTLTVSS	VH; DLL3.3
73	QVQLVQSGAEVKKPGASVKVSKATDYIFSNNYYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVTMTVD TSTSTVYMELSSLRSED TAVYYCARWGDYALFANWGQGTTLTVSS	VH; DLL3.2, DLL3.4
74	SDVQLQESGPGLVKPSQSLSLTCSVTGYSITSAYYWNWIRQFPGN KLEWMGYISDVGHNYNPSLKNRISITRD TSKNQFFLKLNSVTPED TATYYCARDQVFAYWGQGTTLTVSA	VH DLL3.34
75	SDVQLQESGPGLVKPSQSLSLTCSVTGYSITSAYYWNWIRQFPGN KLEWMGYISDVGSNNYNPSLKNRISITRD TSKNQFFLKLNSVTTED TATYFCTRDQVFAYWGQGTTLTVS	VH DLL3.35
76	DIQLTQSPSFLSASVGDRVTITCKASQNVGIAVAWYQQKPGKAPKL LIYAASNRYTGVPSRFSGSGSGTEFTLT ISSLQPEDFATYYCQQYS TYPYTFGQGTKLEIK	VL; DLL3.3
77	DIQMTQSPSFLSASVGDRVTITCKASQNVGTNVAWYQQKPGKAPK PLIYSTSYRYSGVPSRFSGSGSGTEFTLT ISSLQPEDFATYYCQQY NNYPLTFGGGTKVEIK	VL; DLL3.4
78	DIQMTQSPSSLASVGDRVTITCKSSQSLHSDAKTFLYWYQQKP GKAPKLLIYEVSNRFSGVPSRFSGSGSGTDFLT ISSLQPEDFATY YCLQGERLPFTFGQGTKVEIK	VL; DLL3.26, DLL3.27
79	DIQMTQSPSTLSASVGDRVTITCKASQNVGTNVAWYQQKPGKAPK ALIYSASYRYSGVPSRFSGSGSGTEFTLT ISSLQPDDFATYYCQQY NSYPFTFGQGTKLEIK	VL; DLL3.1
80	DIVMTQAAFSNPVTVGTSASISCRSSKSLHNSGITYLYWYLQKPG QSPQLLIYQMSNLASGVPRFSSSGSGTDFLT LRISRVEAEDGVY YCAQNLELPWTFGGGTKLEIK	VL; DLL3.8
81	DIVMTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSP KALIYSASYRYSGVPDRFTGSGSGTDFLT FSSVQSEDLAEYFCQ	VL; DLL3.9

	QYNNYPLTFGGGKLEIK	
82	DIVMTQSPLSLPVTGPGEPAISICKSSQSLLHSDAKTFLYWYLQKPG QSPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGRELPFTFGQGTKVEIK	VL; DLL3.22, DLL3.23, DLL3.24, DLL3.25
83	DIVMTQSPLSLPVTGPGEPAISICKSSQSLLHSDGKTFLYWYLQKPG QSPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGERLPFTFGQGTKVEIK	VL; DLL3.5, DLL3.15, DLL3.16, DLL3.17
84	DIVMTQSPLSLPVTGPGEPAISICRSSQSLLHSDAKTFLDWYLQKPG QSPQLLIYEVS NRAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGRELPFTFGQGTKVEIK	VL DLL3.18, DLL3.19, DLL3.20, DLL3.21
85	DIVMTQSPLSLPVTGPGEPAISICRSSQSLLHSDGKTFLDWYLQKPG QSPQLLIYEVS NRAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGERLPFTFGQGTKVEIK	VL; DLL3.11, DLL3.12, DLL3.13, DLL3.14
86	DIVMTQTPLSLSVTPGQPASISICKSSQSLLHSDAKTFLYWYLQKPG QPPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGRELPFTFGPGTKVEIK	VL DLL3.32, DLL3.33
87	DIVMTQTPLSLSVTPGQPASISICKSSQSLLHSDGKTFLYWYLQKPG QPPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGERLPFTFGPGTKVEIK	VL; DLL3.10, DLL3.31
88	DIVMTQTPLSLSVTPGQPASISICKSSQSLLHSDGKTFLYWYLQKPG QPPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGIHLPFTFGPGTKVEIK	VL; DLL3.29, DLL3.30, DLL3.36
89	DTVLTQSPASLAVSLGQRATISCRASESVHSYGNSLIHWYQQKPG QPPRLLIYRAS NLES GIPARFSGSGSRTDFTLTINPVEADDAVATYYC QQTNEPLTFGAGTKLELK	VL; DLL3.34
90	EIVLTQSPGTLSPGERVTLS CRASQRVNNNYLAWYQQRPQGAP RLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YDRSPLTFGGGKLEIK	VL; DLL3.28
91	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR WIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQW SSNPLTFGAGTKLELK	VL; DLL3.35
92	GFTFSSFGMH	HCDR1; Muc17.7, Mu c17.21, Muc17.22, Muc17.23, Muc17.24
93	GYAFSDYWIN	HCDR1: Muc17.2
94	GYEFSSHWMN	HCDR1; Muc17.1, Muc17.8, Muc17.9, muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14,

		Muc17.25, Muc71.26, Muc17.27, Muc17.28, Muc17.29, Muc17.30, Muc17.31
95	GYIFSNHWMN	HCDR1; Mcu17.3
96	GYTFTSYWLN	HCDR1; Muc17.17, Muc17.42, Muc17.43, Muc17.44, Muc17.46, Muc17.47
97	GYTFTSYWMN	HCDR1; Muc17.4, Muc17.5, Muc17.6, Muc17.15, Muc17.16, Muc17.18, Muc17.19, Muc17.20, Muc17.32, Muc17.33, Muc17.34, Muc17.35, Muc17.36, Muc17.37, Muc17.38, Muc17.39, Muc17.40, Muc17.41, Muc17.45, Muc17.48, Muc17.49
98	GYTFTSYWMN	HCDR1; Mcu17.31
99	MIHPDSESLNQQFKD	HCDR2; Muc17.17, Muc17.39, Muc17.40, Muc17.41, Muc17.46, Muc17.47
100	MIHPDSETRLNQEFD	HCDR2; Muc17.5, Muc17.20
101	MIHPDSETRLNQQFKD	HCDR2; Muc17.4, Muc17.15, Muc17.16,

		Muc17.18, Muc17.19, Muc17.31, Muc17.33, Muc17.34, Muc17.35, Muc17.36, Muc17.37, Muc17.38, Muc17.42, Muc17.43, Muc17.44, Muc17.45, Muc17.48, Muc17.49
102	MIHPDSETRLNQKFTD	HCDR2; Muc17.6
103	QIYPGDGDINYNEKFRG	HCDR2; Muc17.1, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14, Muc17.25, Muc17.26, Muc17.27, Muc17.28, Muc17.29, Muc17.30, Muc17.31
104	QIYPGDGDINYNGKFRG	HCDR2; Muc17.3
105	QVYPGDDDDINYNGKFRG	HCDR2; Muc17.2
106	YISSGSSTIYYADTVKG	HCDR2; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
107	HGNYVMDY	HCDR2; Muc17.8
108	HGNYVMDY	HCDR3; Muc17.1, Muc17.2, Muc17.8, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14,

		Muc17.25, Muc17.26, Muc17.27, Muc17.28, Muc17.29, Muc17.30, Muc17.31
109	QGIITSVQEFAY	HCDR3; Muc17.4, Muc17.6, Muc17.15, Muc17.16, Muc17.17, Muc17.18, Muc17.19, Muc17.31, Muc17.32, Muc17.33, Muc17.34, Muc17.35, Muc17.36, Muc17.37, Muc17.38, Muc17.39, Muc17.40, Muc17.41, Muc17.42, Muc17.43, Muc17.44, Muc17.45, Muc17.46, Muc17.48, Muc17.49
110	QGVITSVQEFAY	HCDR3; Muc17.5, Muc17.20
111	WGYYGSSYFAY	HCDR3; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
112	HGNYLMDY	HCDR3; Muc17.3
113	SASSSLNYIY	LCDR1; Muc17.6
114	SASSSVNYIF	LCDR1; Muc17.18, Muc17.19, Muc17.41, Muc17.44, Muc17.46
115	SASSSVNYIY	LCDR1; Muc17.4,

		Muc17.5, Muc17.15, Muc17.16, Muc17.17, Muc17.31, Muc17.32, Muc17.33, Muc17.34, Muc17.35, Muc17.36, Muc17.37, Muc17.38, Muc17.39, Muc17.40, Muc17.41, Muc17.43, Muc17.45, Muc17.47, Muc17.48, Muc17.49
116	SASSSVSYMF	LCDR1; Muc17.1, Muc17.2, Muc17.8, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14, Muc17.25, Muc17.26, Muc17.27, Muc17.28, Muc17.29, Muc17.30, Muc17.31
117	SVSSNVDYVF	LCDR1; Muc17.3
118	KASEDIYNRLA	LCDR1; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
119	RTSNLAS	LCDR2; Muc17.1, Muc17.2, Muc17.4, Muc17.5, Muc17.6, Muc17.8, Muc17.9, Muc17.10,

		Muc17.11, Muc17.12, Muc17.13, Muc17.14, Muc17.15, Muc17.16, Muc17.17, Muc17.18, Muc17.19, Muc17.20,M uc17.25, Muc17.26, Muc17.27, Muc17.28, Muc17.29, Muc17.30, Muc17.31, Muc17.32, Muc17.33, Muc17.34, Muc17.36, Muc17.37, Muc17.38, Muc17.39, Muc17.40, Muc17.41, Muc17.42, Muc17.43, Muc17.44, Muc17.45, Muc17.46, Muc17.48, Muc17.49
120	RTSNLAT	LCDR2; Muc17.3
121	GATNLET	LCDR2; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
122	QQFHDYPRT	LCDR3; Muc17.1, Muc17.8, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14, Muc17.25, Muc17.26, Muc17.27, Muc17.28,

		Muc17.29, Muc17.30, Muc17.31
123	QQFHSPRT	LCDR3; Muc17.2, Muc17.3
124	QQFWRTPT	LCDR3; Muc17.7, Muc17.21, Muc17.22, Muc17.23
125	QQYHSYPLT	LCDR3; Muc17.4, Muc17.5, Muc17.6, Muc17.15, Muc17.16, Muc17.17, Muc17.18, Muc17.19, Muc17.20M uc17.31, Muc17.32, Muc17.33, Muc17.34, Muc17.35, Muc17.36, Muc17.37, Muc17.38, Muc17.39, Muc17.40, Muc17.41, Muc17.42, Muc17.43, Muc17.44, Muc17.45, Muc17.47, Muc17.48, Muc17.49
126	CQQFWRTPT	LCDR3; Muc17.24
127	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWVRQMPGK GLEWMGQIYPGDGDINYNQKFKDRVTITADKSISTAYLQWSSLKA SDTAMYYCARHGNYVMDYWGQGTTLTVSS	VH; Muc17.1, Muc17.8, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14
128	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPDSESRNQNQKFKDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSS	VH; Muc17.17
129	QVQLVQSGAEVKKPGASVKVSKASGYEFSSHWMNWVRQAPGQ	VH;

	GLEWMGQIYPGDGDINYNKFRGRVTMTTRDTSTSTVYMELSSLRS EDTAVYYCARHGNYVMDYWGQGLTVTVSS	Muc17.29, Muc17.30, Muc17.31
130	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTLTVDKSSSTAYMELSSLRSE DTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.45
131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQEFKDRVTMTTRDTSTSTVYMELSSLR SEDTAVYYCARQGVITSVQEFAYWGQGLTVTVSS	VH; Muc17.5, Muc17.20
132	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTLTRDKSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.37
133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTLTVDKSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH Muc17.35
134	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTLTVDTSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.36
135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTMTTRDTSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.232, Muc17.33, Muc17.34
136	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTMTTRDTSTSTVYMELSSLR SEDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.31, Muc17.48, Muc17.49
137	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTMTVDKSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.38
138	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFTDRVTMTTRDTSTSTVYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH Muc17.6
139	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSDYWINWVRQAPGQ GLEWMGQVYPGDDINYNKFRGRVTITADKSTSTAYMELSSLRS EDTAVYYCARHGNYVMDYWGQGTTVTVSS	VH Muc17.2
140	QVQLVQSGAEVKKPGSSVKVSCKASGYEFSSHWMNWVRQAPGQ GLEWMGQIYPGDGDINYNKFRGRVTITADKSTSTAYMELSSLRS EDTAVYYCARHGNYVMDYWGQGTTVTVSS	Vh Muc17.25, Muc17.26, Muc17.27, Muc17.28
141	QVQLVQSGAEVKKPGSSVKVSCKASGYIFSNHWMNWVRQAPGQ GLEWMGQIYPGDGDINYNKFRGRVTITADKSTSTAYMELSSLRS EDTAVYYCARHGNYLMDYWGQGTTVTVSS	VH; Muc17.3
142	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPSDSESLRNQKFKDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Mucc.17.46, Muc17.47
143	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFKDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.42, Muc17.43, Muc17.44
144	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSESLRNQKFKDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGLTVTVSS	VH; Muc17.39, Muc17.40, Muc17.41

145	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWWMGMHPDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTLLTVSS	VH; Muc17.4, Muc17.15, Muc17.16, Muc17.18, Muc17.19
146	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWRQAPGK GLEWWSYISSGSSTIYYADTVKGRFTISRDNALNSLYLQMNSLRAE DTAVYYCARWGYGSSYFAYWGQGTLLTVSS	VH; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
147	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPKL LIYGATNLETGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQQFW RTPPTFGGGTKVEIK	VL; Muc17.24
148	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLISGATNLETGVPSRFSGSGSGDKDYTLTISLQPEDATYYCQQF WRTPTFGGGTKVEIK	VL; Muc17.21
149	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLISGATNLETGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQQF WRTPTFGGGTKVEIK	VL; Muc17.7
150	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLIYGATNLETGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQQF WRTPTFGGGTKVEIK	VL; Muc17.22
151	EIVLTQSPATLSLSPGERATLSCSASSSVNYIFWYQQKPGQAPRLLI YRTSNLASGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQYHSY PLTFGGGTKVEIK	VL; Muc17.18
152	EIVLTQSPATLSLSPGERATLSCSASSSVNYIYWYQQKPGQAPRLLI YRTSNLASGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQYHSY PLTFGGGTKVEIK	VL; Muc17.16, Muc17.17, Muc17.34, Muc17.39, Muc17.42, Muc17.49
153	EIVLTQSPATLSLSPGERATLSCSASSSVSYMFYQQKPGQAPRL LIYRTSNLASGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQFHD YPRTFGGGTKVEIK	VL; Muc17.8, Muc17.27, Muc17.31
154	EIVLTQSPATLSLSPGERATLSCSASSSVSYMFYQQKPGQAPRL LIYRTSNLASGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQFHS YPRTFGGGTKVEIK	VL; Muc17.2
155	EIVLTQSPATLSLSPGERATLSCSASSSVSYMFYQQKPGQAPRP WIYRTSNLASGIPPRFSGSGSGTDYTLTISLLEPEDFAVYYCQQFH DYPRTFGGGTKVEIK	VL; Muc17.28
156	EIVLTQSPATLSLSPGERATLSCSVSSNVDYVFWYQQKPGQAPRL LIYRTSNLATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQFHS YPRTFGGGTKVEIK	VL; Muc17.3
157	EIVLTQSPATLSVSPGERATLSCSASSSVNYIYWYQQKPGQAPRP WIYRTSNLASGIPARFSGSGSGTEYTLTISLQSEDFAVYYCQQYH SYPLTFGGGTKVEIK	VL; Muc17.20
158	EIVMTQSPATLSVSPGERATLSCSASSSLNYIYWYQQKPGQAPRLL IYRTSNLASGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHS YPLTFGGGTKVEIK	VL; Muc17.6
159	EIVMTQSPATLSVSPGERATLSCSASSSVNYIYWYQQKPGQAPRL	VL;

	LIYRTSNLASGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHS YPLTFGGGKVEIK	Muc17.5, Muc17.15, Muc17.33, Muc17.45, Muc17.48
160	EIVMTQSPATLSVSPGERATLSCSASSSVSYMFYQQKPGQAPRL LIYRTSNLASGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.14, Muc17.26, Muc17.30
161	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPPRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.13
162	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPPRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIKR	VL; Muc17.11
163	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.9, Muc17.25, Muc17.29
164	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.10
165	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKPW IYRTSNLASGVPPRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.12
166	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKPW IYRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGGKVEIK	VL; Muc17.1
167	IQMTQSPSSLSASVGDRVITITCSASSSVNYIFWYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYHS YPLTFGGGKVEIK	VL; Muc17.19, Muc17.41, Muc17.44, M uc17.46
168	IQMTQSPSSLSASVGDRVITITCSASSSVNYIYWYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYHS YPLTFGGGKVEIK	VL; Muc17.4, Muc17.31, Muc17.32, Muc17.35, Muc17.36, Muc17.387, Muc17.38, Muc17.40, Muc17.43, Muc17.47
169	DIQMTQSPSSLSASVGDRVITITCKASEDIYNRLAWYQQKPGKAPKL LIYGATNLETGVPSRFSGSGSGKDYTLTISLQPEDFATYYCQQFW RTPPTFGGGKVEIK	VL; Muc17.23
170	GFTFSSFGMH	HCDR1; CLDN182.3, CLDN182.& , CLDN182.1 2, CLDN182.1

		3
171	GYAFNNYWMN	HCDR1; CLDN182.5
172	GYAFSSYWMN	HCDR1; CLDN182.6, CLDN182.9, CLDN182.1 5, CLDN182.1 6
173	GYTFTNFGIT	HCDR1; CLDN182.4, CLDN182.8, CLDN182.1 0, CLDN18.11
174	GYTFTNSGMN	HCDR1; CLDN182.2, CLDN182.1 4, CLDN182.1 7
175	GYTFTNYGMN	HCDR1; CLDN182.1
176	EIYPSSGNTFYNEKFKG	HCDR2; CLDN182.4, CLDN182.8, CLDN182.1 0, CLDN182.1 1
177	QISPGNGNSNFNGKFKG	HCDR2; CLDN182.5
178	QIYPGNGNSNFNGKFKA	HCDR2; CLDN182.6, CLDN182.9, CLDN182.1 5, CLDN182.1 6
179	WINTNTGEPTFAEEFRG	HCDR2; CLDN182.2, CLDN182.1 4, CLDN182.1 7
180	WINTNTGEPTYAEEFKG	HCDR2; CLDN182.1
181	YISSGNSAIYYADTVNG	HCDR2; CLDN182.3, CLDN182.7, CLDN182.1 2, CLDN182.1

		3
182	GGGPLRSRYFDY	HCDR3; CLDN182.4, CDLN182.8, CLDN182.1 0, CLDN182.1 1
183	GGRFGNAMDY	HCDR3; CLDN182.6, CLDN182.9, CLDN182.1 5, CLDN182.1 6
184	GGRYGNAMDY	HCDR3; CLDN182.5
185	LRYGNSFDY	HCDR3; CLDN182.3, CLDN182.7, CLDN182.1 2, CLDN182.1 3
186	YFYGNSFVY	HCDR3; CLDN182.1
187	YYYGNSFAY	HCDR3; CLDN182.2, CLDN182.1 4, CLDN182.1 7
188	KSSQSLLNSGNQKNYLT	LCDR1; CLDN182.1, CLDN182.2, CLDN182.3, CLDN182.6, CLDN182.7, CLDN182.9, CLDN182.1 2, CLDN182.1 3, CLDN182.1 4, CLDN182.1 5, CLDN182.1 6, CLDN182.1 7
189	KSSQSLLNSGNQQRNYLT	LCDR1; CLDN182.5
190	RSSQSLFSSGNQKNYLT	LCDR1;

		CLDN182.4, CLDN182.8, CLDN182.1 0, CLDN182.1 1
191	WASTRES	LCDR2; CLDN182.1, CLDN182.2, CLDN182.3, CLDN182.4, CLND182.5, CLDN182.6, CLDN182.7, CLDN182.8, CLDN182.9, CLND182.1 0, CLDN182.1 1, CLDN182.1 2, CLDN182.1 3, CLDN182.1 4, CLDN182.1 5, CLDN182.1 6, CLDN182.1 7
192	QNAYFYPT	LCDR3; CLDN182.5, CLDN182.6, CLND182.9, CLDN182.1 5, CLDN182.1 6
193	QNDYYYPLT	LCDR3; CLDN182.4, CLDN182.8, CLND182.1 0, CLDN182.1 1
194	QNNYFYPLT	LCDR3; CLDN182.2, CLND182.1 4, CLND182.1 7
195	QNNYNFPLT	LCDR3;

		CLDN182.1
196	QNNYYYPLT	LCDR3; CLDN182.3, CLND182.7, CLND182.1 2, CLND182.1 3
197	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWRQAPGK GLEWWAYISSGNSAIYYADTVNGRFTISRDNPKNTLYLQMNSLRAE DTAVYYCARLRYGNSFDYWGQGTLVTVSS	VH; CLDN182.1 2, CLND182.1 3
198	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWRQAPGK GLEWWSYISSGNSAIYYADTVNGRFTISRDNKNSLYLQMNSLRAE DTAVYYCARLRYGNSFDYWGQGTLVTVSS	VH; CLDN182.3, CLDN182.7
199	QIQLVQSGAEVKKPGASVKVSCKASGYTFTNSGMNWRQAPGQ GLEWMGWINTNTGEPTFAEEFRGRVTFTLDTASTAYMELSRLRS DDTAVYYCARYYYGNSFAYWGQGTLVTVSS	VH; CLDN182.1 4
200	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNFGITWVRQAPGQG LEWIGEIPSSGNTFYNEKFKGRVTLTADKSSSAAYMELRSLRSD TAVYYCARGGGPLRSRYFDYWGQGTLVTVSS	VH; CLDN182.1 0, CLND182.1 1
201	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNFGITWVRQAPGQG LEWMGEIYPSSGNTFYNEKFKGRVTMTTDTSTSTAYMELRSLRSD DTAVYYCARGGGPLRSRYFDYWGQGTLVTVSS	VH; CLDN182.4, CLND182.8
202	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNSGMNWRQAPGQ GLEWMGWINTNTGEPTFAEEFRGRVTMTDRDTSISTAYMELSRLRS DDTAVYYCARYYYGNSFAYWGQGTLVTVSS	VH; CLND182.2, CLND182.1 7
203	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWRQAPGQ GLEWMGWINTNTGEPTYAEEFKGRVTMTDRDTSISTAYMELSRLRS DDTAVYYCARYFYGNSFVYWGQGTLVTVSS	VH; CLDN182.1
204	QVQLVQSGAEVKKPGSSVKVSCKASGYAFNNYWMNWRQAPGQ GLEWMGQISPGNGNSNFNGKFKGRVTITADKSTSTAYMELSSLRS EDTAVYYCARGGRYGNAMDYWGQGTTVTVSS	VH; CLND182.5
205	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSYWMNWRQAPGQ GLEWIGQIYPGNGNSNFNGKFKARVTLTADKSSSTAYMELSSLRS EDTAVYYCARGGRFGNAMDYWGQGTTVTVSS	VH; CLND182.1 5, CLND182.1 6
206	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSYWMNWRQAPGQ GLEWMGQIYPGNGNSNFNGKFKARVTITADKSTSTAYMELSSLRS EDTAVYYCARGGRFGNAMDYWGQGTTVTVSS	VH; CLDN182.6, CLDN182.9
207	DIVMTQSPDSLAVSLGERATINCKSSQSLNSGNQKNYLTWYQQK PGQPPKLLIFWASTRESGVDPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNYYYPLTFGGGKVEIK	VL; CLND182.7, CLND182.1 3
208	DIVMTQSPDSLAVSLGERATINCKSSQSLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNYNFPLTFGGGKVEIK	VL; CLND182.1
209	DIVMTQSPDSLAVSLGERATINCKSSQSLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISSLQAEDVAV	VL; CLDN182.3,

	YYCQNNYYYPLTFGGGKVEIK	CLND182.1 2
210	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQRNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLQAEDVAV YYCQNAVYFYPYTFGGGKVEIK	VL; CLND182.5
211	DIVMTQSPDSLAVSLGERATINCRSSQSLFSSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGADFTLTISLQAEDVAV YYCQNDYYYPLTFGGGKVEIK	VL; CLND182.8, CLND182.1 1
212	DIVMTQSPDSLAVSLGERATINCRSSQSLFSSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLQAEDVAV YYCQNDYYYPLTFGGGKVEIK	VL; CLND812.4, CLND182.1 0
213	DIVMTQSPDSLAVSLGERATMNCKSSQSLLNSGNQKNYLTWYQQ KPGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLQAEDVA VYYCQNAVYFYPYTFGGGKVEIK	VL; CLND182.9, CLND182.1 6
214	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLQAEDVAV YYCQNAVYFYPYTFGGGKVEIK	VL; CLND182.6, CLND182.1 5
215	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLQAEDVAV YYCQNNYFYPLTFGGGKVEIK	VL; CLND182.2, CLND182.1 4, CLND182.1 7
216	SGGGGS	1xG4S
217	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1
218	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (N297A)
219	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVKPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (L234F/L23 5E/P331S)
220	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN	CH1-3 IgG1 (Y349C/K37)

	TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSCLTVDKSRWQQGNVFSCSVMHEALH NHYTQESLSLSPGK	0E/K409D/K 439E)
221	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPCRKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (S354C/ D356K/ E357K/ D399K)
222	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (S354C/T36 6W)
223	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (Y349C/ T366S/ L368A/ Y407V)
224	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSCLTVDKSRWQQGNVFSCSVMHEALH NHYTQESLSLSPGK	CH1-3 IgG1 (L234F/L23 5E/P331S/ Y349C/K37 0E/K409D/K 439E)
225	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVYTLPPCRKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (L234F/L23 5E/P331S/ S354C/ D356K/ E357K/ D399K)
226	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (L234F/L23 5E/P331S/ S354C/T36 6W)

227	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (L234F/L23 5E/P331S/ Y349C/ T366S/ L368A/ Y407V)
228	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSDLTVDKSRWQQGNVFSCSVMHEALH NHYTQESLSLSPGK	CH1-3 IgG1 (N297A/ Y349C/K37 0E/K409D/K 439E)
229	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPCRKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (N297A/ S354C/ D356K/ E357K/ D399K)
230	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (N297A/ S354C/T36 6W)
231	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	CH1-3 IgG1 (N297A/ Y349C/ T366S/ L368A/ Y407V)
232	EPKSSDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	Fc IgG1
233	EPKSSDKTHTCPPCPAPELLGGGPSVFLFPPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (N297A)
234	EPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV	Fc IgG1 (L234F/L23

	LTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	5E/P331S)
235	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVCTL PPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQES LSLSPGK	Fc IgG1 (Y349C/K37 0E/K409D/K 439E)
236	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVYTL PPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLKSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (S354C/ D356K/ E357K/ D399K)
237	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (S354C/T36 6W)
238	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLVSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (Y349C/ T366S/ L368A/ Y407V)
239	EPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTL PPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQES LSLSPGK	Fc IgG1 (L234F/L23 5E/P331S/ Y349C/K37 0E/K409D/K 439E)
240	EPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTL PPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLKSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (L234F/L23 5E/P331S/ S354C/ D356K/ E357K/ D399K)
241	EPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (L234F/L23 5E/P331S/ S354C/T36 6W)
242	EPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLVSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (L234F/L23 5E/P331S/ Y349C/ T366S/ L368A/ Y407V)

243	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTL PPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSCLTVDKSRWQQGNVSCSVMHEALHNHYTQES LSLSPGK	Fc IgG1 (N297A/ Y349C/K37 0E/K409D/K 439E)
244	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLKSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (N297A/ S354C/ D356K/ E357K/ D399K)
245	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (N297A/ S354C/T36 6W)
246	EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLVSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKS LSLSPGK	Fc IgG1 (N297A/ Y349C/ T366S/ L368A/ Y407V)
247	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRQAKVQWKVDN ALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	CL1
248	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGKG LEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTLYLQMNSL EDTAMYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vA
249	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vB
250	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vC
251	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vD
252	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKLNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vE
253	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKVNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vF
254	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vG
255	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMDWRQAPGK GLEWGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vH
256	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMNWRQAPGK GLEWGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFEYWGQGTLLTVSS	VH; CD3vI

257	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLLTVSS	VH; CD3vJ
258	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFNYWGQGTLLTVSS	VH; CD3vK
259	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSFYAYWGQGTLLTVSS	VH; CD3vL
260	QLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLE WVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAE DTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	VH; CD3vB2
261	QAVVTQEPSLTVSPGGTVTLTCSSTGAVTTSNYANWWQKPGK SPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYY CALWYSNHWVFGGGTKLTVL	VL; CD3
262	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSLTVSPGGTVTLTCSSTGAVT TSNYANWWQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vB scfv-Fc
263	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSLTVSPGGTVTLTCSSTGAVT TSNYANWWQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vC scfv-Fc
264	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKINNYATYYADSVKGRFTISRDDSKNTLYLQMNSLR AEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSSGKPGSGK PGSGKPGSGKPGSQAVVTQEPSLTVSPGGTVTLTCSSTGAVTT SNYANWWQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTC PPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vD scfv-Fc
265	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGK GLEWVGRIIRSKLNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSLTVSPGGTVTLTCSSTGAVT TSNYANWWQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT	CD3vE scfv-Fc

	CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	
266	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGK GLEWVGRIIRSKVNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWWQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vF scfv- Fc
267	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGK GLEWVGRIIRSKSNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWWQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vG scfv-Fc
268	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMDWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWWQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vH scfv-Fc
269	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFEYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWWQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vI scfv- Fc
270	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWWQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA	CD3vJ scfv- Fc

	LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVYTLPPCRKKLT NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	
271	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSWFNYWGQGTLLTVVSSGKPGSG KPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVT TSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVYTLPPCRKKLT NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vK scfv-Fc
272	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGK GLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSL RAEDTAVYYCVRHGNFGDSYVSFYAWGQGTLLTVVSSGKPGSGK PGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVTT SNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTC PPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPASIIEKTISKAKGQPREPQVYTLPPCRKKLT NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vL scfv- Fc
273	QLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLE WVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAE DTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVVSSGKPGSGKPG SGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCGSSTGAVTT SNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAA LTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTC PPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPASIIEKTISKAKGQPREPQVYTLPPCRKKLT NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFF LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD3vB2scfv -Fc
274	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVISGSGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGTLLTVVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL T KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.11, DLL3.15
275	EVQLLES GGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVISGSGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYFIDYWGQGTLLTVVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV EPKSCDKT	HC; DLL3.11, DLL3.15

	HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	
276	EVQLLESQGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPGK GLEWVAIVISHHGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.18, DLL3.22
277	EVQLLESQGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPGK GLEWVAIVISHHGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.5, DLL3.12, DLL3.26
278	EVQLLESQGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPGK GLEWVAIVISYDGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.19, DLL3.23
279	EVQLLESQGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPGK GLEWVAIVISYDGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.13, DLL3.16,
280	EVQLLESQGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPGK GLEWVSVISHHGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCAKDWFFYLFIDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF	HC; DLL3.20, DLL3.24

	FLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	
281	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYGMHWVRQAPGK GLEWWSVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAKDWFYFIDYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; DLL3.14, DLL3.17
282	EVQLQQSGPVLVKPGASVKMSCKASGFTFTDYYMNWVKQSHGK SLEWIGVINPDNGITTYNQKFKGKATLTVDKSSSTAYMELNGLTSE DSAVYYCARGVWNYERSFDYWGQGTLLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC DKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLS PGK	HC; DLL3.21, DLL3.25
283	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWVAVISHHGSSKYYADSVKGRYTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFIDYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; DLL3.9
284	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGL EWIGYVYYSGTTNYPNPSLKSRTISVDTSKNQFSLKLSSVTAADTA VYYCASIATGIFYFDYWGQGTLLTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT CPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSRDELTK NQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; DLL3.27
285	QVQLQQSGPVLVKPGASVKMSCKASGYSTFDYYVNWVKQSHGK SLEWIGIISPNDGGTNYNQKFKGKATLTVDKSSSTAYMEVNSLTSE DSAVYYCARDDDLGWYFDVWGTGTTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSP GK	HC; DLL3.28
286	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK	HC; DLL3.8

	GLEWWAVISHHGSSKYYARSVKGRFTISRDN SKNTLYLEMNSLRA EDTAVYYCARDWWELVFDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSDDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSP GK	
287	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWWAVISHHGSSKYYARSVKGRFTISRDN SKNTLYLEMNSLRA EDTAVYYCARDWWELVFDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSDDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSP GK	HC; DLL3.29, DLL3.30, DLL3.36
288	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWWAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYLFYDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSDDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSPGK	HC DLL3.10, DLL3.31
289	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGK GLEWWAVISHHGSSKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARDWFFYFIFDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSDDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSPGK	HC; DLL3.32, DLL3.33
290	QVQLVQSGAEVKKPGASVKVSCKASDYTFSTNYIEWVRQAPGQG LEWMGEILPGNGNTVYNEKFKDRVTMTVDTSTSTAYMELRSLRSD DTAVYYCARWGDYALFANWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF LYSDDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSPGK	HC; DLL3.1
291	QVQLVQSGAEVKKPGASVKVSCKASGYTFDYFMNWRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLR EDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSASTKGPSVFP	HC; DLL3.3

	LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	
292	QVQLVQSGAEVKKPGASVKVSCKATDYIFSNNYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVTMTVDTSTSTVYMESSLRSED TAVYYCARWGDYALFANWGQGLTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.2, DLL3.4
293	SDVQLQESGPGGLVKPSQSLSLTCSVTGYSITSAYYWNWIRQFPGN KLEWMGYISDVGHNNYNP SLKNRISITRDTSKNQFFLKLNSVTPED TATYYCARDQVFAYWGQGLTVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.34
294	SDVQLQESGPGGLVKPSQSLSLTCSVTGYSITSAYYWNWIRQFPGN KLEWMGYISDVGSNNYNP SLKNRISITRDTFKNQFFLKLNSVTTED TATYFCTRDQVFAYWGQGLTVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSPGK	HC; DLL3.35
295	DIQLTQSPSFLSASVGDRVTITCKASQNVGIAVAWYQQKPGKAPKLLIYAASNRYTGVP SRFSGSGSGTEFTLTISLQPEDFATYYCQQYS TYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.3
296	DIQMTQSPSFLSASVGDRVTITCKASQNVGTNVAWYQQKPGKAPKPLIYSTSYRYSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQYNNYPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.4
297	DIQMTQSPSSLSASVGDRVTITCKSSQSLHSDAKTFLYWYQQKPGKAPKLLIYEVSNRFSGVPSRFSGSGSGTDFTLTISLQPEDFATY YCLQGERLPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.26
298	DIQMTQSPSTLSASVGDRVTITCKASQNVGTNVAWYQQKPGKAPK	LC;

	ALIYSASYRYSVPSRFSGSGSGTEFTLTISLQPDDEFATYYCQQY NSYPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	DLL3.27
299	DIVMTQAAFSNPVTVGTSASISCRSSKSLHSHNGITYLYWYLQKPG QSPQLLIYQMSNLASGVDPDRFSSSGSGTDFTLRISRVEAEDVGVY YCAQNLELPWTFGGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.1
300	DIVMTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQKPGQSP KALIYSASYRYSVGPDRFTGSGSGTDFTLTFSSVQSEDLAEYFCQ QYNNYPLTFGGGKLEIKRRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTL TLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.2
301	DIVMTQSPLSLPVTGPGEPAISICKSSQSLHSDAKTFLYWYLQKPG QSPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGRELPFTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.8
302	DIVMTQSPLSLPVTGPGEPAISICKSSQSLHSDGKTFLYWYLQKPG QSPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGERLPFTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.9
303	DIVMTQSPLSLPVTGPGEPAISICKSSQSLHSDAKTFLDWYLQKPG QSPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGRELPFTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.22, DLL3.23, DLL3.24, DLL3.25
304	DIVMTQSPLSLPVTGPGEPAISICKSSQSLHSDGKTFLDWYLQKPG QSPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGERLPFTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.5, DLL3.15, DLL3.16, DLL3.17
305	DIVMTQTPLSLSVTPGQPASISCKSSQSLHSDAKTFLYWYLQKPG QPPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGRELPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC DLL3.18, DLL3.19, DLL3.20, DLL3.21
306	DIVMTQTPLSLSVTPGQPASISCKSSQSLHSDAKTFLYWYLQKPG QPPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGRELPFTFGPGTKVEIKSTFGQGTKVEIKRTVAAPSVFIFPPS EQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	LC; DLL3.11, DLL3.12, DLL3.13, DLL3.14
307	DIVMTQTPLSLSVTPGQPASISCKSSQSLHSDGKTFLYWYLQKPG QPPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGERLPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC DLL3.32, DLL3.33
308	DIVMTQTPLSLSVTPGQPASISCKSSQSLHSDGKTFLYWYLQKPG QPPQLLIYEVSNNRFSVGPDRFSGSGSGTDFTLKISRVEAEDVGVY CLQGERLPFTFGPGTKVEIKSTFGQGTKVEIKRTVAAPSVFIFPPS EQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ	LC; DLL3.10, DLL3.31

	DSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
309	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTFLYWYLQKPG QPPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGIHLPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.29, DLL3.30, DLL3.36
310	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTFLYWYLQKPG QPPQLLIYEVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYY CLQGIHLPFTFGPGTKVEIKSTFGQGTKEIKRTVAAPSVFIFPPSD EQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.29.1
311	DTVLTQSPASLAVSLGQRATISCRASESVHSYGNSLIHWYQQKPG QPPRLLIYRAS NLES GIPARFSGSGSRTDFTLTINPVEADDVATYYC QQTNE DPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.34
312	EIVLTQSPGTLSPGERVTLS CRASQRVNNNYLAWYQQRPGQAP RLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YDRSPLTFGGG TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.28
313	QIVLTQSPA IMSASPG EKVTMTCSASSSVSYMHWYQQKSGTSPKR WIYDTSKLASGV PARFSGSGSGTSYSLTISSMEAEDAATYYCQQW SSNPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVC LLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; DLL3.35
314	G	Linkers
315	GS	Linkers
316	GSS	Linkers
317	GSSSG	Linkers
318	GGGS	Linkers
319	GGGSGGGGS	Linkers
320	GGGSGGGGSGGGGS	Linkers
321	GGGSGGGGSGGGGSGGGGS	Linkers
322	GGGSGGGGSGGGGSGGGGSGGGGS	Linkers
323	PGGGGSP	Linkers
324	PGGGGSPGGGGSPGGGGSP	Linkers
325	GEPGSGE	Linkers
326	GEPGSGEGEPGSGE	Linkers
327	GEPGSGEGEPGSGEEGEPGSGE	Linkers
328	EGEPGSGEEGEPGSGEEGEPGSGEEGEPGSGE	Linkers
329	GKPGS	Linkers
330	GKPGSGKPGS	Linkers
331	GKPGSGKPGSGKPGS	Linkers
332	GKPGSGKPGSGKPGSGKPGS	Linkers
333	GKPGSGKPGSGKPGSGKPGSGKPGS	Linkers
334	SSSSG	Linkers
335	SSSSGSSSSG	Linkers
336	SSSSGSSSSGSSSSG	Linkers
337	SSSSGSSSSGSSSSGSSSSG	Linkers
338	GRPGSGPGSGRPGSGRPGS	Linkers

339	GRPGSGPGSGRPGSGRPGSGRPGS	Linkers
340	GKPGSGRPGSGKPGSGRPGS	Linkers
341	QVQLVQSGAEVKKPGASVKVSCKASDYTFSNYYIEWVRQAPGQG LEWMGEILPGNGNTVYNEKFKDRVMTMTVDTSTSTAYMELRSLRSD DTAVYYCARWGDYALFANWGQGTTLTVSSGGGGSGGGGSGGGG GSDIQMTQSPSTLSASVGDRVITICKASQNVGTNVAWYQQKPGK APKALIYSASYRSGVPSRFSGSGSGTEFTLTISLQPDDEFATYYC QQYNSYPFTFGQGTKLEIKSGGGSEVQLVESGGGLVQPGGSLRL SCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYAD SVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYV SWFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQE PSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRGLIGG TNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNH WVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKA KGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSV HEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
342	QVQLVQSGAEVKKPGASVKVSCKATDYIFSNNYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVMTMTVDTSTSTVYMELSSLRSED TAVYYCARWGDYALFANWGQGTTLTVSSGGGGSGGGGSGGGG SDIQMTQSPSTLSASVGDRVITICKASQNVGTNVAWYQQKPGKAP KALIYSASYRSGVPSRFSGSGSGTEFTLTISLQPDDEFATYYCQQ YNSYPFTFGQGTKLEIKSGGGSEVQLVESGGGLVQPGGSLRLSCA ASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVK GRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSW FAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS LTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNH VFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK GQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSV HEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
343	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMNWVRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLR EDTAVYYCAREGVLYDGYEGAYWGQGTTLTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITICKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSPRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPYTFGQGTKLEIKSGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
344	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMNWVRQAPGQ	DLL3Scfv-

	CLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITICKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPYTFGCGTKLEIKSGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFEYWGQGLTVTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWWFGGGTKLTVLEPKSSDKHTCPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	CD3Scfv-Fv
345	QVQLVQSGAEVKKPGASVKVSCKATDYIFSNNYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVMTVDTSTSTVYMELSSLRS EDTAVYYCARWGDYALFANWGQGLTVTVSSGGGGSGGGGSGGGG SDIQMTQSPSFLSASVGDRVITICKASQNVGTNVAWYQQKPGKAP KPLIYSTSYRYSVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQ YNNYPLTFGGGTKEIKSGGGSEVQLVESGGGLVQPGGSLRLSC AASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSV KGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVS WFAYWGQGLTVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRGLIGGT NKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNH WWFGGGTKLTVLEPKSSDKHTCPCPAPEFEGGPSVFLFPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKT ISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
346	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMNWRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITICKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPYTFGCGTKLEIKSGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWWFGGGTKLTVLEPKSSDKHTCPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
347	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMNWRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITICKASQNVGIAVAWYQQK	DLL3Scfv- CD3Scfv-Fv

	PGKAPKLLIYAASNRYTGVPSRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPYTFGQGTKLEIKSGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFEYWGGGTLTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWWFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	
348	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMNWRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGLYDGYEGAYWGQGTTLTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITICKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPYTFGQGTKLEIKSGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFNYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWWFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	DLL3Scfv- CD3Scfv-Fv
349	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWRQMPGK CLEWMGQIYPGDGDINYNKFRGQVTISADKSISTAYLQWSSLKAS DTAMYYCARHGNYVMDYWGGGTLTVSSGGGGSGGGGSGGGG SGGGGSIQLTQSPSFLSASVGDRVITCSASSSVSYMFYQQKPG KAPKPWIYRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYY CQQFHDPRTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLR LSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYATYYA DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFEYWGGGTLTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQ EPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPRGLIG GTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSN HWWFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISK AKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
350	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWRQMPGK GLEWMGQIYPGDGDINYNKFRGQVTISADKSISTAYLQWSSLKA SDTAMYYCARHGNYVMDYWGGGTLTVSSGGGGSGGGGSGGGG SGGGGSIQLTQSPSFLSASVGDRVITCSASSSVSYMFYQQKPG GKAPKPWIYRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATY YCQQFHDPRTFGGGTKVEIKSGGGSEVQLVESGGGLVQPGGSL RLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYATYY	Muc17scfv- CD3scfv

	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDS YVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSGKPGSQAVVT QEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLI GGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYS NHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTIS KAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	
351	QVQLQQWGAGLLKPSETLSLTCVAVYGGSGYYSWIRQPPGKC LEWIGDIDASGSTKYNP SLKSRVTISLDTSKNQFSLKLSVTAADTA VYFCARKKYSTVWSYFDNWGQGLTVTVSSGGGGSGGGGSGGG GSSYELTQPSSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQS PVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYC QAWGSSTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSL KLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS YISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRW VFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSG GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	Muc17scfv- CD3scfv
352	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNHGMHWVRQAPGK CLEWVAGIWSEGSNKYYADAVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARATYTTGWSYFDYWGQGLTVTVSSGGGGSGGGGS GGGGSSYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKS GQSPVLVIYQDAKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAFHQSTWVFGCGTQLTVLSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG NSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR WVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT	Muc17scfv- CD3scfv

	QKSLSLSPGK	
353	QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPDSESRNLNQKFKDRVITADKSTSTAYMELSSLR EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIFWYQQ KPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQYHSYPLTFGGGTKEIKSGGGGSEVQLVESGGGLVQPGG SLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYAT YYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFG DSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSPR GLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCAL WYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASI EKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
354	QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPDSESRNLNQKFKDRVITADKSTSTAYMELSSLR EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIFWYQQ KPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQYHSYPLTFGGGTKEIKSGGGGSEVQLVESGGGLVQPGGS LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNYATY YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGD SYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSPRG LIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALW YSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
355	QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPDSESRNLNQKFKDRVITADKSTSTAYMELSSLR EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGTKEIKSGGGGSEVQLVESGGGLVQP GGSRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGN FGDSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQ AVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKS PRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYC ALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA SIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
356	QVQLVQSGAEVKKPGSSVKVSCASGYTFTSYWLNWVRQAPGQ GLEWMGMIHPDSETRNLNQKFKDRVITADKSTSTAYMELSSLR	Muc17scfv- CD3scfv

	EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIEFWYQQ KPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQYHSYPLTFGGGKVEIKSGGGGGSEVQLVESGGGLVQPGG SLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYAT YYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFG DSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPR GLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCAL WYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASI EKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH ~~EA~~ LHNHYTQKSLSLSPGK	
357	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWLNWVRQAPGQ GLEWMGMHPDSE ~~TR~~ LNQKF ~~DR~~ VTITADKSTSTAYMELSSRLS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGGGSEVQLVESGGGLVQP GGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGN FGDSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQ AVVTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKS PRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYC ALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA SIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGN VFSCSVMH ~~EA~~ LHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
358	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMHPDSE ~~S~~ RLN ~~Q~~ KF ~~DR~~ VTITADKSTSTAYMELSSRLS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIEFWYQQ KPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQYHSYPLTFGGGKVEIKSGGGGGSEVQLVESGGGLVQPGG SLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYAT YYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFG DSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPR GLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCAL WYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASI EKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH ~~EA~~ LHNHYTQKSLSLSPG	Muc17scfv- CD3scfv
359	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMHPDSE ~~S~~ RLN ~~Q~~ KF ~~DR~~ VTITADKSTSTAYMELSSRLS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF	Muc17scfv- CD3scfv

	ATYYCQQYHSYPLTFGGGKVEIKSGGGGSEVQLVESGGGLVQP GSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGN FGDSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQ AVVTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKS PRGLIGGTNKRAGVPARFSGSLLGGKAALTISGAQPEDEADYYC ALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA SIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK	
360	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIEWYQQ KPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQYHSYPLTFGGGKVEIKSGGGGSEVQLVESGGGLVQPGG SLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYAT YYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFG DSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKSPR GLIGGTNKRAGVPARFSGSLLGGKAALTISGAQPEDEADYYCAL WYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASI EKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
361	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGGSEVQLVESGGGLVQP GSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGN FGDSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQ AVVTQEPLSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQQKPGKS PRGLIGGTNKRAGVPARFSGSLLGGKAALTISGAQPEDEADYYC ALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA SIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPG	Muc17scfv- CD3scfv
362	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGGSEVQLVESGGGLVQPG GSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKINNYAT YYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFG	Muc17scfv- CD3scfv

	DSYVSWFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSPR GLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCAL WYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASI EKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	
363	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGSEVQLVESGGGLVQPG GSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYA TYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF GDSYVSWFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSP RGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCA LWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAS IEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
364	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGSEVQLVESGGGLVQPG GSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYA TYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF GDSYVSWFEYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSP RGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCA LWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAS IEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- CD3scfv
365	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPSDSETRLNQKFDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFNYWGQGTTLTVSSGGGGSGGGGGSG GGGSGGGGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQ QKPGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQYHSYPLTFGGGKVEIKSGGGSEVQLVESGGGLVQPG GSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYA TYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF GDSYVSWFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWWQKPGKSP RGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCA	Muc17scfv- CD3scfv

	LWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPEFEGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAS IEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	
366	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWVRQMPGK GLEWMGQIYPGDGDINYEKFRGQVTISADKSISTAYLQWSSLKA SDTAMYYCARHGNVMDYWGQGTLLTVSSGKPGSGKPGSGKPG SGKPGSIQLTQSPSFLSASVGDRVTITCSASSSVSYMFYQQKPG KAPKPWIYRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYY CQQFHDPRTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA SIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- Fc
367	QVQLVQSGAEVKKPGSSVKVSKASGYFTTSYWMNWVRQAPGQ GLEWMGMHPDSETRLNQKFKDRVTITADKSTSTAYMELSSLRS EDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSGKPGSGKPGSGK PGSGKPGSIQMTQSPSSLSASVGDRVTITCSASSSVNYIYWYQQK PGKAPKLLIYRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFATY YCQQYHSYPLTFGGGTKEIKEPKSSDKTHTCPPCPAPEFEGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPS SDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK	Muc17scfv- Fc
368	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWVRQAPGK GLEWWSYISSGSSTIYYADTVKGRFTISRDNALNSLYLQMNSLRAE DTAVYYCARWGYGSSYFAYWGQGTLLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSC DKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLS PGK	HC; Muc17.7, Muc17.21, Muc17.22, Muc17.23, Muc17.24
369	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWVRQMPGK GLEWMGQIYPGDGDINYEKFRGQVTISADKSISTAYLQWSSLKA SDTAMYYCARHGNVMDYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPSRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSF FLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; Muc17.1, Muc17.8, Muc17.9, Muc17.10, Muc17.11, Muc17.12, Muc17.13, Muc17.14
370	QVQLVQSGAEVKKPGASVKVSKASGYEFSSHWMNWVRQAPGQ GLEWMGQIYPGDGDINYEKFRGRVTMTTRDTSTSTVYMELSSLRS EDTAVYYCARHGNVMDYWGQGTLLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKT	HC; Muc17.29, Muc17.30, Muc17.31

	HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRDEL KNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSPGK	
371	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYWMNWVRQAPGQ GLEWIGMIHPDSETRLNQKFKDRVTLTVDKSSSTAYMELSSLRSE DTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSP GK	HC; Muc17.45
372	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQEFKDRVTMTTRDTSTSTVYMELSSLR SEDTAVYYCARQGVITSVQEFAYWGQGTLLTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSP RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSL SPGK	HC; Muc17.5, Muc17.20
373	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTLTRDKSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSP RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSL SPGK	HC; Muc17.37
374	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTLTVDKSISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSP RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSL SPGK	HC; Muc17.35
375	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTLTVDTISISTAYMELSRLRS DDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS	HC; Muc17.36

	CDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSS RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSGLTVDDSRWQQGNVSCSVMHEALHNHYTQESLSL SPGK	
376	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTMTTRDTSISTAYMELSLRS DDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSDDLGTQTYICNVNHKPSNTKVDKRVKPS CDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSS RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSGLTVDDSRWQQGNVSCSVMHEALHNHYTQESLSL SPGK	HC; Muc17.232, Muc17.33, Muc17.34
377	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTMTTRDTSISTAYMELSLRS SEDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSDDLGTQTYICNVNHKPSNTKVDKRVKPS CDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSS RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSGLTVDDSRWQQGNVSCSVMHEALHNHYTQESLSL SPGK	HC; Muc17.31, Muc17.48, Muc17.49
378	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTMTVDDKISTAYMELSLRS DDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSDDLGTQTYICNVNHKPSNTKVDKRVKPS CDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSS RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSGLTVDDSRWQQGNVSCSVMHEALHNHYTQESLSL SPGK	HC; Muc17.38
379	QVQLVQSGAEVKKPGSSVKVSCKASGYEFSSHWMNWVRQAPGQ GLEWMGQIYPGDGDINYNKFRGRVTITADKSTSTAYMELSSRLRS EDTAVYYCARHGNVMDYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSDDLGTQTYICNVNHKPSNTKVDKRVKPS HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSSRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSGLTVDDSRWQQGNVSCSVMHEALHNHYTQESLSLSPGK	HC Muc17.25, Muc17.26, Muc17.27, Muc17.28
380	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMNWVRQAPGQ GLEWMGMIHPDSETRLNQKFKDRVTITADKSTSTAYMELSSRLRS EDTAVYYCARQGIITSVQEFAYWGQGTLLTVSSASTKGPSVFPLA SSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVPSDDLGTQTYICNVNHKPSNTKVDKRVKPS	HC; Muc17.4, Muc17.15, Muc17.16, Muc17.18,

	DKHTCPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD DGSFFLYSDLTVDKSRWQQGNVFCSCVMHEALHNHYTQESLSLS PGK	Muc17.19
381	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPKL LIYGATNLETGVPSRFSGSGSGKDYLTLTISSLQPEDATYYCQQFW RTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.23
382	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPKL LIYGATNLETGVPSRFSGSGSGDFTFTISSLQPEDATYYCQQFW RTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.24
383	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLISGATNLETGVPSRFSGSGSGKDYLTLTISSLQPEDATYYCQQF WRTPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.21
384	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLISGATNLETGVPSRFSGSGSGDFTFTISSLQPEDATYYCQQF WRTPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.7
385	DIQMTQSPSSLSASVGDRVTITCKASEDIYNRLAWYQQKPGKAPK PLIYGATNLETGVPSRFSGSGSGDFTFTISSLQPEDATYYCQQF WRTPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.22
386	EIVLTQSPATLSLSPGERATLSCSASSSVNYIYWYQQKPGQAPRLI YRTSNLASGIPARFSGSGSGDFTLTISLEPEDFAVYYCQQYHSY PLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.16, Muc17.17, Muc17.34, Muc17.39, Muc17.42, Muc17.49
387	EIVLTQSPATLSLSPGERATLSCSASSSVSYMFYQQKPGQAPRL LIYRTSNLASGIPARFSGSGSGDFTLTISLEPEDFAVYYCQQFHD YPRTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.8, Muc17.27, Muc17.31
388	EIVLTQSPATLSLSPGERATLSCSASSSVSYMFYQQKPGQAPRP WIYRTSNLASGIPPRFSGSGSGDFTLTISLEPEDFAVYYCQQFH DYPRTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.28
389	EIVLTQSPATLSVSPGERATLSCSASSSVNYIYWYQQKPGQAPRP WIYRTSNLASGIPARFSGSGSGTEYTLTISSLQSEDFAVYYCQQYH SYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.20
390	EIVMTQSPATLSVSPGERATLSCSASSSVNYIYWYQQKPGQAPRL	LC;

	LIYRTSNLASGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHS YPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	Muc17.5, Muc17.15, Muc17.33, Muc17.45, Muc17.48
391	EIVMTQSPATLSVSPGERATLSCSASSSVSYMFYQQKPGQAPRL LIYRTSNLASGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.14, Muc17.26, Muc17.30
392	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPPRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.13
393	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPPRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.11
394	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.9, Muc17.25, Muc17.29
395	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQFHQ YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.50
396	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.10
397	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKPW YRTSNLASGVPPRFSGSGSGTEYTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.12
398	IQLTQSPSFLSASVGDRVITITCSASSSVSYMFYQQKPGKAPKPW YRTSNLASGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQFHD YPRTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.1
399	IQMTQSPSSLSASVGDRVITITCSASSSVNYIYWFYQQKPGKAPKLLI YRTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYHS YPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; Muc17.4, Muc17.31, Muc17.32, Muc17.35, Muc17.36, Muc17.387, Muc17.38, Muc17.40,

		Muc17.43, Muc17.47
400	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGK SPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYY CALWYSNHWVFGGGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CD3
401	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWVRQAPGK GLEWWAYISSGNSAIYYADTVNGRFTISRDNPKNTLYLQMNSLRAE DTAVYYCARLRYGNSFDYWGQGTTLTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH TCPGPCAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRDELTK NQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFF LYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; CLDN182.1 2, CLND182.1 3
402	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGMHWVRQAPGK GLEWWSYISSGNSAIYYADTVNGRFTISRDNKNSLYLQMNSLRAE DTAVYYCARLRYGNSFDYWGQGTTLTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH TCPGPCAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRDELTK NQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFF LYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSPGK	HC; CLDN182.3, CLDN182.7
403	QIQLVQSGAEVKKPGASVKVSCKASGYFTFTNSGMNWRQAPGQ GLEWMGWINTNTGEPTFAEEFRGRVTFTLDTASTAYMELSLRSLRS DDTAVYYCARYYYGNSFAYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSP GK	HC; CLDN182.1 4
404	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNFGITWVRQAPGQG LEWIGEIPSSGNTFYNEKFKGRVTLTADKSSSAAYMELRSLRSD TAVYYCARGGGPLRSRYFDYWGQGTTLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC DKHTTCPGPCAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLS PGK	HC; CLDN182.1 0, CLND182.1 1
405	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNFGITWVRQAPGQG LEWMGEIPSSGNTFYNEKFKGRVTMTTDTSTSTAYMELRSLRSD DTAVYYCARGGGPLRSRYFDYWGQGTTLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS	HC; CLDN182.4, CLND182.8

	CDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSS RDELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSL SPGK	
406	QVQLVQSGAEVKKPGASVKVSCKASGYFTTNSGMNWVRQAPGQ GLEWMGWINTNTGEPTFAEEFRGRVTMTRDTSISTAYMELSLRS DDTAVYYCARYYYGNSFAYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSSRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSP GK	HC; CLND182.2, CLND182.1 7
407	QVQLVQSGAEVKKPGASVKVSCKASGYFTTNYGMNWVRQAPGQ GLEWMGWINTNTGEPTYAEEFKGRVTMTRDTSISTAYMELSLRS DDTAVYYCARYFYGNSFVYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSSRDEL TKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLSPGK	HC; CLDN182.1
408	QVQLVQSGAEVKKPGSSVKVSCKASGYAFNNYWMNWVRQAPGQ GLEWMGQISPGNGNSNFNGKFKGRVTITADKSTSTAYMELSSLS EDTAVYYCARGGRYGNAMDYWGQGTITVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC DKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSSR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD DGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLS PGK	HC; CLND182.5
409	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSYWMNWVRQAPGQ GLEWIGQIYPGNGNSNFNGKFKARVTLTADKSSSTAYMELSSLS EDTAVYYCARGGRFGNAMDYWGQGTITVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC DKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSSR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPPVLDSD DGSFFLYSDLTVDKSRWQQGNVFCSSVMHEALHNHYTQESLSLS PGK	HC; CLND182.1 5, CLND182.1 6
410	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSYWMNWVRQAPGQ GLEWMGQIYPGNGNSNFNGKFKARVTITADKSTSTAYMELSSLS EDTAVYYCARGGRFGNAMDYWGQGTITVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC	HC; CLDN182.6, CLDN182.9

	DKHTCPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVWVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPQVCTLPSPR DELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPVLDS DGSFFLYSDLTVDKSRWQQGNVFCSCVMHEALHNHYTQESLSLS PGK	
411	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIFWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNYYYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.7, CLND182.1 3
412	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNAFYFYPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.6, CLND182.1 5
413	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNFYFYPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.2, CLND182.1 4, CLND182.1 7
414	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNFYFYPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.1
415	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNNYYYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.3, CLND182.1 2
416	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNAFYFYPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.5
417	DIVMTQSPDSLAVSLGERATINCRSSQSLSFSSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGADFTLTISSLQAEDVAV YYCQNDYYYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.8, CLND182.1 1
418	DIVMTQSPDSLAVSLGERATINCRSSQSLSFSSGNQKNYLTWYQQK PGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQNDYYYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.4, CLND182.1 0
419	DIVMTQSPDSLAVSLGERATINCRSSQSLSFSSGNQKNYLTWYQQK KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQNAFYFYPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTA SVWCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CLND182.9, CLND182.1 6
420	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGGG LEWIGCIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRIRSD	VH; CD28

	TAVYFCTRSHYGLDWNFDVWGQGTTVTVSS	
421	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGSIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSS	VH; CD28 (C50S)
422	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGAIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSS	VH; CD28 (C50A)
423	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGGIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSS	VH; CD28 (C50G)
424	DIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQG QTPYTFGGGKVEIK	VL CD28
425	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGCIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSP GK	HC; CD28
426	DIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQG QTPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CD28
427	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGCIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQ QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQGQTPYTFGGGKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVK FYPSDIAVEWESNGQPENNYKTPPVLSKSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD28 Scfv- Fc
428	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGGIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQ QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQGQTPYTFGGGKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVK FYPSDIAVEWESNGQPENNYKTPPVLSKSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD28 (C50G) Scfv-Fc
429	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWRQAPGQG LEWIGAIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTTVTVSSGKPGSGKPGSGKP	CD28 (C50A) scfv- Fc

	GSGKPGSDIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQ QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQGQTYPTYTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	
430	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYIHWRQAPGQG LEWIGSIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSLRSD TAVYFCTRSHYGLDWNFDVWGQGTITVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQ QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQGQTYPTYTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD28 (C50S) scfv- Fc
431	QVQLVQSGAEVKKPGASVKVSCKASDYTFSNYYIEWVRQAPGQG LEWMGEILPGNGNTVYNEKFKDRVTMTVDTSTSTAYMELSLRSD DTAVYYCARWGDYALFANWGQGTITVTVSSGGGGSGGGGGSGGG GSDIQMTQSPSTLSASVGDRVTITCKASQNVGTNVAWYQQKPGK APKALIYSASYRYSVPSRFSGSGSGTEFTLTISLQPDDEFATYYC QQYNSYPFTFGQGTKLEIKEPKSSDKTHTCPPCPAPEFEGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAS IEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGIFYPSDIA VEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	DLL3scfv- Fc
432	QVQLVQSGAEVKKPGASVKVSCKASGYFTDYFMNWVRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLR EDTAVYYCAREGVLYDGYEGAYWGQGTITVTVSSGGGGSGGGGG SGGGGSDIQLTQSPSFLSASVGDRVTITCKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSPRFSGSGSGTEFTLTISLQPEDFAT YYCQQYSTYPTYTFGQGTKLEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFI PSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	DLL3scfv- Fc
433	QVQLVQSGAEVKKPGASVKVSCKATDYIFSNNYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVTMTVDTSTSTVYMELSSLRSED TAVYYCARWGDYALFANWGQGTITVTVSSGGGGSGGGGGSGGGG SDIQMTQSPSFLSASVGDRVTITCKASQNVGTNVAWYQQKPGKAP KPLIYSTSYRYSVPSRFSGSGSGTEFTLTISLQPEDFATYYCQQ YNNYPLTFGGGKVEIKEPKSSDKTHTCPPCPAPEFEGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEK TISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGIFYPSDIAVE WESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	DLL3scfv- Fc
434	QVQLVQSGAEVKKPGASVKVSCKATDYIFSNNYIEWVRQAPGQGL EWMGEILPGTGNTVYNEKFKDRVTMTVDTSTSTVYMELSSLRSED	DLL3scfv- Fc

	TAVYYCARWGDYALFANWQGTLTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVITICKASQNVGTNVAWYQQKPGKAPKALIYSASYRYSVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQYNSYPFTFGQGTKLEIKEPKSSDKTHTCPPCPAPEFEGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFS	
435	CSVMHEALHNHYTQKSLSLSPGK QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWWVRQAPGQC LEWIGSIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTITVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVITICHASQNIYVWLNWYQ QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQGQTYPTYFGCGTKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFS	CD28 (C50S) Scfv(CC)-Fc
436	CSVMHEALHNHYTQKSLSLSPGK QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWWVRQAPGQG LEWIGSIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSD TAVYFCTRSHYGLDWNFDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVITICHASQNIYVWLNWY QKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQGQTYPTYFGGGTKVEIKEPKSSDKTHTCPPCPAPEFE GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKS RWQQGNVFS	CD28 (C50S) Scfv(G4S)- Fc
437	CSVMHEALHNHYTQKSLSLSPGK QVQLQQWGAGLLKPSETLSLCAVYGGSFSGYYWSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWFYDLWGRGTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSDLTVDKSRWQQGNVFS	HC; CD137.U
438	CSVMHEALHNHYTQKSLSLSPGK EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGTDFTLTISLQPEDFAVYYCQQRS NWPPALTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CD137.U
439	CSVMHEALHNHYTQKSLSLSPGK QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYSQKFQGRVTITVDKSASTAYMELSSLR EDTAVYYCARSFTTARAFAYWGQGTITVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ	HC; CD137.B

	DWLNKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTPVLDS GSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSP GK	
440	DIVMTQSPPTLSLSPGERVTLSRASQSSISDYLHWYQQKPGQSPR LLIKYASQSSISGIPARFSGSGSGTDFTLTSSLEPEDFAVYYCQDGH SFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	LC; CD137.B
441	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWYFDLWGRGTLVTVSSGKPGSGKPGSGKP GSGKPGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQ KPGQAPRLIYDASNRTGIPARFSGSGSGTDFTLTSSLEPEDFAV YYCQQRSNWPPALTFGGGTKEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv(CL)-Fc
442	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWYFDLWGRGTLVTVSSGGGGSGGGGSGG GGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQ APRLIYDASNRTGIPARFSGSGSGTDFTLTSSLEPEDFAVYYCQ QRSNWPPALTFGGGTKEIKEPKSSDKTHTCPPCPAPEFEGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNKEYKCKVSNKAL PASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKSRWQQ GNVFCFSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv(G4S)- Fc
443	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWYFDLWGRGTLVTVSSGGGGSGGGGSGG GGSGGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATLSRAS QSVSSYLAWYQQKPGQAPRLIYDASNRTGIPARFSGSGSGTDF TLTSSLEPEDFAVYYCQQRSNWPPALTFGGGTKEIKEPKSSDKT HTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLKSDGSF FLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv (6x)-Fc
444	EIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPR LLIYDASNRTGIPARFSGSGSGTDFTLTSSLEPEDFAVYYCQQRS NWPPALTFGGGTKEIKGKPGSGKPGSGKPGSGKPGSQVQLQQ WGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPEKGLEWIGE INHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTAVYYCAR DYGPNGYDWYFDLWGRGTLVTVSSEPKSSDKTHTCPPCPAPEFE GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPVLKSDGSFFLYSKLTVDKS RWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv(VLVH) Fc
445	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPEKG	CD137.U(G

	LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPGNYDWYFDLWGRGTLTVSSGGGGSGGGSGG GGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ APRLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQ QRSNWPPALTFSGGKVEIKREPSSDKTHTCPPCPAPEFEGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFP SDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK	99S) scfv- Fc
446	QVQLQESGPGLVKPSSETLSLTCTVSGGSFSGYYWSWIRQPPGKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPGNYDWYFDLWGRGTLTVSSGKPGSGKPGSGKP GSGKPGSEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQ QKPGQAPRLIYDASNRATGIPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQRSNWPPALTFGGGKVEIKEPKSSDKTHTCPPCPAPEF EGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLV KGFYPSPDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.Uv1 scfv-Fc
447	EVQLLESGGGLVQPGGSLRLSCAASGGSFSGYYWSWVRQAPGK GLEWVSEINHGGYVTYNPSLESRTISRDNSTLYLQMNSLRAE DTAVYYCAKDYGPGNYDWYFDLWGRGTLTVSSGKPGSGKPGS GKPGSGKPGSEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQ QKPGQAPRLIYDASNRATGIPDRFSGSGSGTDFTLTISRLEP EDFAVYYCQQRSNWPPALTFGGGKVEIKEPKSSDKTHTCPPCPA PEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLT CLVKGFPSPDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.Uv2 scfv-Fc
448	QVQLVQSGAEVKKPGSSVKVSCKASGGSFSGYYWSWVRQAPGQ GLEWMGEINHGGYVTYNPSLESRTITADESTSTAYMELSSLRSE DTAVYYCARDYGPGNYDWYFDLWGRGTLTVSSGKPGSGKPGS GKPGSGKPGSEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQ QKPGQAPRLIYDASNRATGIPDRFSGSGSGTDFTLTISRLEP EDFAVYYCQQRSNWPPALTFGGGKVEIKEPKSSDKTHTCPPCPA PEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLT CLVKGFPSPDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.Uv3 scfv-Fc
449	QVQLQQWGAGLLKPSSETLSLTCAVYGGSFSGYYWSWIRQSPEKC LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPGNYDWYFDLWGRGTLTVSSGKPGSGKPGSGKP GSGKPGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAV YYCQQRSNWPPALTFGCGTKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv(CC)-Fc

450	QVQLQQWGAGLLKPSETLSLTCAVYGGSGYYSWIRQSPEKC LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWFYDLWGRGTLTVSSGKPGSGKPGSGKP GSGKPGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLLIYDASNRTGIPARFSGSGSGTDFTLTISSELEPEDFAV YYCQQRSNWPPALTFGCGTKVEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTIKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.U scfv(CC)-Fc
451	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSSISDYLHWYQQ KPGQSPRLLIKYASQSSIGIPARFSGSGSGTDFTLTISSELEPEDFAV YYCQDGHSFPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTIKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.B scfv-Fc
452	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYAQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSSISDYLHWYQQ KPGQSPRLLIKYASQSSIGIPARFSGSGSGTDFTLTISSELEPEDFAV YYCQDGHSFPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTIKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.b(S6 0A) scfv-fc
453	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYNQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSSISDYLHWYQQ KPGQSPRLLIKYASQSSIGIPARFSGSGSGTDFTLTISSELEPEDFAV YYCQDGHSFPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTIKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.B (S50N) scfv- fc
454	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMWVRQAPGK GLEWVADIKNDGSYTNAPSLTNRFTISRDNKNSLYLQMNSLRA EDTAVYYCARELTGTWGQGTMTVSSGKPGSGKPGSGKPGSGK PGSDIVMTQSPDSLAVSLGERATINCKSSQSLLSSGNQKNYLAWY QQKPGQPPKLLIYYASTRQSGVPDRFSGSGSGTDFTLTISSLQAED VAVYYCLQYDRYPFTFGGQTKLEIKEPKSSDKTHTCPPCPAPEFE GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPASIEKTIKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKS	CD137.39 scfv-Fc

	RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	
455	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMSWVRQAPGK GLEWWADIKNDGSYTNVDSVKGRFTISRDNANKNSLYLQMNSLRA EDTAVYYCARELTGTWGGGTLTVSSGKPGSGKPGSGKPGSGKP GSDIIMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLAWYQ QKPGQPPELLIYYASTRQSGVPDRFSGSGSGTDFTLTISLQAEDV AVYYCLQYDRYPFTFGGQTKLEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.39v 1 scfv-Fc
456	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMSWVRQAPGK GLEWWADIKNDGSYTNVDSVKGRFTISRDNANKNSLYLQMNSLRA EDTAVYYCARELTGTWGGGTLTVSSGKPGSGKPGSGKPGSGKP GSDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLAWYQ QKPGQPPELLIYYASTRQSGVPDRFSGSGSGTDFTLTISLQAEDV AVYYCLQYDRYPFTFGGQTKLEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.39v 2 scfv-Fc
457	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMSWVRQAPGK GMEWVGDIKNDGSYTNAPSLTNRFTISRDNARNNSLYLQMNSLRA EDTAVYYCTRELGTWGGGTLTVSSGKPGSGKPGSGKPGSGKP GSDIIMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLAWYQ QKPGQPPELLIYYASTRQSGVPDRFSGSGSGTDFTLTISLQAEDV AVYYCLQYDRYPFTFGGQTKLEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.39v 3 scfv-Fc
458	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMSWVRQAPGK GMEWVGDIKNDGSYTNAPSLTNRFTISRDNARNNSLYLQMNSLRA EDTAVYYCTRELGTWGGGTLTVSSGKPGSGKPGSGKPGSGKP GSDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLAWYQ QKPGQPPELLIYYASTRQSGVPDRFSGSGSGTDFTLTISLQAEDV AVYYCLQYDRYPFTFGGQTKLEIKEPKSSDKTHTCPPCPAPEFEG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.39v 4 scfv-Fc
459	QVKLVESGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQ VLEWMGEINPGNGHTSYAQKFQGRVTLTVDKSTSTAYMELSSRLS EDTAVYYCARSFTTARAFAYWGQGTITVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRTITCRASQSISDYLHWYQQ KPGKAPKLLIKYASQSIGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQDSHSFPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFY	CD137.Bv1 scfv-Fc

	PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGK	
460	QVKLVESGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQ VLEWMGEINPGNGHTSYAQKFQGRVTLTVDKSTSTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSISDYLHWYQQ KPGQSPRLIKYASQSIGIPARFSGSGSGTDFTLTISSELEDFAV YYCQDGHSPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFI PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGK	CD137.Bv2 scfv-fc
461	QVQLVQSGAEVKKPGASVKLSCKASGYTFTSSYWMHWVRQAPGQ GLEWIGEINPGNGHTNYNEKFKSRVTMTRDTSTSTAYMELSSLRS EDTAVYYCARSFKTARAFAYWGQGTTLTVVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPAFLSVTPGEKVTITCRASQTISDYLHWYQQ KPDQAPKLLIKYASQSIGIPSRFSGSGSGTDFTFTISSELEAEDAT YYCQDGHSPPTFGGGTKLEIKEPKSSDKTHTCPPCPAPEFEGGP PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFI YPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRW QGNVFSCSVMEALHNHYTQKSLSLSPGK	CD137.Bv3 scfv-fc
462	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQ GLEWMGIINPGNGHTSYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVTITCRASQSISDYLHWYQQ KPGKAPKLLIKYASQSIGVPSRFSGSGSGTDFTLTISSELEDFAT YYCQDSHSPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFI PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGK	CD137.Bv4 scfv-fc
463	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQ GLEWMGIINPGNGHTSYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSISDYLHWYQQ KPGQSPRLIKYASQSIGIPARFSGSGSGTDFTLTISSELEDFAV YYCQDGHSPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKLTKNQVSLTCLVKGFI PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGK	CD137.Bv5 scfv-fc
464	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQ RLEWMGEINPSNGHTKYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRVTITCRASQSISDYLHWYQQ KPGKAPKLLIKYASQSIGVPSRFSGSGSGTDFTLTISSELEDFAT YYCQDSHSPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA	CD137.Bv6 scfv-fc

	LPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHLEALHNHYTQKSLSLSPGK	
465	QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYWMHWVRQAPGQ RLEWMGEINPSNGHTKYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPPTLSLSPGERVTLSRASQSSISDYLHWYQQ KPGQSPRLLIKYASQSSIGIPARFSGSGSGTDFTLTISSEPEDFAV YYCQDGHFSFPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHLEALHNHYTQKSLSLSPGK	CD137.Bv7 scfv-fc
466	QVQLVQSGAEVKKPGASVKVSCKASGYFTDYFMNHWVRQAPGQ CLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGLYDGYEGAYWGQGTTLTVSSGKPGSGKPG SGKPGSGKPGSDIQLTQSPSFLSASVGDRVITCKASQNVGIAVA WYQQKPGKAPKLLIYAASNRYTGVPSTRFSGSGSGTEFTLTISLQ EDFATYYCQYSTYPYTFGCGTKLEIKEPKSSDKTHTCPPCPAPEF EGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHLEALHNHYTQKSLSLSPGK	DLL3 scfv- Fc
467	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYGMHWVRQAPGK GLEWVAVISHHGSSKYYADSVKGRFTISRDNSTLYLQMNSLRA EDTAVYYCARDWFFYLFQDYWGQGTTLTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPLSLPVTPGEPASISCKSSQSLHSDGKTF WYLQKPGQSPQLLIYEVSNRFSGVDPDRFSGSGSGTDFTLKIS AEDVGVIYCLQGERLPFTFGGQTKVEIKEPKSSDKTHTCPPCPAP EFEGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK KVSNAKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHLEALHNHYTQKSLSLSPGK	DLL3 scfv- Fc
468	QVQLVQSGAEVKKPGASVKVSCKASGYFTDYFMNHWVRQAPGQ GLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTVYMELSSLRS EDTAVYYCAREGLYDGYEGAYWGQGTTLTVSSGGGGSGGGG SGGGGSDIQLTQSPSFLSASVGDRVITCKASQNVGIAVAWYQQK PGKAPKLLIYAASNRYTGVPSTRFSGSGSGTEFTLTISLQPEDFAT YYCQYSTYPYTFGQGTKEIKSGGGGSQVQLVQSGAEVKKPGA SVKVSCASGYTFSSYWMHWVRQAPGQRLEWMGEINPGNGHTN YSQKFQGRVTITVDKSASTAYMELSSLRSEDVAVYYCARSFTTARA FAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSDIVMTQSPPT LSLSPGERVTLSRASQSSISDYLHWYQQKPGQSPRLLIKYASQSS GIPARFSGSGSGTDFTLTISSEPEDFAVYYCQDGHFSFPPTFGGGT KVEIKEPKSSDKTHTCPPCPAPEFEGGPSVFLFPKPKDTLMISRT PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREP QVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHLEALHNH YTQKSLSLSPGK	DLL3scFv- CD137.Bsc Fv-fc
469	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ	CD137.Bsc

	RLEWMGEINPGNGHTNYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSGGGGSGGGSGG GGSGGGGSDIVMTQSPPTLSLSPGERVTLSRASQSISDYLHWYQ QKPGQSPRLLIKYASQSISGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQDGHSPPTFGGGTKVEIKSGGGGSQVQLVQSGAEVKKPG ASVKVSCKASGYTFSSYWMHWVRQAPGQRLEWMGEINPGNGHT NYSQKFQGRVTITVDKSASTAYMELSSLRSEDVAVYYCARSFTTA RAFAYWGQGTTLTVSSGKPGSGKPGSGKPGSGKPGSDIVMTQSP PTLSLSPGERVTLSRASQSISDYLHWYQKPGQSPRLLIKYASQS ISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQDGHSPPTFGG GTKVEIKEPKSSDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMIS RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPR EPQVYTLPPCRKLTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	Fv- CD137.Bsc Fv-Fc
470	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPSPRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSDLTVDKSRWQQGNVFSCSVMHEALHNHYTQESLSLSP GKSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMN WVRQAPGQGLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTV YMELSSLRSEDVAVYYCAREGVLYDGYEGAYWGQGTTLTVSSG GGSGGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCKASQNVGI AVAWYQQKPGKAPKLLIYAASNRYTGVPSPRFSGSGSGTEFTLTISS LQPEDFATYYCQYSTYPYTFGGGTKLEIK	CD137.BFa b-Fc- DLL3scFv
471	QVQLQQWGAGLLKPSETLSLCAVYGGSFSGYYWSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWFYDLWGRGTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRK KLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GKSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMN WVRQAPGQGLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTV YMELSSLRSEDVAVYYCAREGVLYDGYEGAYWGQGTTLTVSSG GGSGGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCKASQNVGI AVAWYQQKPGKAPKLLIYAASNRYTGVPSPRFSGSGSGTEFTLTISS LQPEDFATYYCQYSTYPYTFGGGTKLEIK	CD137.UFa b-Fc- DLL3scFv
472	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSYWMHWVRQAPGQ RLEWMGEINPGNGHTNYSQKFQGRVTITVDKSASTAYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS	CD137.BFa b-Fc- DLL3scFv

	HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRK KLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSD GSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP GKSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMN WVRQAPGQGLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTV YMESSLRSEDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSG GGSGGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCKASQNVGI AVAWYQQKPGKAPKLLIYAASNRYTGVPSTRFSGSGSGTEFTLTSS LQPEDFATYYCQYSTYPYTFGGGTKLEIK	
473	QVQLQQWGAGLLKPSETLSLCAVYGGSGYYSWIRQSPEKG LEWIGEINHGGYVTYNPSLESRTISVDTSKNQFSLKLSSVTAADTA VYYCARDYGPNGYDWYFDLWGRGTLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCD KTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVCTLPVSRD ELTKNQVSLTCLVEGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSDLTVDKSRWQQGNVFCFSVMHEALHNHYTQESLSLSP GKSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYFMN WVRQAPGQGLEWMGVINPYNDITIYNQKFQGRVTMTVDRSTSTV YMESSLRSEDTAVYYCAREGVLYDGYEGAYWGQGLTVTVSSG GGSGGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCKASQNVGI AVAWYQQKPGKAPKLLIYAASNRYTGVPSTRFSGSGSGTEFTLTSS LQPEDFATYYCQYSTYPYTFGGGTKLEIK	CD137.UFa b-Fc- DLL3scFv
474	EVQLVQSGAEVKKPGESLKISCKGSGYEFSSHWMNWVRQMPGK CLEWMGQIYPGDGDINYNKFRGQVTISADKSISTAYLQWSSLKAS DTAMYYCARHGNYVMDYWGQGLTVTVSSGKPGSGKPGSGKPGS GKPGSIQLTQSPSFLSASVGDRVTITCSASSSVSYMFYQQKPGK APKPWIYRTSNLASGVPSRFSGSGSGTEFTLTSSSLQPEDFATYYC QQFHDYPRTFGCGTKVEIKEPKSSDKTHTCPPCPAPEFEGGPSVF LFPPKPKDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAS IEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQQGNV FSCSMHEALHNHYTQKSLSLSPGK	Muc17scfv- fc
475	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNFGITWVRQAPGQG LEWMGEIYPSSGNIFYNEKFKGRVTMTTDTSTSTAYMELRSLRSD DTAVYYCARGGGPLRSRYFDYWGQGLTVTVSSGKPGSGKPGSG KPGSGKPGSDIVMTQSPDSLAVSLGERATINCRSSQSLFSSGNQK NYLTWYQQKPGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLT SSLQAEDVAVYYCQNDYYYPLTFGGGKTKVEIKEPKSSDKTHTCPP CPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKL TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	CLDN182. scfv-Fc
476	EVQLVESGGGLVQPGLSLRLSCAASGFTFSSFGMHWWVRQAPGK GLEWWSYISSGNSAIYYADTVNGRFTISRDNKNSLYLQMNSLRAE DTAVYYCARLRYGNSFDYWGQGLTVTVSSGKPGSGKPGSGKPG SGKPGSDIVMTQSPDSLAVSLGERATINCKSSQSLNLSGNQKNYL TWYQQKPGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTSS QAEDVAVYYCQNNYYYPLTFGGGKTKVEIKEPKSSDKTHTCPPCPA	CLDN182. scfv-Fc

	PEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLT CLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	
477	QVQLVQSGAEVKKPGSSVKVSCASGYAFNNYWMNWVRQAPGQ GLEWMGQISPGNGNSNFNGKFKGRVTITADKSTSTAYMELSSLRS EDTAVYYCARGGRYGNAMDYWGQGTTVTVSSGKPGSGKPGSGK PGSGKPGSDIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQRN YLTWYQQKPGQPPELLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCQNAFYFYPYTFGGGTKEIKEPKSSDKTHTCPPC PAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSL TCLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CLDN182. scfv-Fc
478	QVQLVQSGAEVKKPGASVKVSCASGYFTTNSGMNWVRQAPGQ GLEWMGWINTNTGEPTFAEEFRGRVTMTDRDTSISTAYMELSSLRS DDTAVYYCARYYYGNSFAYWGQGLTVTVSSGKPGSGKPGSGKP GSGKPGSDIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNY LTWYQQKPGQPPELLIYWASTRESGVPDRFSGSGSGTDFTLTIS LQAEDVAVYYCQNNFYPLTFGGGTKEIKEPKSSDKTHTCPPCP APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLT CLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	CLDN182. scfv-Fc
479	QVQLVQSGAEVKKPGASVKVSCASGYFTTSYWMHWVRQAPGQ GLEWMGIINPGNGHTSYAQKFQGRVTMTDRDTSSTVYMELSSLRS EDTAVYYCARSFTTARAFAYWGQGTITVTVSSGKPGSGKPGSGKP GSGKPGSDIQMTQSPSSLSASVGDRTITCRASQSISDYLHWYQQ KPGKAPKLLIKYASQSIGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQDSHSFPPTFGGGTKVEIKEPKSSDKTHTCPPCPAPEFEGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPCRKKLTKNQVSLTCLVKGIFY PSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	CD137.bV8 scfv-Fc

CLAIMS

1. A bispecific molecule comprised of an antibody against DLL3 paired with an agonist antibody that activates one or more of CD3, CD28 or CD137.
2. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific molecule of claim 1.
3. A method of treating cancer using the bispecific molecule of claim 1.
4. The method of claim 3, wherein the cancer is at least one of breast, lung, kidney, bladder, urinary tract, urethra, penis, vulva, vagina, cervical, colon, ovarian, prostate, pancreas, stomach, brain, head and neck, skin, uterine, testicular, esophagus and liver cancer.
5. The method of claim 3, wherein the bispecific molecule is administered with one or more checkpoint regulators.
6. The bispecific molecule of claim 1, further comprised of an immune checkpoint agonist or immune checkpoint antagonist.
7. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific molecule of claim 6.
8. A method of treating cancer using the bispecific molecule of claim 6.
9. The method of claim 8, wherein the cancer is at least one of breast, lung, kidney, bladder, urinary tract, urethra, penis, vulva, vagina, cervical, colon, ovarian, prostate, pancreas, stomach, brain, head and neck, skin, uterine, testicular, esophagus and liver cancer.
10. An antibody which binds to DLL3 paired with an agonist antibody that activates CD3, CD28 or CD137, the antibody selected from the group consisting of:
 - (1) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 7, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 14, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 27, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 31, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 40, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 47;

(2) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 1, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 11, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 22, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 39, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 54;

(3) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(4) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 5, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(5) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 2, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 10, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 22, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 46, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 55;

(6) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 1, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 11, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 22, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 46, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 55;

(7) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 3, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 13, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 28, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 46, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 54;

(8) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 15, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(9) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(10) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 18, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(11) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(12) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 15, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(13) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(14) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 18, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(15) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(16) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 15, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 37, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(17) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 37, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(18) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 18, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 37, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(19) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 37, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(20) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 7, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 15, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 38, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(21) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 38, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(22) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 18, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 38, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(23) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 6, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 38, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 42, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 49;

(24) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 5, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 25, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 33, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 51;

(25) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 5, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 16, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 24, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 50;

(26) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 5, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 17, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 26, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 34, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 43, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 50;

(27) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 8, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 19, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 23, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 35, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 45, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 52.

(28) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 9, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 21, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 29, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 32, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 39, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 54.

11. An antibody according to claim 10, wherein its CDR domains have one, two, three, four or five amino acids mutated, deleted or added.
12. An antibody according to claim 10, wherein the antibody is humanized.
13. A composition comprising:
 - a) the antibody of claim 10, and

- b) a pharmaceutically acceptable diluent, adjuvant, or carrier.
14. A method of activating T-cell cytotoxicity against DLL3 expressing cells comprising administering to a subject in need thereof an effective amount of the antibody of claim 10.
15. The method of claim 14, wherein the antibody is administered with an anti-PD1 and/or anti-PDL1 antagonist.
16. A method of treating cancer in a mammal comprising administering to a subject in need thereof an effective amount of the antibody of claim 10.
17. The method of claim 16, wherein the antibody is administered with one or more immune checkpoint regulators.
18. A humanized antibody which binds to human DLL3 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 1 – 28 or 29.
19. A humanized antibody which binds to human DLL3 protein comprising a light chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 76 – 90 or 91.
20. A nucleic acid sequence which encodes a humanized human DLL3 antibody heavy chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 1 – 28 or 29.
21. A nucleic acid sequence which encodes a humanized human DLL3 antibody light chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 76 – 90 or 91.
22. A bispecific antibody comprising:
a first targeting domain having a first binding specificity to DLL3,
a second targeting domain having a second binding specificity to a cluster of differentiation receptor,
wherein the first targeting domain and the second targeting domain each comprises one or more antibody variable regions.
23. The bispecific antibody of claim 22, wherein the cluster of differentiation receptor is at least one of CD3, CD28 or CD137.

24. The bispecific antibody of claim 22, wherein the first targeting domain and the second targeting domain are each comprised at least one antibody fragment selected from the group consisting of single domain antibody (sdAb), a fragment variable (Fv) heterodimer, a single chain Fv (scFv), Fab fragment and combinations thereof.
25. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific antibody of claim 22.
26. A method of treating cancer using the bispecific antibody of claim 22.
27. The method of claim 25, further comprising administration of one or more immune checkpoint regulators.
27. The method of claim 26, further comprising administration of one or more immune checkpoint regulators.
28. An antibody that binds to human DLL3 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a heavy chain variable domain selected from the group consisting of SEQ ID NO: 170 – 186 and 187.
29. An antibody that binds to human DLL3 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a light chain variable domain selected from the group consisting of SEQ ID NO: 188 – 195 and 196.
30. A bispecific molecule comprised of an antibody against MUC17 paired with an agonist antibody that activates one or more of CD3, CD28 or CD137.
31. A method of activating T-cell cytotoxicity against MUC17 expressing cells using the bispecific molecule of claim 1.
32. A method of treating cancer using the bispecific molecule of claim 30.
33. The method of claim 32, wherein the cancer is at least one of pancreatic, appendiceal and colon cancer.
34. The method of claim 32, wherein the bispecific molecule is administered with one or more checkpoint regulators.
35. The bispecific molecule of claim 30, further comprised of an immune checkpoint agonist or immune checkpoint antagonist.

36. A method of activating T-cell cytotoxicity against MUC17 expressing cells using the bispecific molecule of claim 35.
37. A method of treating cancer using the bispecific molecule of claim 35.
38. The method of claim 37, wherein the cancer is at least one of pancreatic, appendiceal and colon cancer.
39. An antibody which binds to MUC17 paired with an agonist antibody that activates CD3, CD28 or CD137, the antibody selected from the group consisting of:
- (1) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 92, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 106, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 111, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 118, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 121, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 124;
 - (2) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 92, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 106, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 111, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 118, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 121, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 126;
 - (3) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 93, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 105, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 108, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 116, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 123;

(4) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 94, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 103, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 108, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 116, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 122;

(5) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 95, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 104, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 112, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 117, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 120, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 123;

(6) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(7) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 99, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(8) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(9) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 98, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(10) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(11) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 100, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 110, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(12) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 99, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(13) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 99, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(14) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(15) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(16) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(17) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 99, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 114, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(18) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 96, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 99, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(19) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID

NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(20) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 100, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 110, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125;

(21) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 97, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 101, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 109, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 115, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 119, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 125.

40. An antibody according to claim 39, wherein its CDR domains have one, two, three, four or five amino acids mutated, deleted or added.
41. An antibody according to claim 39, wherein the antibody is humanized.
42. A composition comprising:
- a) the antibody of claim 39, and
 - b) a pharmaceutically acceptable diluent, adjuvant, or carrier.
43. A method of activating T-cell cytotoxicity against MUC17 expressing cells comprising administering to a subject in need thereof an effective amount of the antibody of claim 39.
44. The method of claim 43, wherein the antibody is administered with an anti-PD1 and/or anti-PDL1 antagonist.

45. A method of treating cancer in a mammal comprising administering to a subject in need thereof an effective amount of the antibody of claim 39.
46. The method of claim 45, wherein the antibody is administered with one or more immune checkpoint regulators.
47. A humanized antibody which binds to human MUC17 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 127 - 245 or 246.
48. A humanized antibody which binds to human MUC17 protein comprising a light chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 113 – 125 or 126.
49. A nucleic acid sequence which encodes a humanized human MUC17 antibody heavy chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 92 – 111 or 112.
50. A nucleic acid sequence which encodes a humanized human MUC17 antibody light chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 147 – 168 or 169.
51. A bispecific antibody comprising:
a first targeting domain having a first binding specificity to MUC17,
a second targeting domain having a second binding specificity to a cluster of differentiation receptor,
wherein the first targeting domain and the second targeting domain each comprises one or more antibody variable regions.
52. The bispecific antibody of claim 51, wherein the cluster of differentiation receptor is at least one of CD3, CD28 or CD137.
53. The bispecific antibody of claim 51, wherein the first targeting domain and the second targeting domain are each comprised at least one antibody fragment selected from the group consisting of single domain antibody (sdAb), a fragment variable (Fv) heterodimer, a single chain Fv (scFv), Fab fragment and combinations thereof.

54. A method of activating T-cell cytotoxicity against MUC17 expressing cells using the bispecific antibody of claim 51.
55. A method of treating cancer using the bispecific antibody of claim 51.
56. The method of claim 25, further comprising administration of one or more immune checkpoint regulators.
57. The method of claim 26, further comprising administration of one or more immune checkpoint regulators.
58. An antibody that binds to human MUC17 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a heavy chain variable domain selected from the group consisting of SEQ ID NO: 92 – 111 and 112.
59. An antibody that binds to human MUC17 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a light chain variable domain selected from the group consisting of SEQ ID NO: 113 – 125 and 126.
60. A bispecific molecule comprised of an antibody against CLDN18.2 paired with an agonist antibody that activates one or more of CD3, CD28 or CD137.
61. A method of activating T-cell cytotoxicity against CLDN18.2 expressing cells using the bispecific molecule of claim 60.
62. A method of treating cancer using the bispecific molecule of claim 60.
63. The method of claim 62, wherein the cancer is at least one of pancreatic, appendiceal and colon cancer.
64. The method of claim 62, wherein the bispecific molecule is administered with one or more checkpoint regulators.
65. The bispecific molecule of claim 60, further comprised of an immune checkpoint agonist or immune checkpoint antagonist.

66. A method of activating T-cell cytotoxicity against CLDN18.2 expressing cells using the bispecific molecule of claim 65.
67. A method of treating cancer using the bispecific molecule of claim 65.
68. The method of claim 8, wherein the cancer is at least one of colorectal cancer, gastric cancer, liver cancer, esophageal cancer and pancreatic cancer.
69. An antibody which binds to CLDN18.2 paired with an agonist antibody that activates CD3, CD28 or CD137, the antibody selected from the group consisting of:
- (1) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 175, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 180, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 186, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 195;
 - (2) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 174, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 179, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 187, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 194;
 - (3) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 170, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 181, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 185, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 196;

(4) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 173, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 176, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 182, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 190, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 193;

(5) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 171, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 177, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 184, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 189, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 192;

(6) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 172, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 178, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 173, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 192;

(7) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 173, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 176, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 182, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 190, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 193;

(8) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 170, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 181, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 185, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 196;

(9) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 174, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 179, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 187, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 194; or

(10) an antibody comprising a heavy chain variable region comprising heavy chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 172, heavy chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 178, and heavy chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 183, and a light chain variable region comprising light chain CDR1 containing at least the amino acid sequence as set forth in SEQ ID NO: 188, light chain CDR2 containing at least the amino acid sequence as set forth in SEQ ID NO: 191, and light chain CDR3 containing at least the amino acid sequence as set forth in SEQ ID NO: 192.

70. An antibody according to claim 69, wherein its CDR domains have one, two, three, four or five amino acids mutated, deleted or added.

71. An antibody according to claim 69, wherein the antibody is humanized.

72. A composition comprising:

- a) the antibody of claim 69, and
- b) a pharmaceutically acceptable diluent, adjuvant, or carrier.

73. A method of activating T-cell cytotoxicity against CLDN18.2 expressing cells comprising administering to a subject in need thereof an effective amount of the antibody of claim 69.

74. The method of claim 73, wherein the antibody is administered with an anti-PD1 and/or anti-PDL1 antagonist.

75. A method of treating cancer in a mammal comprising administering to a subject in need thereof an effective amount of the antibody of claim 69.

76. The method of claim 75, wherein the antibody is administered with one or more immune checkpoint regulators.

77. A humanized antibody which binds to human CLDN18.2 protein comprising a heavy chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 170 – 186 or 187.

78. A humanized antibody which binds to human CLDN18.2 protein comprising a light chain variable domain having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 188 – 195 or 196.

79. A nucleic acid sequence which encodes a humanized human CLDN18.2 antibody heavy chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 170 – 186 or 187

80. A nucleic acid sequence which encodes a humanized human CLDN18.2 antibody light chain, which comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 207 – 212 or 213.

81. A bispecific antibody comprising:
a first targeting domain having a first binding specificity to CLDN18.2,
a second targeting domain having a second binding specificity to a cluster of differentiation receptor,
wherein the first targeting domain and the second targeting domain each comprises one or more antibody variable regions.

82. The bispecific antibody of claim 81, wherein the cluster of differentiation receptor is at least one of CD3, CD28 or CD137.
83. The bispecific antibody of claim 81, wherein the first targeting domain and the second targeting domain are each comprised at least one antibody fragment selected from the group consisting of single domain antibody (sdAb), a fragment variable (Fv) heterodimer, a single chain Fv (scFv), Fab fragment and combinations thereof.
84. A method of activating T-cell cytotoxicity against CLDN18.2 expressing cells using the bispecific antibody of claim 81.
85. A method of treating cancer using the bispecific antibody of claim 81.
86. The method of claim 25, further comprising administration of one or more immune checkpoint regulators.
87. The method of claim 26, further comprising administration of one or more immune checkpoint regulators.
88. An antibody that binds to human CLDN18.2 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a heavy chain variable domain selected from the group consisting of SEQ ID NO: 170 – 186 and 187.
89. An antibody that binds to human CLDN18.2 paired with an agonist antibody that activates CD3, CD28 or CD137, comprising a light chain variable domain selected from the group consisting of SEQ ID NO: 188 – 195 and 196.
90. A bispecific antibody comprised of:
- a) an anti-DLL3 single chain fragment variable region (scFv),
 - b) an anti-CD3 single chain fragment variable region (scFv), and
 - c) an anti-DLL3 antigen-binding fragment (Fab) – fragment crystallizable region (Fc region).
91. A method of treating cancer comprised of administering a therapeutic amount of the bispecific antibody of claim 90.

92. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific antibody of claim 90.
93. The bispecific molecule of claim 90, comprised of SEQ. ID NO: 269, SEQ. ID NO: 276 and SEQ. ID NO: 297.
94. A bispecific antibody comprised of:
- a) an anti-CD3 single chain fragment variable region (scFv) – fragment crystallizable region (Fc region), and
 - b) an anti-DLL3 antigen-binding fragment (Fab) – fragment crystallizable region (Fc region).
95. A method of treating cancer comprised of administering a therapeutic amount of the bispecific antibody of claim 94.
96. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific antibody of claim 94.
97. The bispecific molecule of claim 90, comprised of SEQ. ID NO: 263, SEQ. ID NO: 279 and SEQ. ID NO: 303.
98. A bispecific antibody comprised of:
- a) an anti-CD3 single chain fragment variable region (scFv) – fragment crystallizable region (Fc region), and
 - b) an anti-Claudin 18.2 antigen-binding fragment (Fab) – fragment crystallizable region (Fc region).
95. A method of treating cancer comprised of administering a therapeutic amount of the bispecific antibody of claim 98.
96. A method of activating T-cell cytotoxicity against DLL3 expressing cells using the bispecific antibody of claim 98.
97. The bispecific molecule of claim 90, comprised of SEQ. ID NO: 430, SEQ. ID NO: 405 and SEQ. ID NO: 418.

Scfv-Fc x Fab-Fc molecules

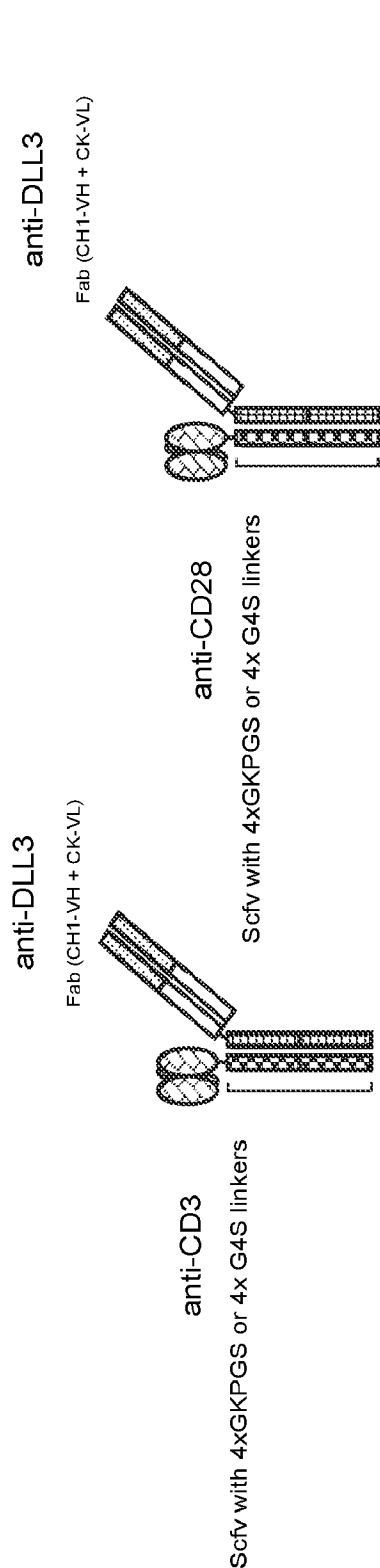


FIG. 1A

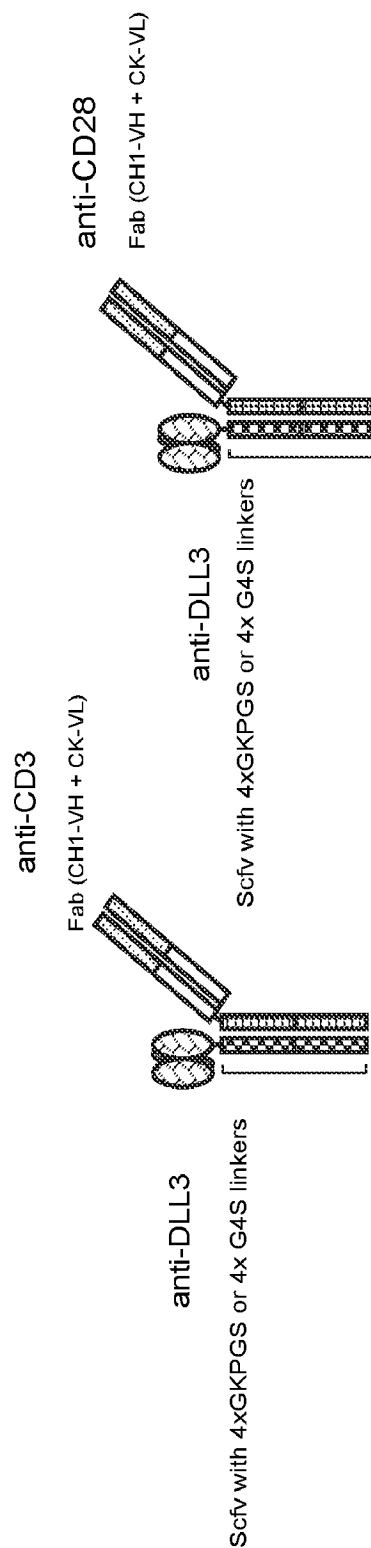


FIG. 1B

FIG. 1C

FIG. 1D

Scfv-Fc x Fab-Fc molecules

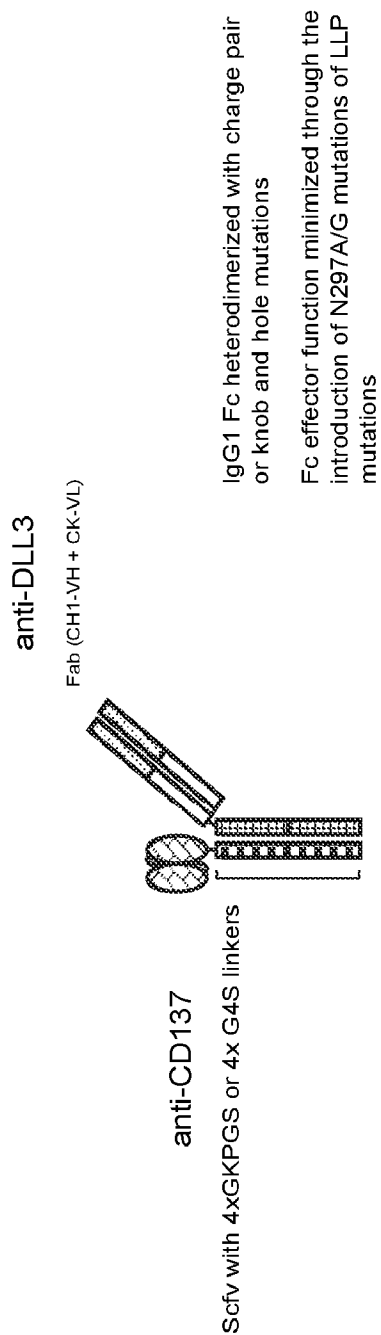


FIG. 1E

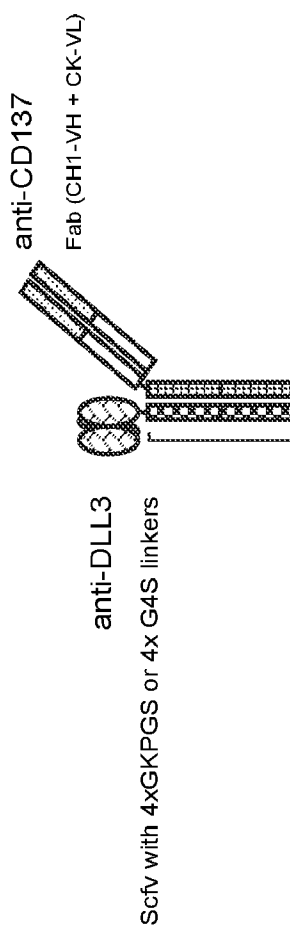


FIG. 1F

Scfv-scfv-Fc x Fc molecules

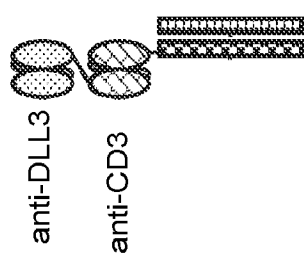


FIG. 2A

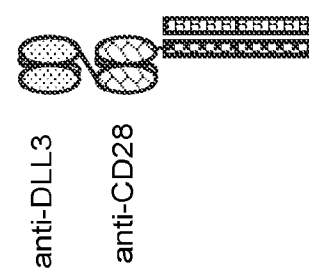


FIG. 2B

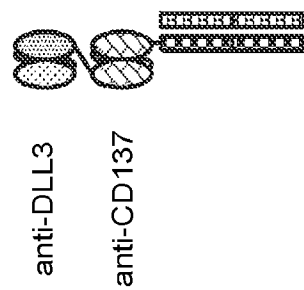


FIG. 2C

Scfv-scfv-Fc x Fab-Fc bispecific molecules



FIG. 2D



FIG. 2E

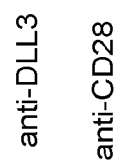
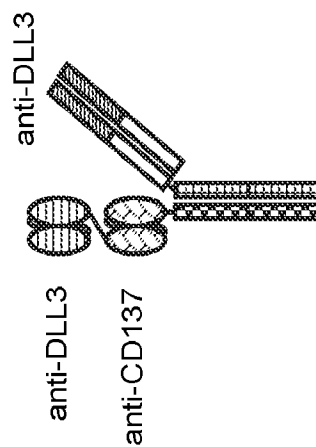


FIG. 2F



Anti-DLL3 antibodies binding to huDLL3 Expressing CHO cells

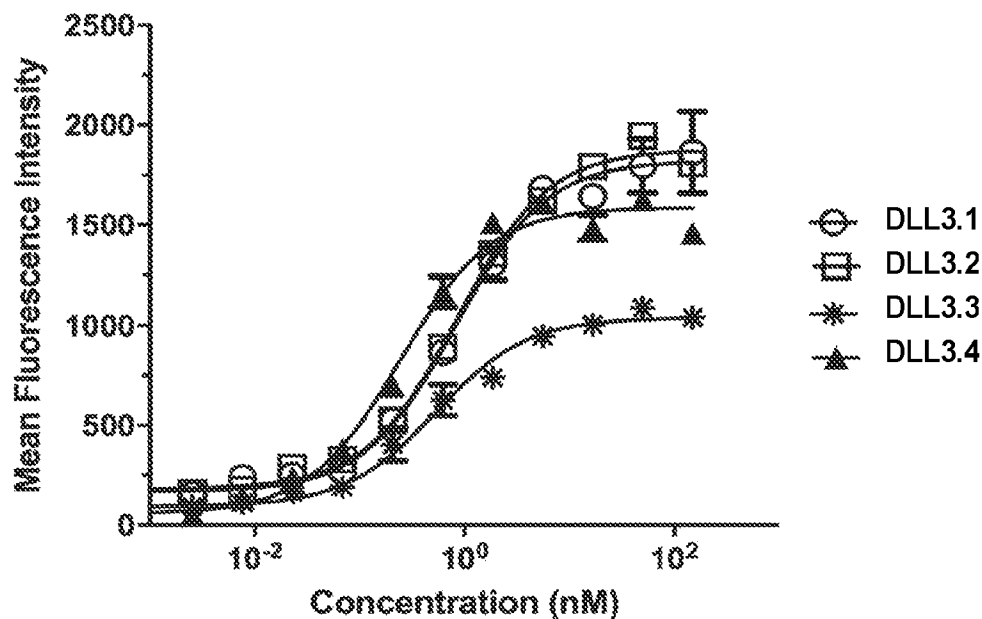


FIG. 3A

Anti-DLL3 binding to Cyno DLL3 CHO

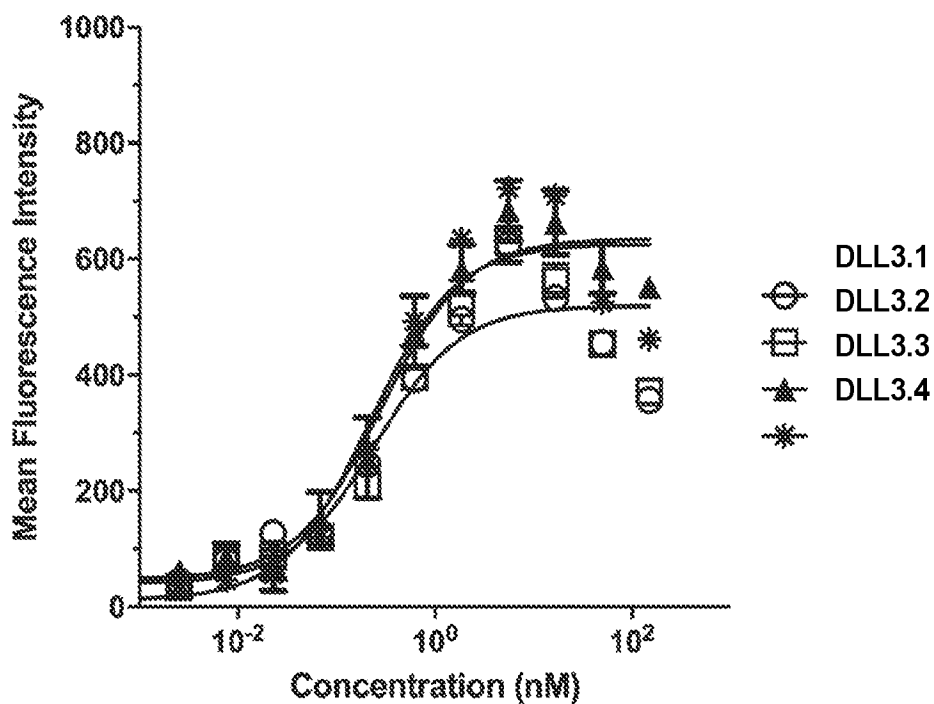


FIG. 3B

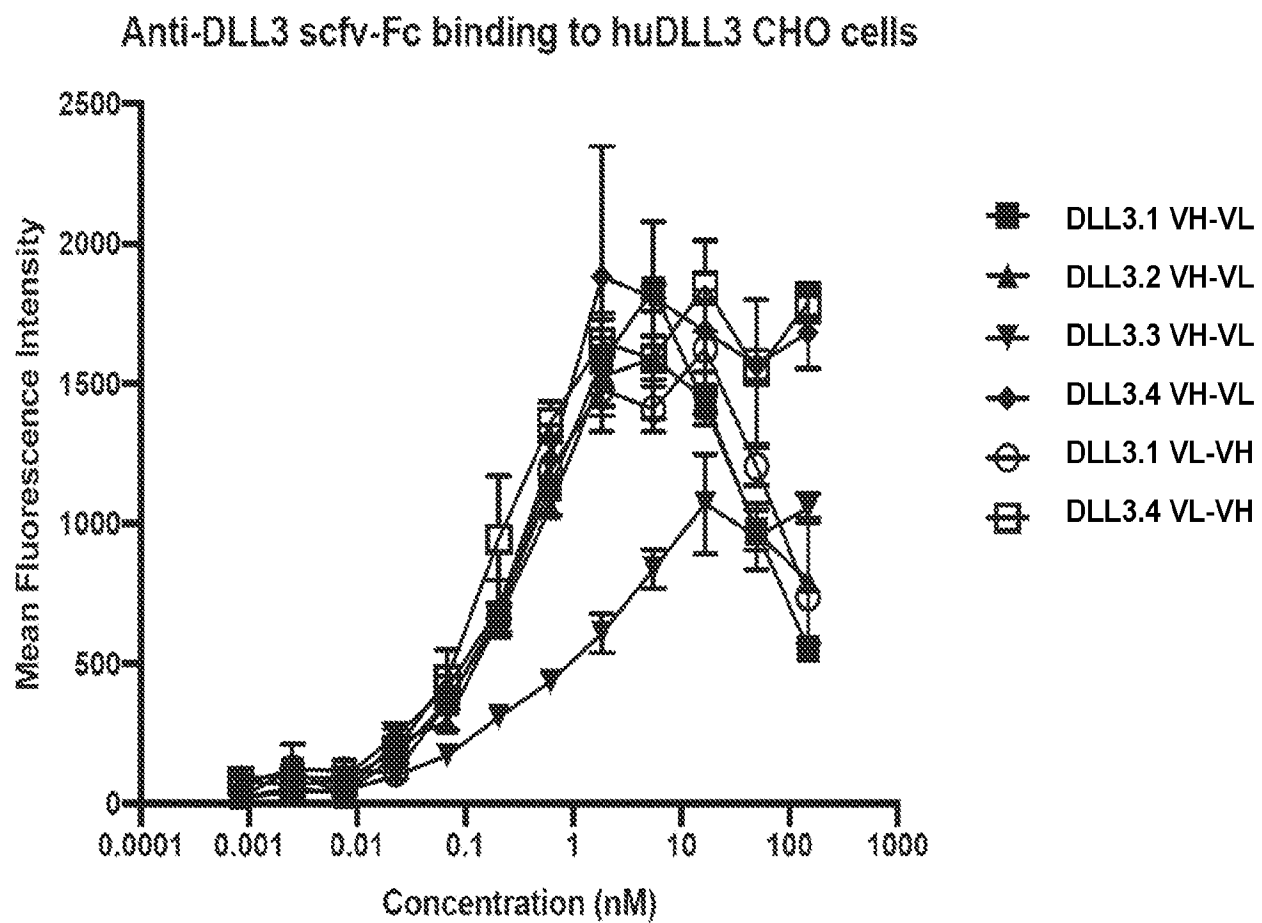


FIG. 4

DLL3Fab-Fc x CD3scfv-Fc mediated killing of huDLL3 expressing CHO cells by human PBMC cells

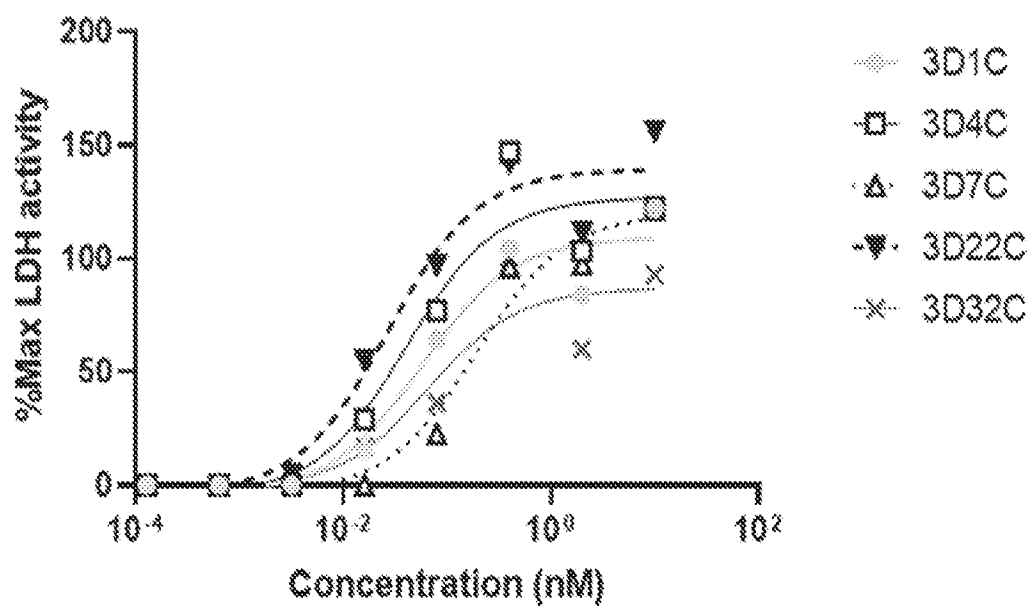


FIG. 5

DLL3Fab-Fc x CD3scfv-Fc mediated activation of human PBMC cells in the presence of huDLL3 expressing CHO cells

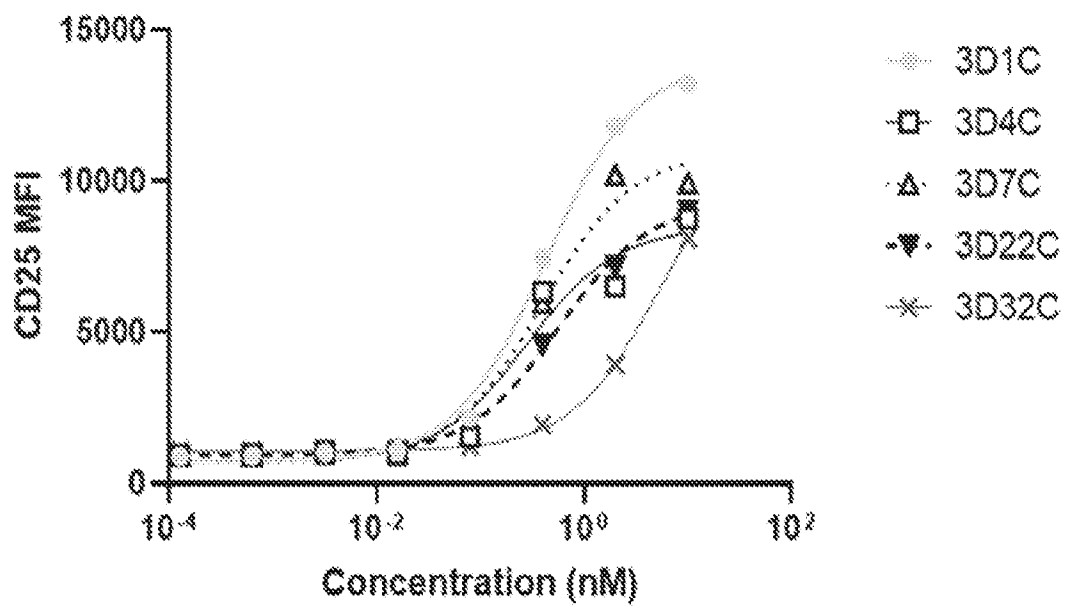


FIG. 6

DLL3scfv-CD3scfv-Fc x Fc killing of huDLL3 expressing CHO cells
by human PBMC cells

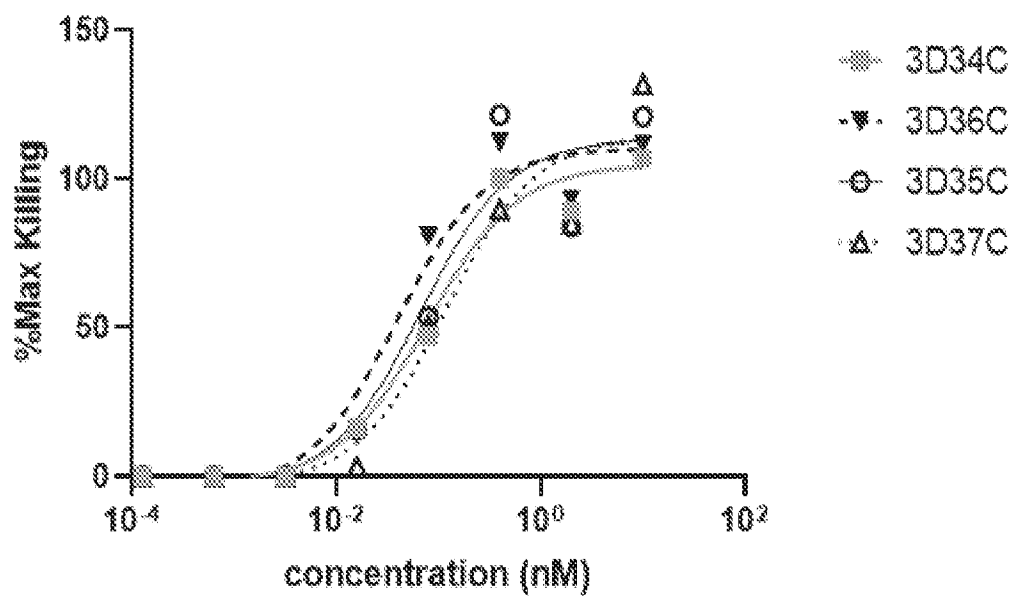


FIG. 7

DLL3scfv-CD3scfv-Fc x Fc mediated activation of human PBMC cells in the presence of huDLL3 expressing CHO cells

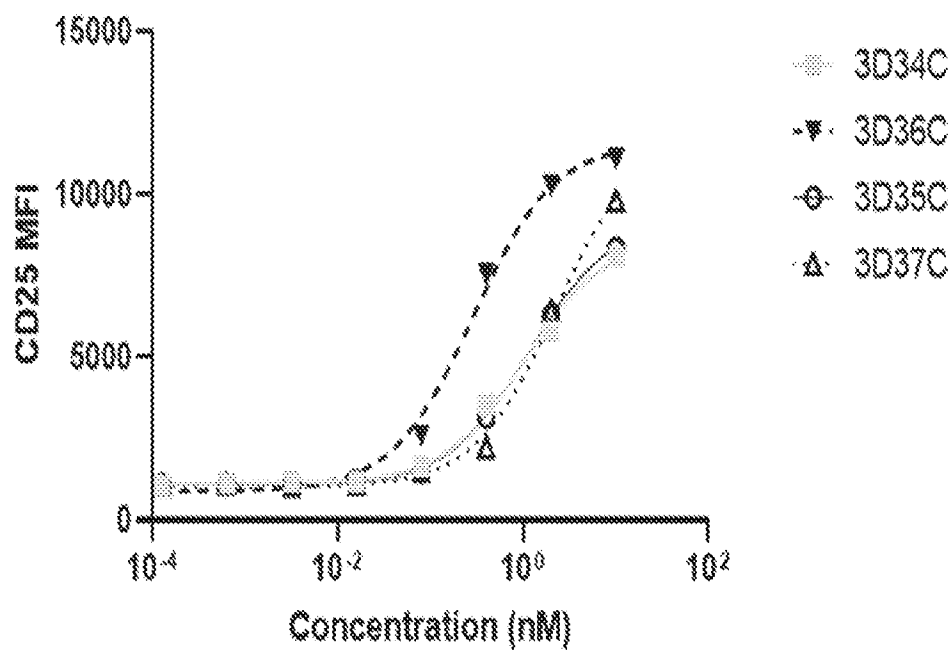


FIG. 8

DLL3Fab-Fc x DLL3scfv-CD3scfv-Fc mediated killing of huDLL3
expressing NCI-H82 cells by human PBMC cells

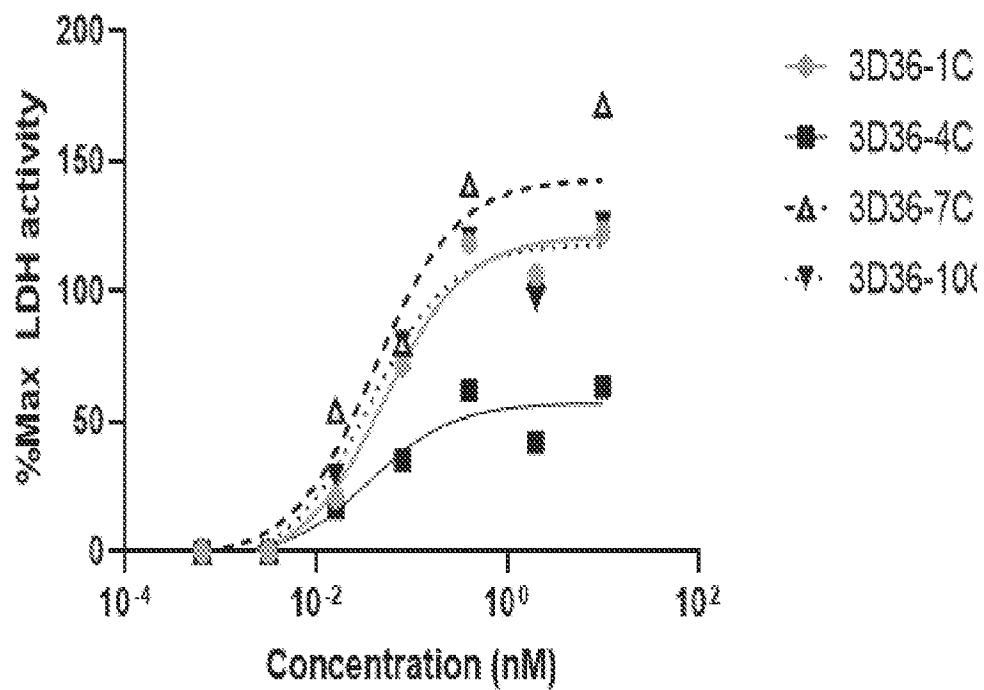


FIG. 9A

DLL3Fab-Fc x DLL3scfv-CD3scfv-Fc mediated killing of huDLL3
expressing NCI-H82 cells by human PBMC cells

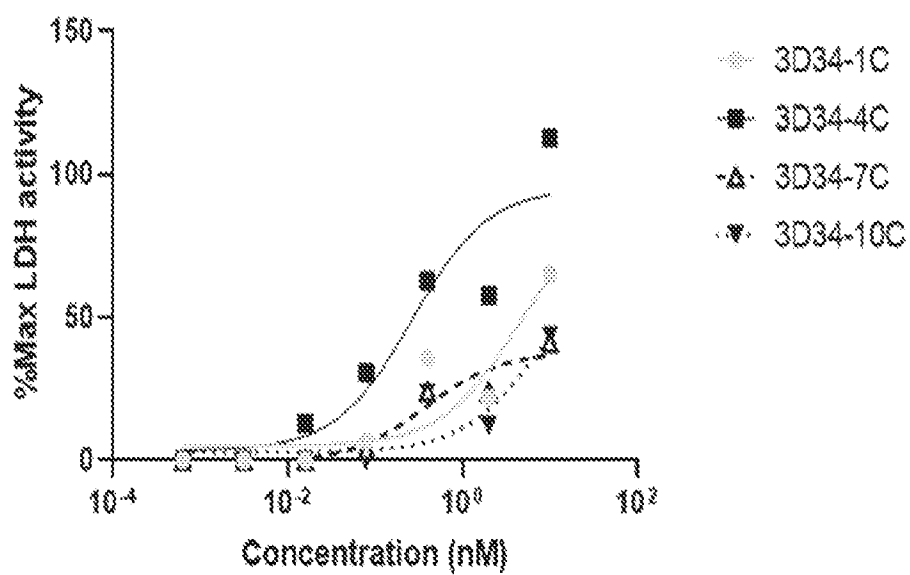


FIG. 9B

DLL3Fab-Fc x DLL3scfv-CD3scfv-Fc mediated killing of huDLL3
expressing NCI-H82 cells by human PBMC cells

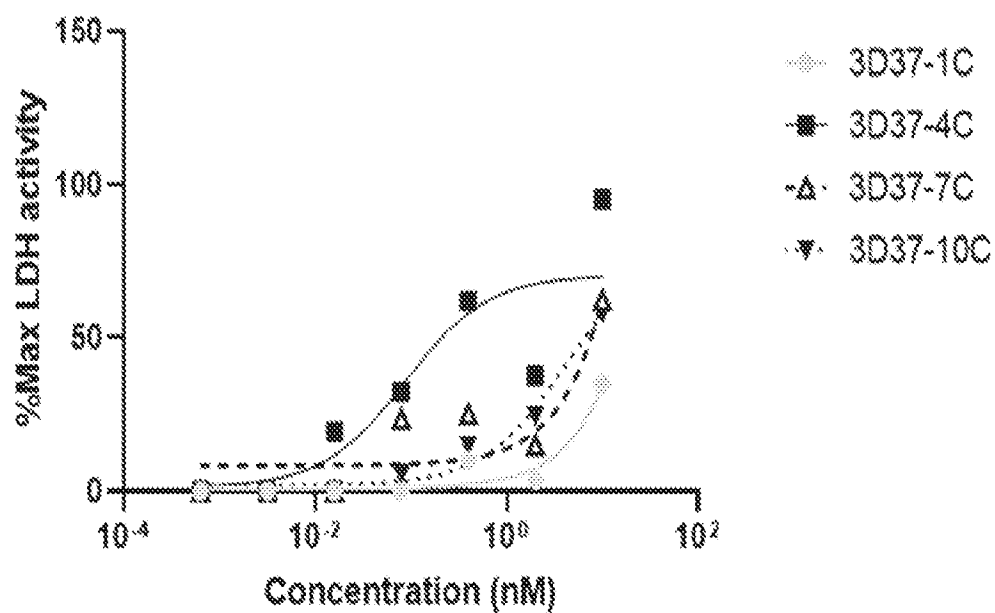


FIG. 9C

anti-CD3 variants of DLL3Fab-Fc x CD3scfv-Fc and DLL3scfv-
CD3scfv-Fc formatted molecules mediating the killing of huDLL3
expressing NCI-H82 cells by human PBMC cells

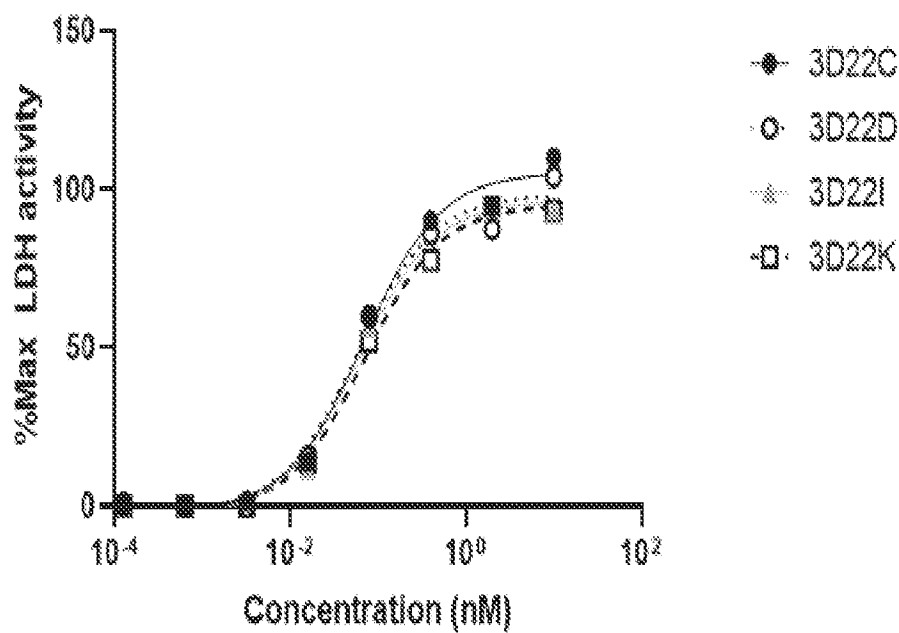


FIG. 10A

anti-CD3 variants of DLL3Fab-Fc x CD3scfv-Fc and DLL3scfv-
CD3scfv-Fc formatted molecules mediating the killing of huDLL3
expressing NCI-H82 cells by human PBMC cells

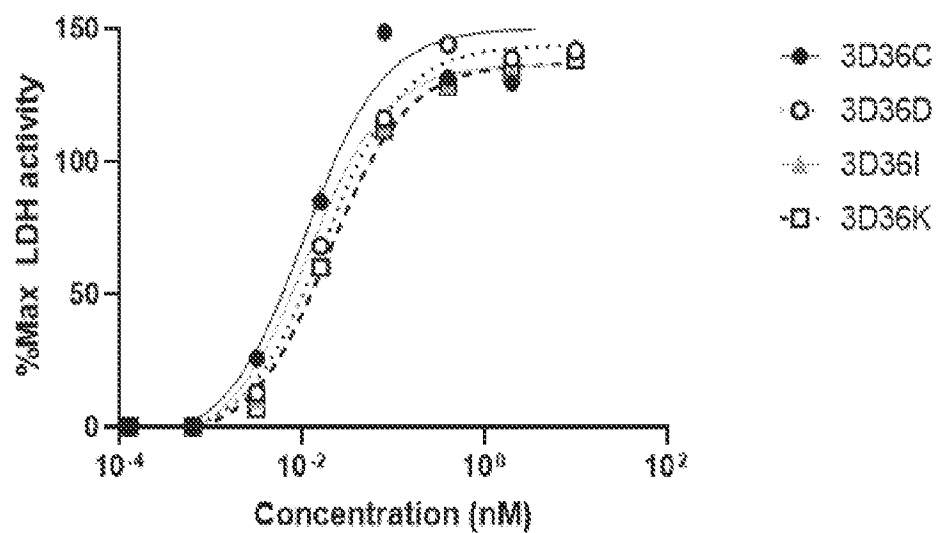


FIG. 10B

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

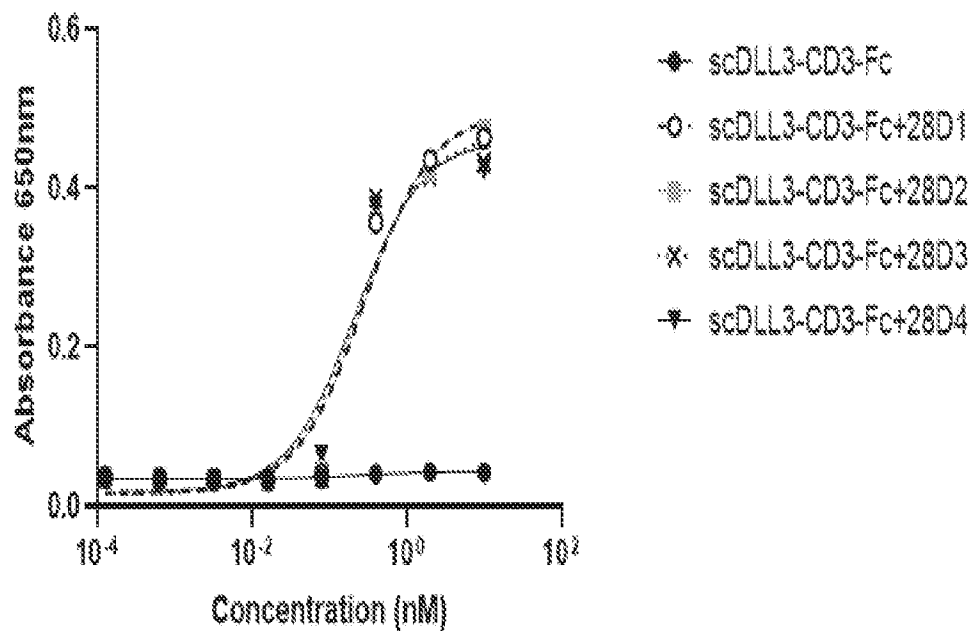


FIG. 11A

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

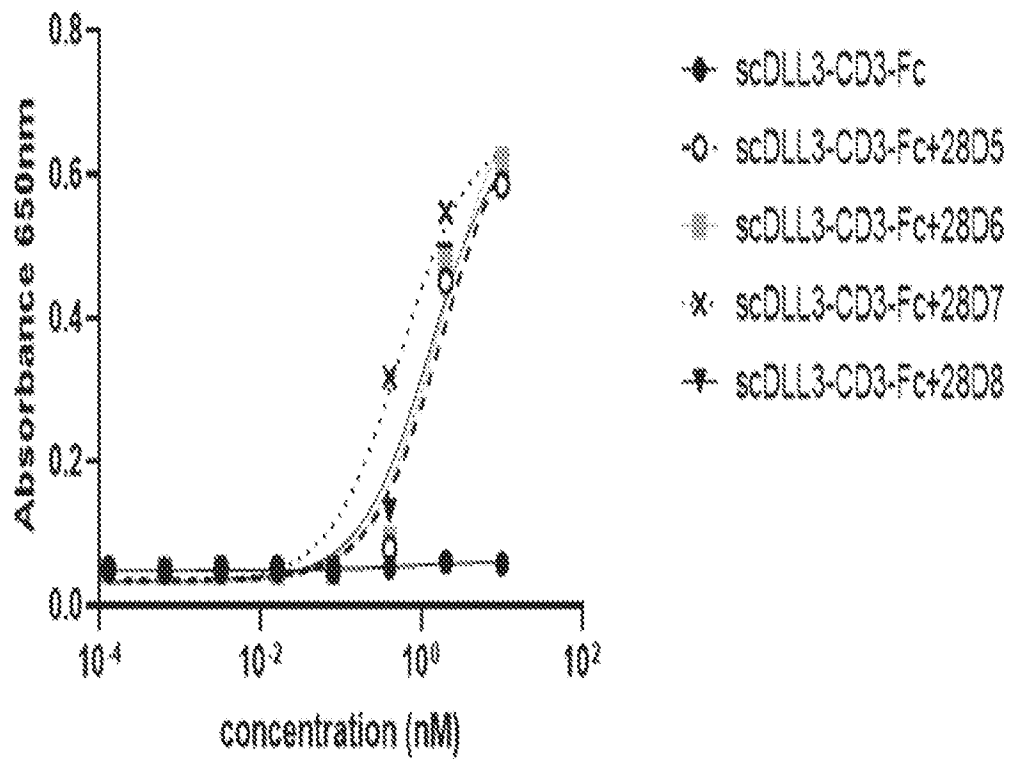


FIG. 11B

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

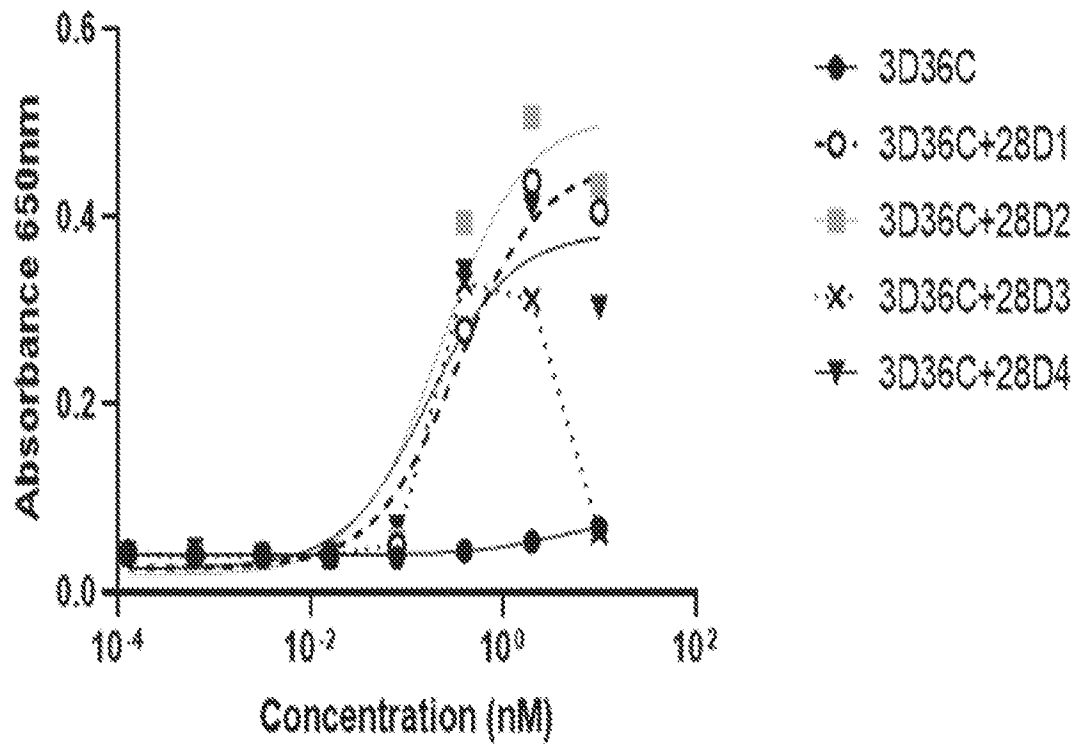


FIG. 11C

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

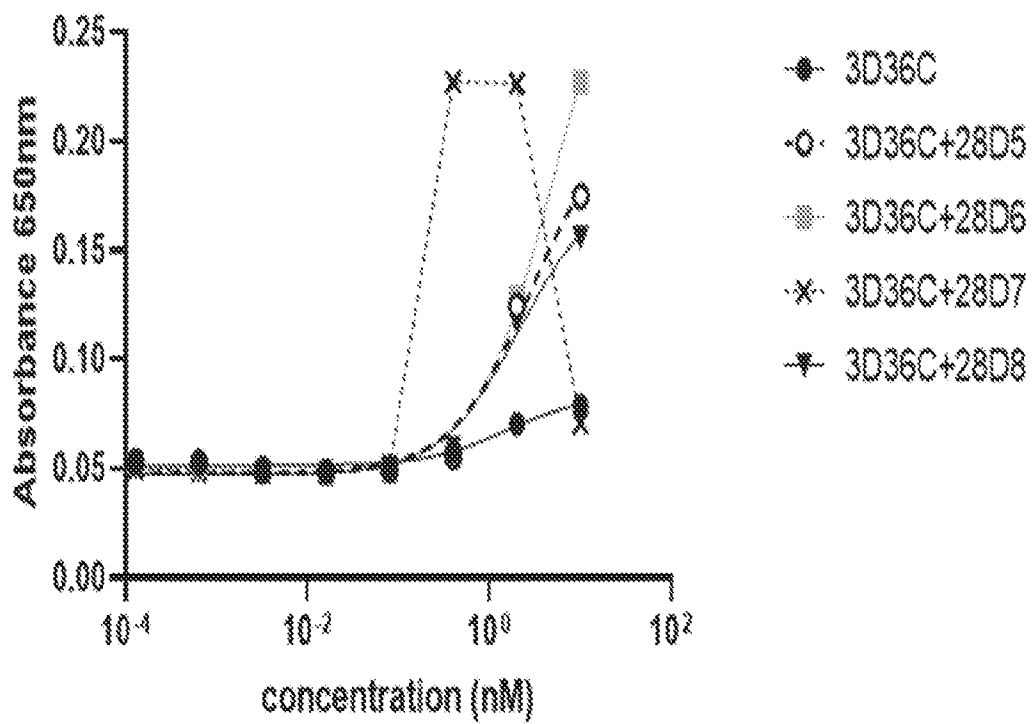


FIG. 11D

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

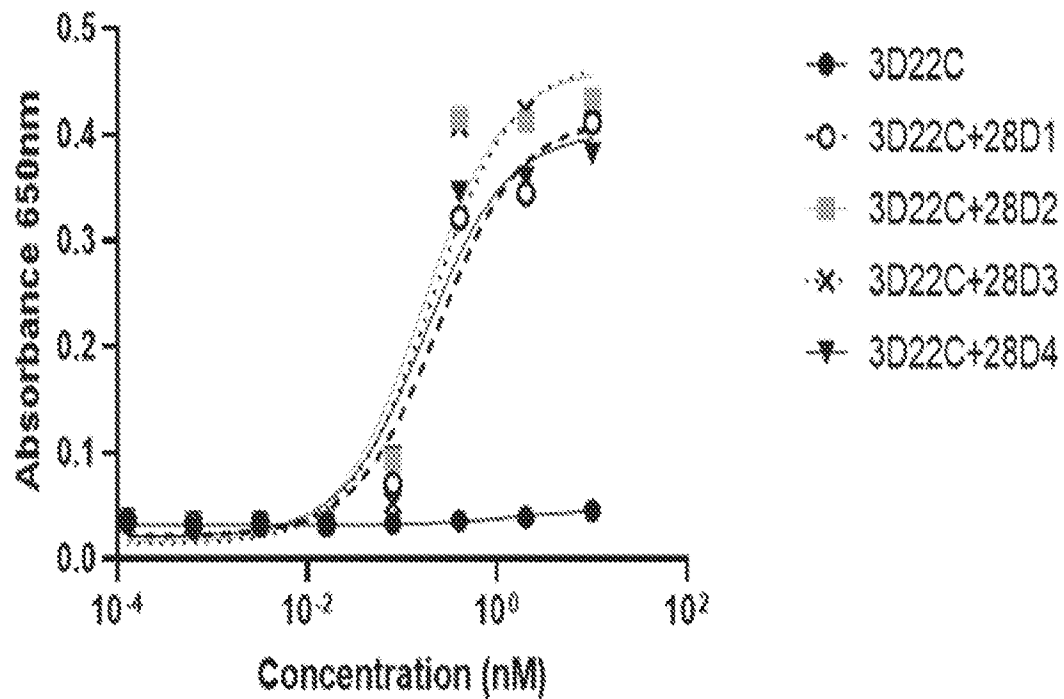


FIG. 11E

DLL3Fab-Fc x CD28Scfv-Fc mediated IL-2 secretion by huPBMCs in the presence of huDLL3 expressing NCI-H82 cells in combination with DLL3scfv-CD3scfv-scFc or DLL3Fab-CD3scfv-Fc

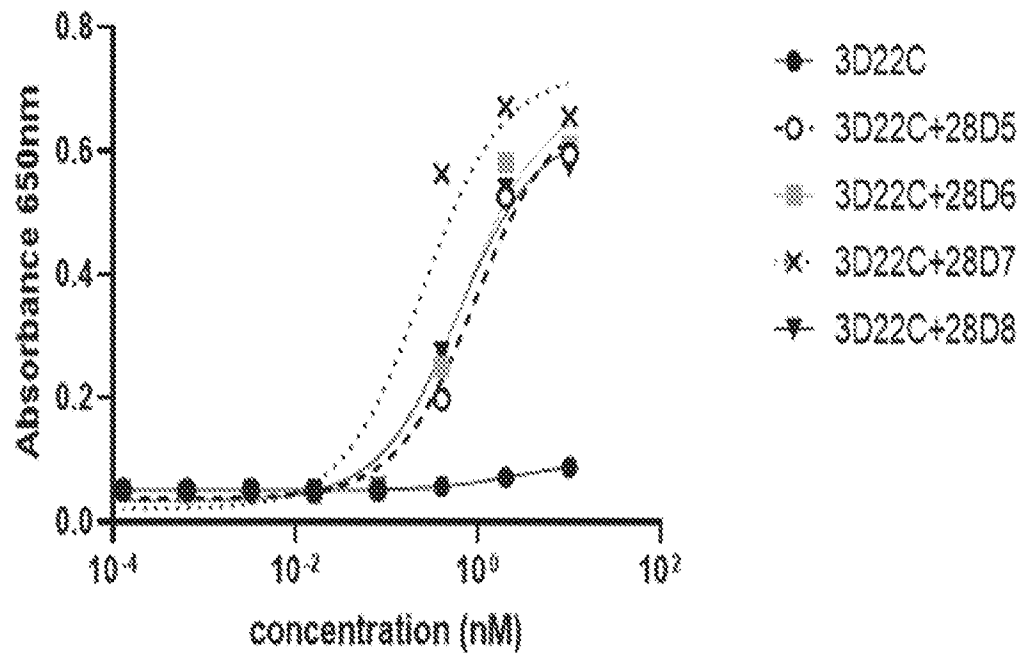


FIG. 11F

HPLC-size exclusion chromatography analysis of HEK293 transiently expressed and Protein A purified bispecifics using various CD3 variants

Name	DLL3 antibody	CD3 variant	conc (ug/ml)	%HMW	%Main Peak	%LMW
3D4B	D139A	Y52cA	602.7	2.1	97.7	0.2
3D4C	D139A	WT	511.4	2.5	97.0	0.6
3D4D	D139A	Y52cI	803.6	1.8	97.8	0.3
3D4E	D139A	Y52cL	351.6	2.1	97.3	0.6
3D4F	D139A	Y52cV	477.1	2	97.3	0.6
3D4G	D139A	Y52cS	288.8	2.3	97.2	0.5
3D4H	D139A	N35D	2070	2.2	97.2	0.6
3D4I	D139A	A101E	511.4	1.6	97.5	0.9
3D4J	D139A	A101D	1297.2	1.9	97.0	1.1
3D4K	D139A	A101N	449	1.8	97.4	0.8
3D4L	D139A	W100eY	267	3.3	96.1	0.6

FIG. 12

Killing of NC1-H82 tumor cells of PBMCs with variants of 3D22I

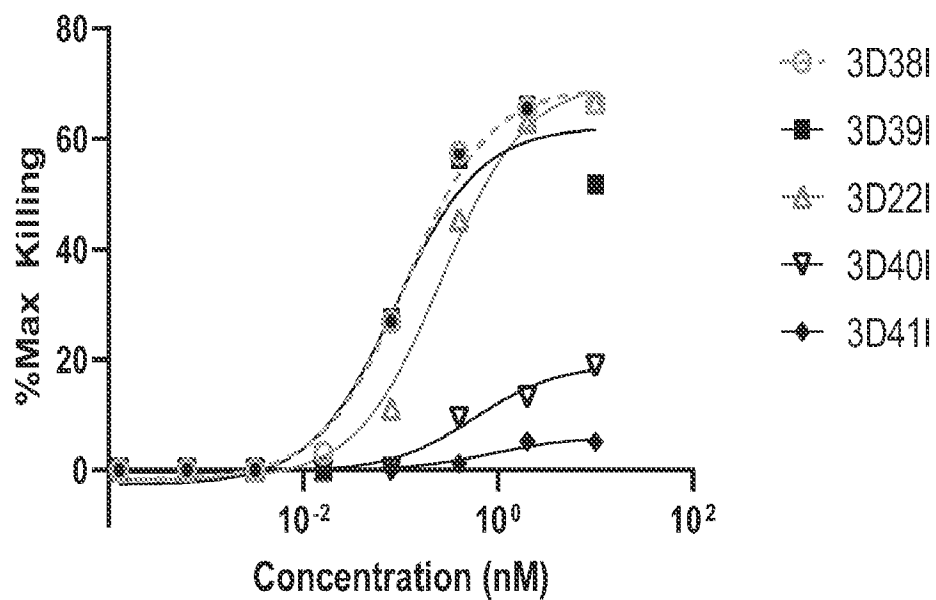


FIG. 13

Expression of CD25 by PBMCs when stimulated with variants of
3D22I in the presence of NC1-H82 tumor cells

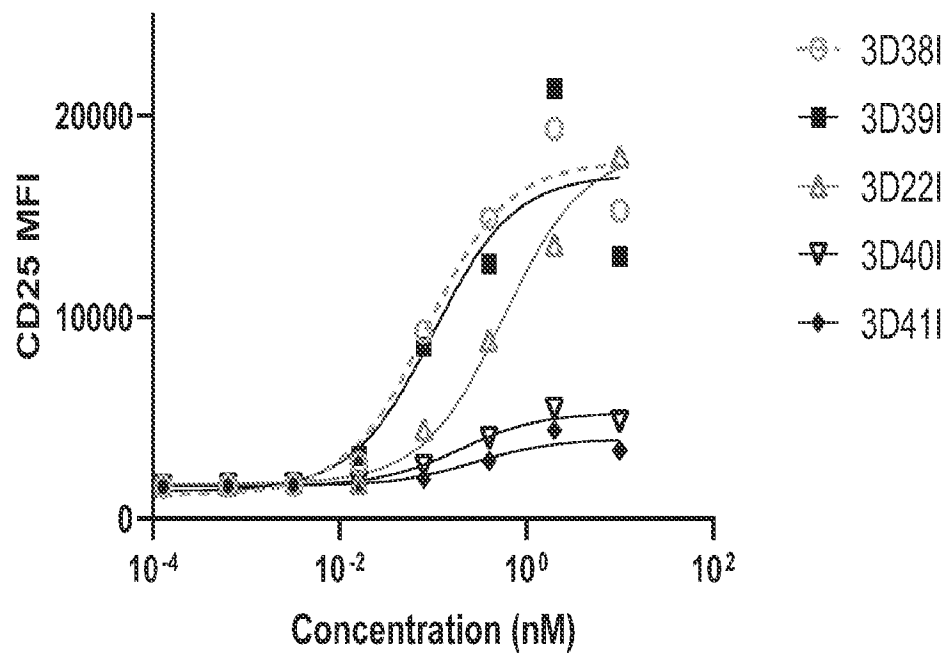


FIG. 14

DLL3 scfv x CD3scfv x DLL3 Fab variant 3D45I more potently stimulates killing of NCI-H82 cells by PBMCs than 3D39I

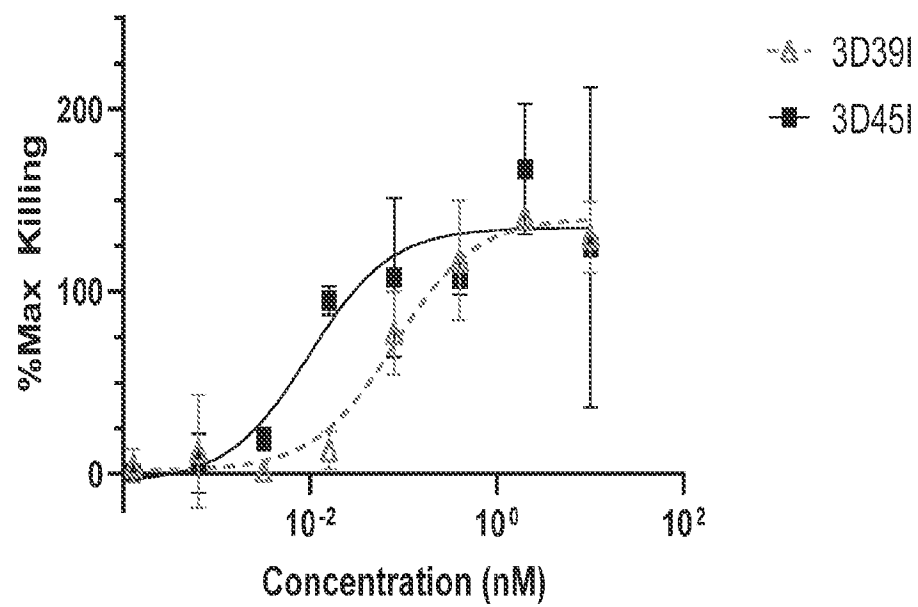


FIG. 15

DLL3 scfv x CD3scfv x DLL3 Fab variant 3D45I more potently stimulates expression of CD25 by PBMCs in the presence of NCI-H82 cells than 3D39I

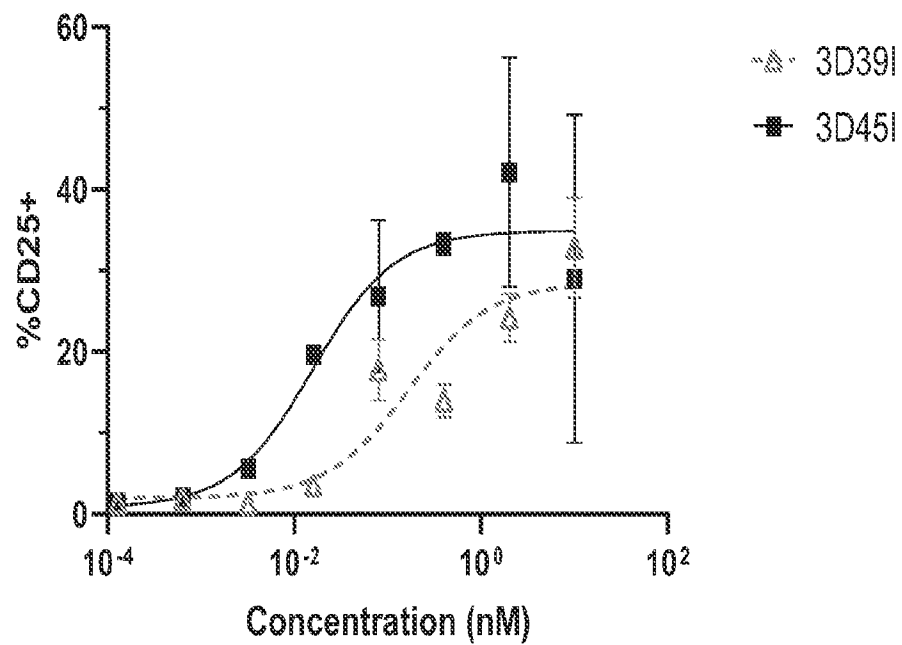


FIG. 16

CD28scfv-Fc x DLL3Fab-Fc bispecific molecules in combination with 50M of CD3-DLL3 benchmark, 3DBM, activate T-cells to secrete IL-2 better than 3DBM alone

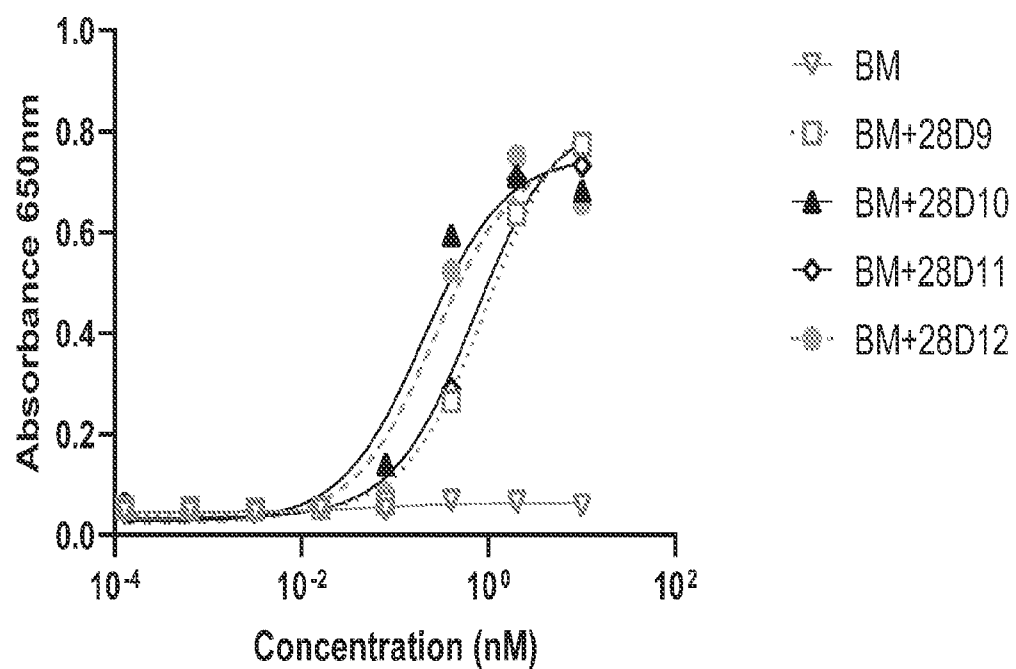


FIG. 17

CD28-Scfv-Fc (C50S) x DLL3-Fab-Fc variants 28D13 and 28D15, with the free cysteine in the anti-CD28 molecule engineered out, induce IL-2 secretion by PBMCs similarly to the parental molecule, 28D10, when combined with 50pM benchmark, 3DBM in the presence of NCI-H82 cells

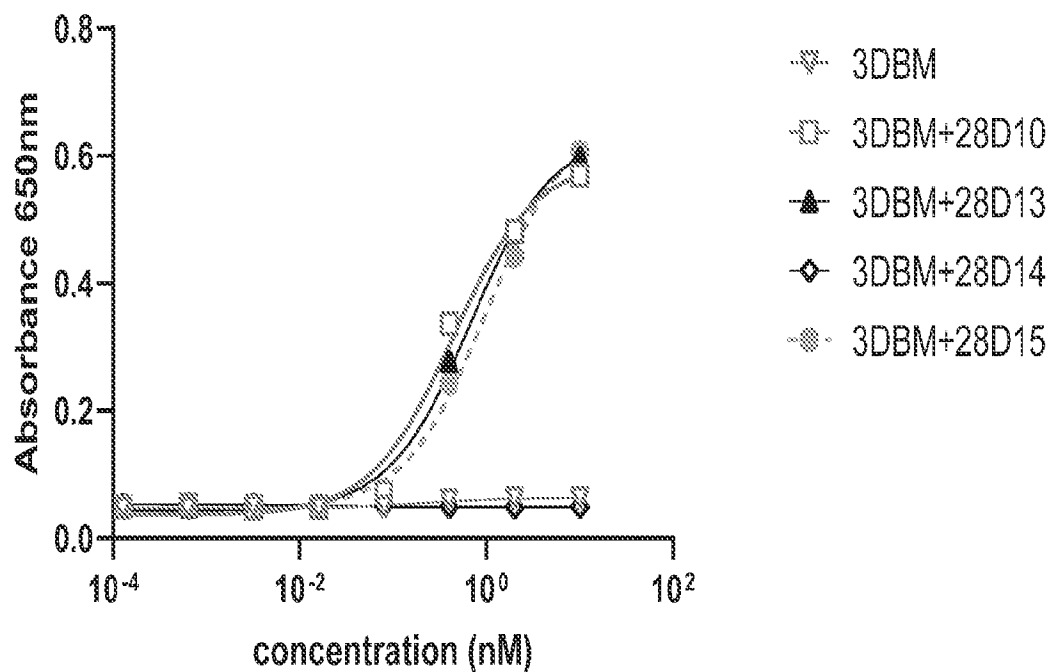


FIG. 18

Urelumab increases IFN γ secretion when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule

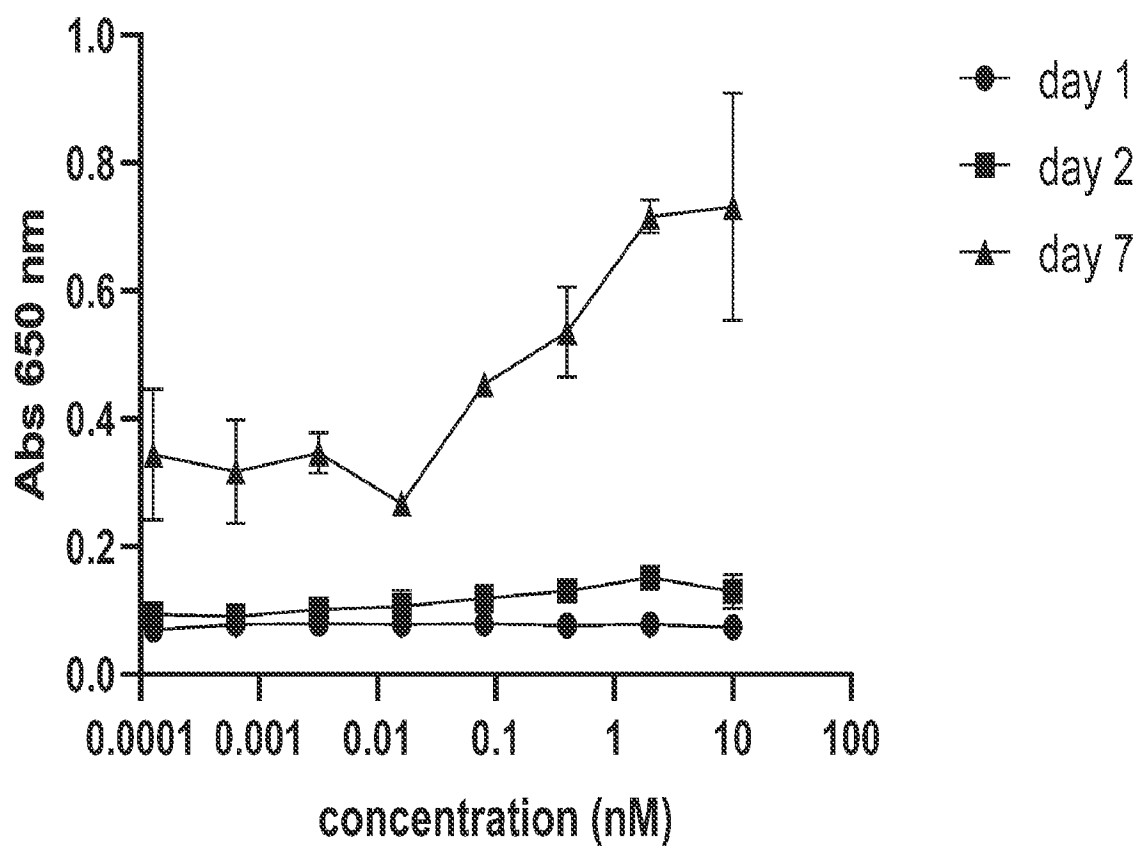


FIG. 19A

4-1BB Fab-Fc x DLL3scfv-Fc bispecific 4D3 increases IFN γ secretion when in combination with 50pM CD3xDLL3 T cell engager benchmark (BM) molecule

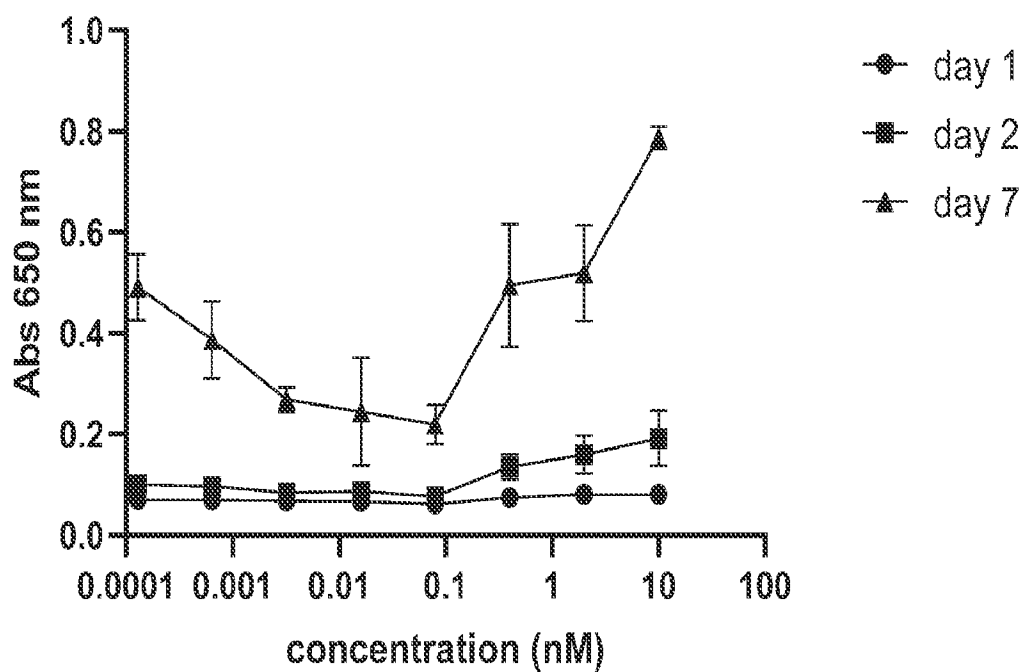


FIG. 19B

Bispecific molecules with two CD137 Fab fragments

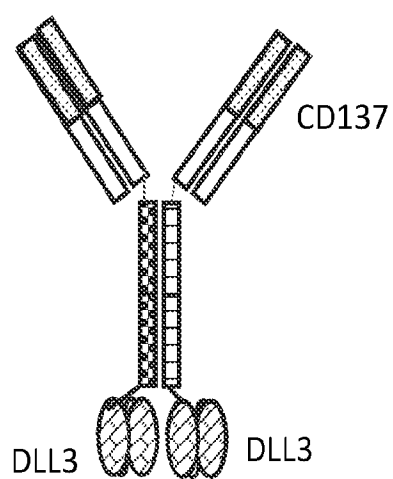


FIG. 20A

Scfv-Fc x Fab-Fc molecules

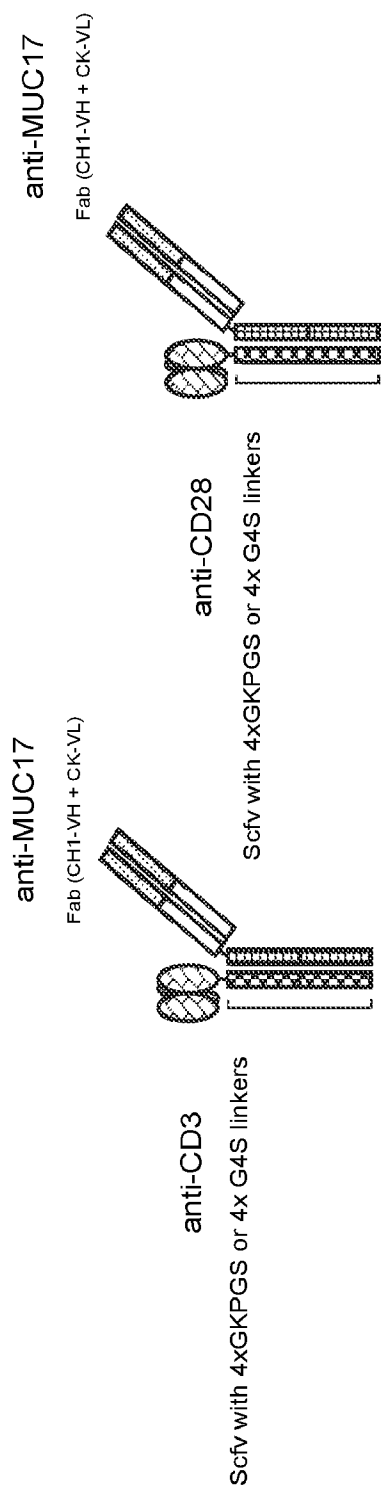


FIG. 21A

FIG. 21B

Scfv-Fc x Fab-Fc molecules

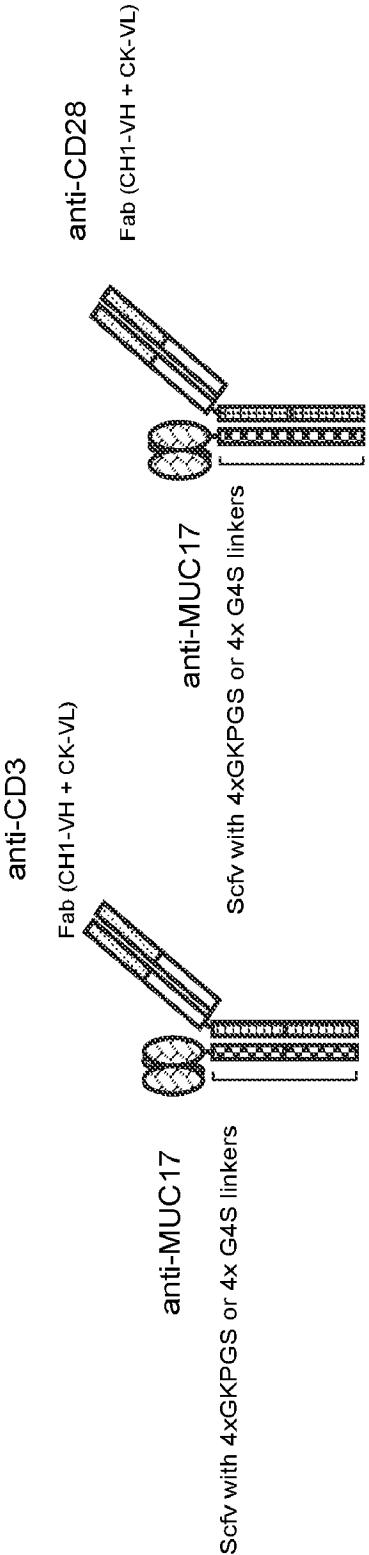


FIG. 21C

FIG. 21D

Scfv-Fc x Fab-Fc molecules

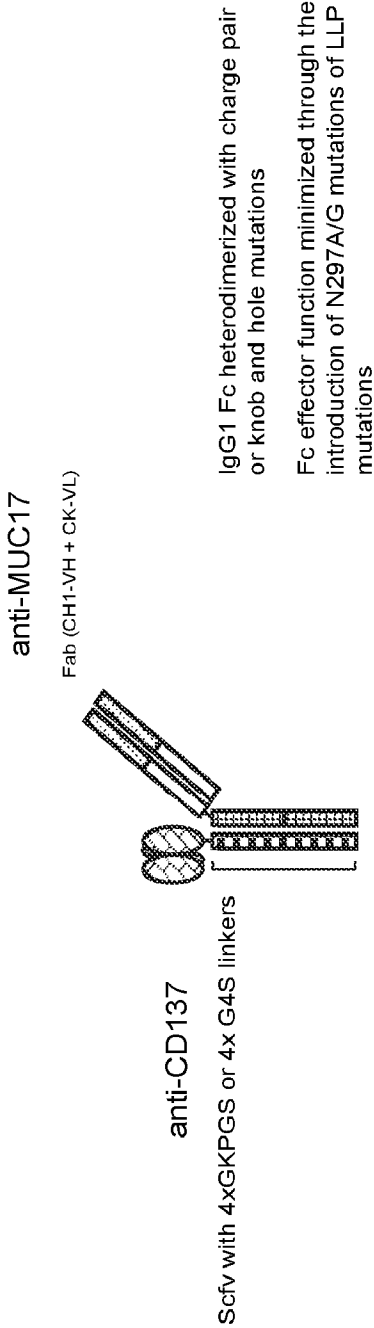


FIG. 21E

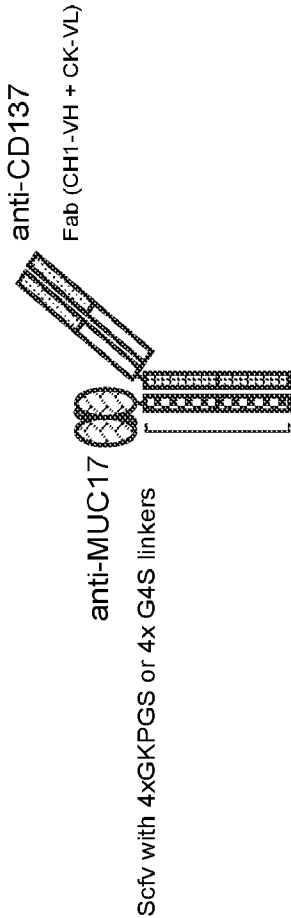


FIG. 21F

Scfv-scfv-Fc x Fc molecules

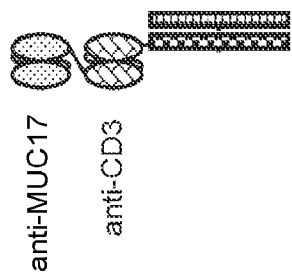


FIG. 22A

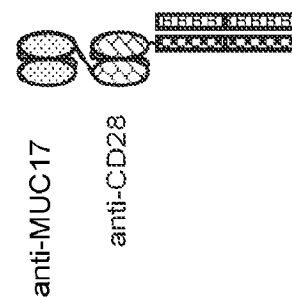


FIG. 22B



FIG. 22C

Scfv-scfv-Fc x Fab-Fc bispecific molecules



FIG. 22D

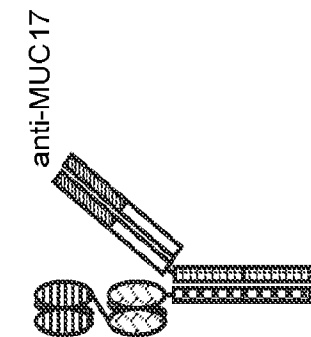


FIG. 22E

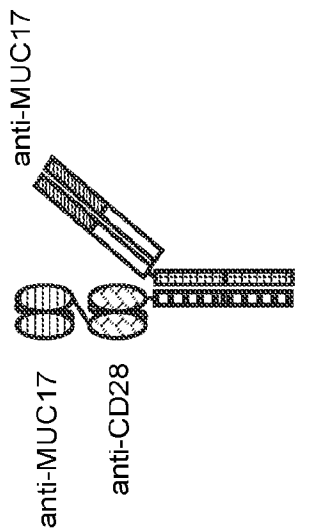


FIG. 22F

MUC17xCD3 Bispecifics bind ASPC1 cells

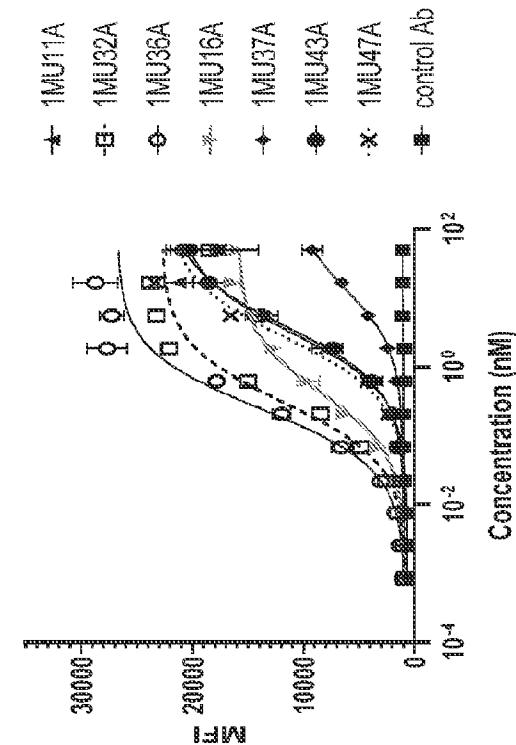


FIG. 24

MUC17xCD3 Bispecifics bind CHO Cell Expressing Muc17

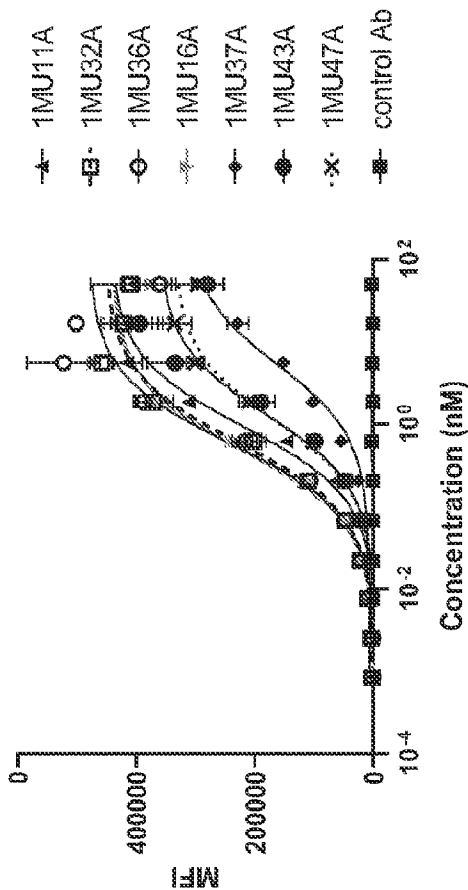


FIG. 23

MUC17xCD3 bispecific molecules, 3M55C, 3M46C, and 3M32C, kill
Muc17 expressing CHO cells with PBMCs

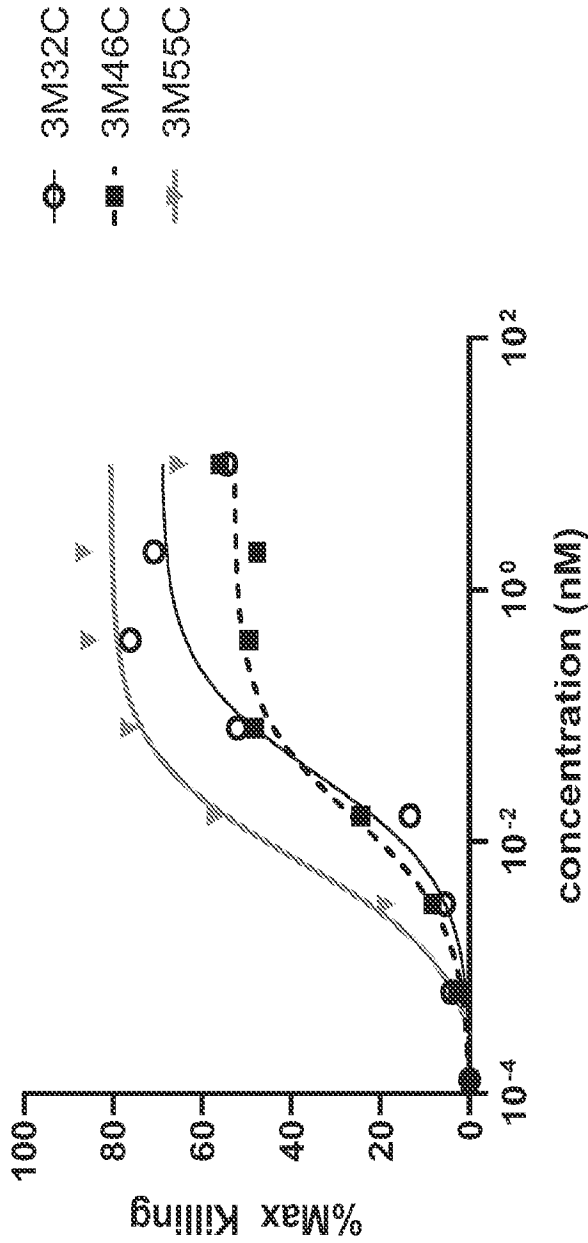


FIG. 25

PBMC killing of ASPC1 cells with MUC17xCD3 bispecifics of various formats of antibody 1MU32A

MUC17xCD3 Bispecifics Activate PBMC T-cells
to Kill ASPC1 Cells

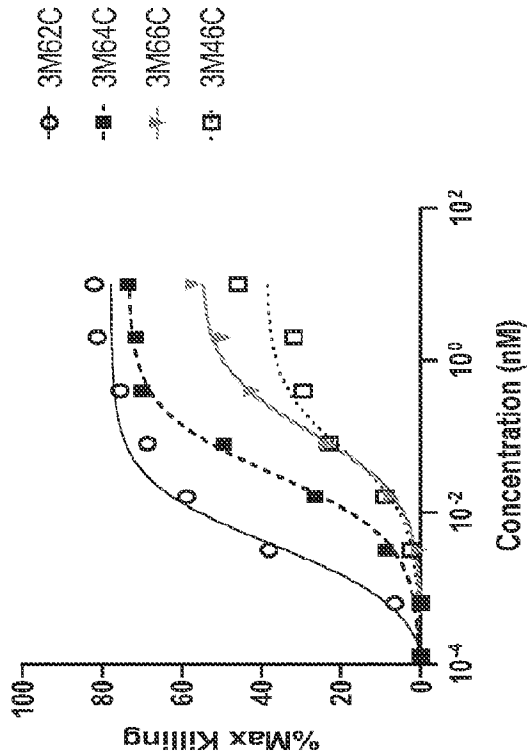


FIG. 26A

MUC17xCD3 Bispecifics increase levels of CD25 in
the presence of ASPC1 Cells

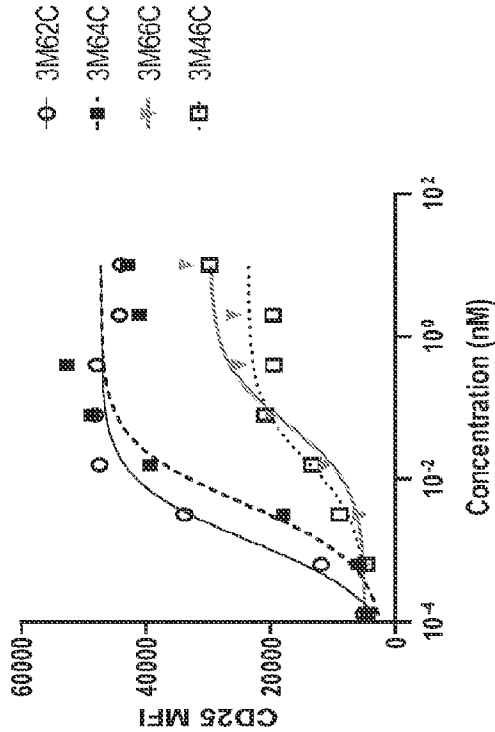
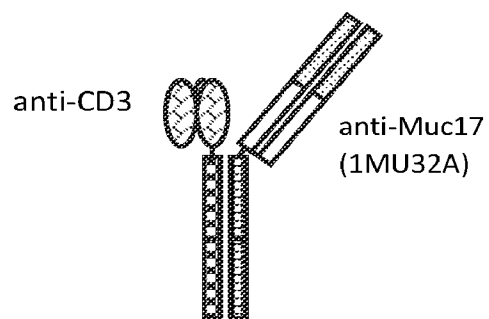
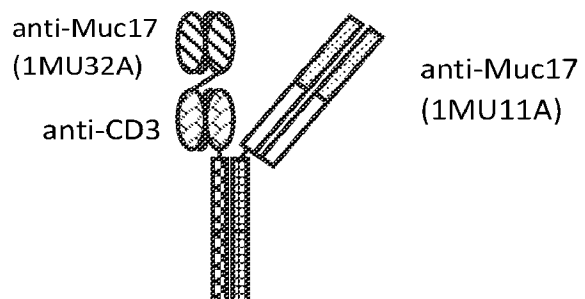


FIG. 26B



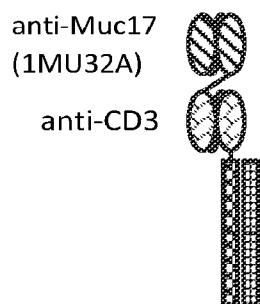
3M46C

FIG. 26C



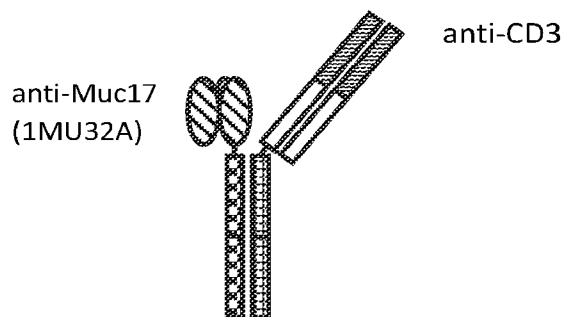
3M64C

FIG. 26D



3M62C

FIG. 26E



3M66C

FIG. 26F

PBMC killing of ASPC1 cells with MUC17xCD3 bispecifics of various formats of antibody 1MU11A

MUC17xCD3 Bispecifics Activate PBMC T-cells to Kill ASPC1 Cells

MUC17xCD3 Bispecifics increase levels of CD25 in the presence of ASPC1 Cells

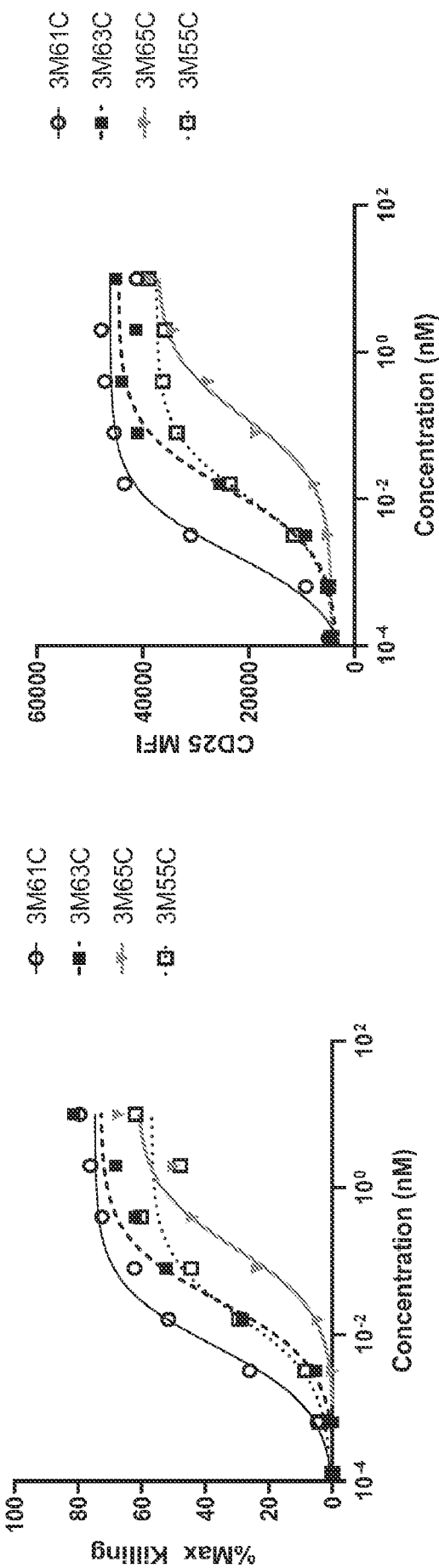
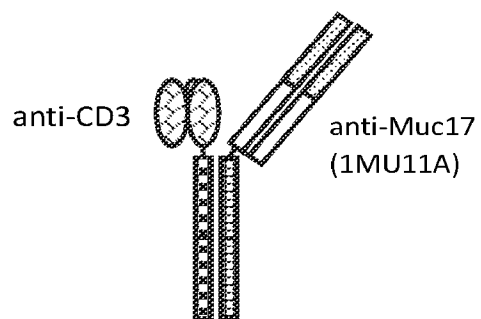


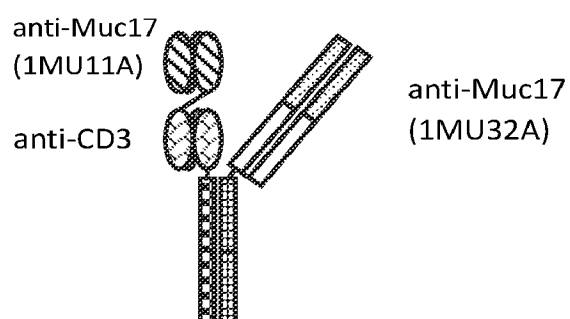
FIG. 27A

FIG. 27B



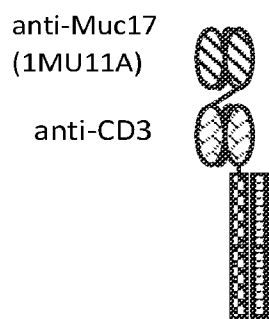
3M55C

FIG. 27C



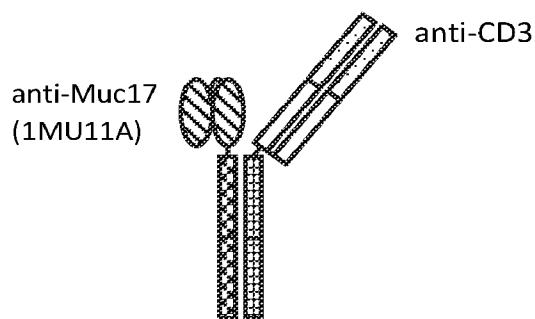
3M63C

FIG. 27D



3M61C

FIG. 27E



3M65C

FIG. 27F

CD28xMuc17 bispecific in combination with 10pM of MUC17xCD3 (3M62C) bispecific
activates T-cells to express IL-2 and CD25

CD28xMUC17 Bispecifics combined with MUC17xCD3
Bispecifics activate T-cells to Secrete IL-2 in the
presence of ASPC1 Cells

IL-2 secretion

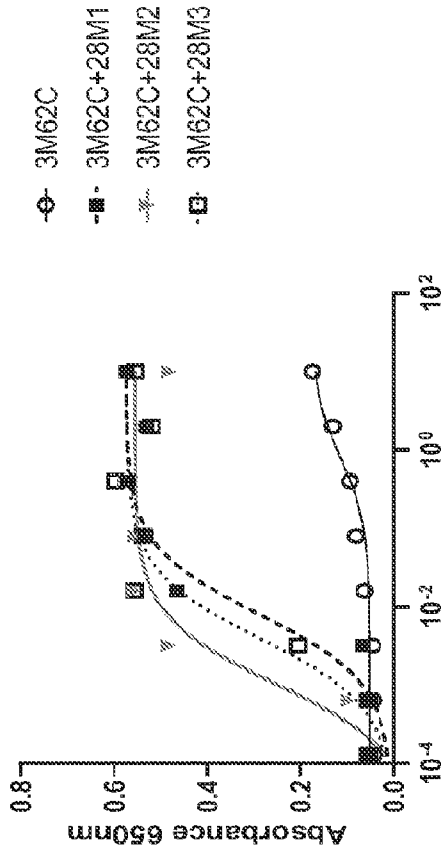


FIG. 28A

CD28xMUC17 Bispecifics combined with MUC17xCD3
Bispecifics activate T-cells to Express CD25 in the
presence of ASPC1 Cells

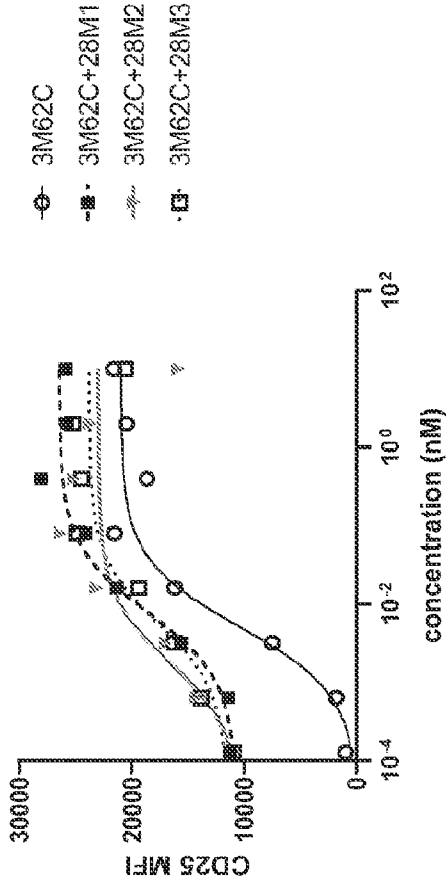
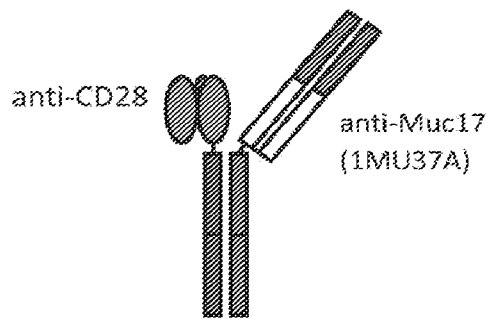
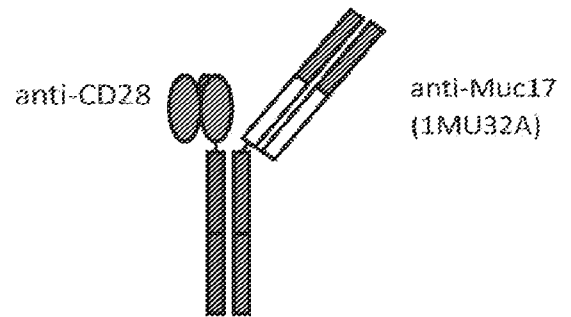


FIG. 28B



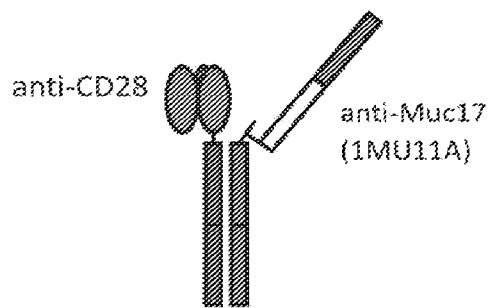
28M1

FIG. 28C



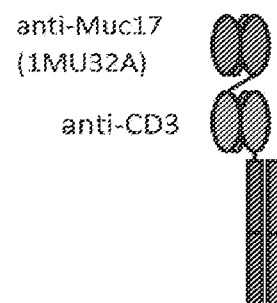
28M2

FIG. 28D



28M3

FIG. 28E



3M62C

FIG. 28F

CD28xMuc17 bispecific in combination with 20pM of MUC17xCD3 (3M55C)
bispecific activates T-cells to express IL-2 and CD25

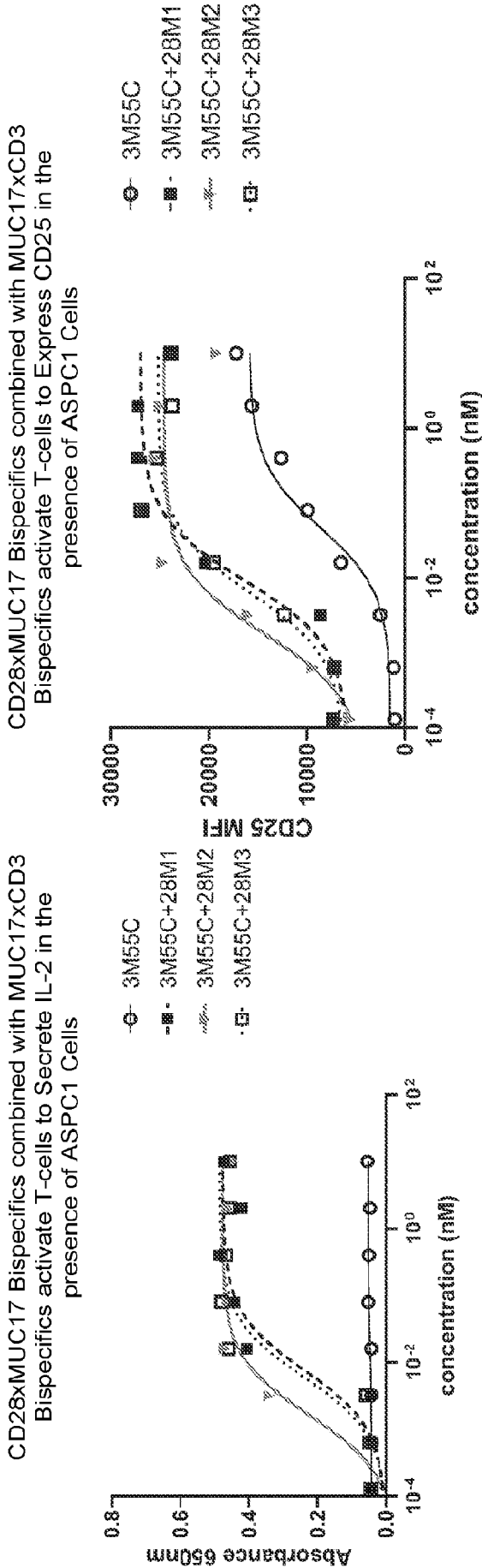


FIG. 29A

FIG. 29B

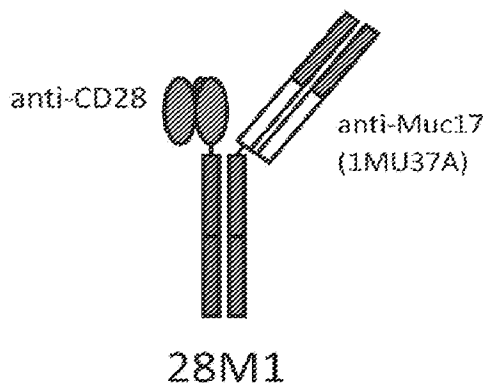


FIG. 29C

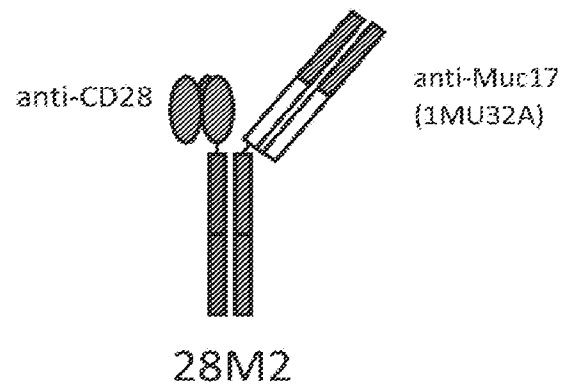


FIG. 29D

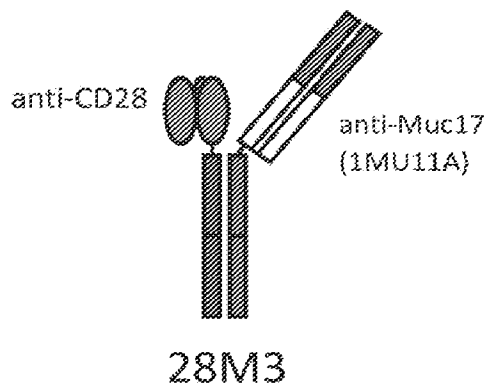


FIG. 29E

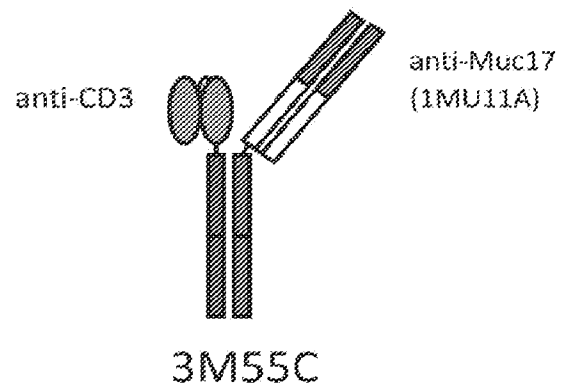


FIG. 29F

CD28xMUC17 Bispecifics alone do not activate T-cells
to Secrete IL-2 in the presence of ASPC1 Cells

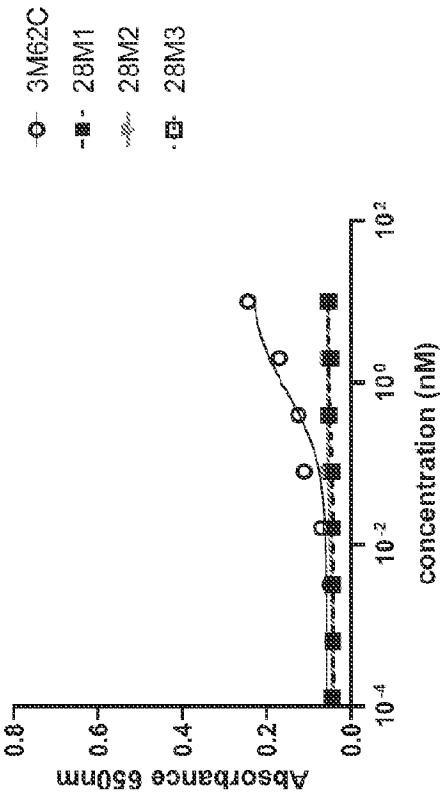


FIG. 30A

CD28xMUC17 Bispecifics alone do not activate T-cells
to Express CD25 in the presence of ASPC1 Cells

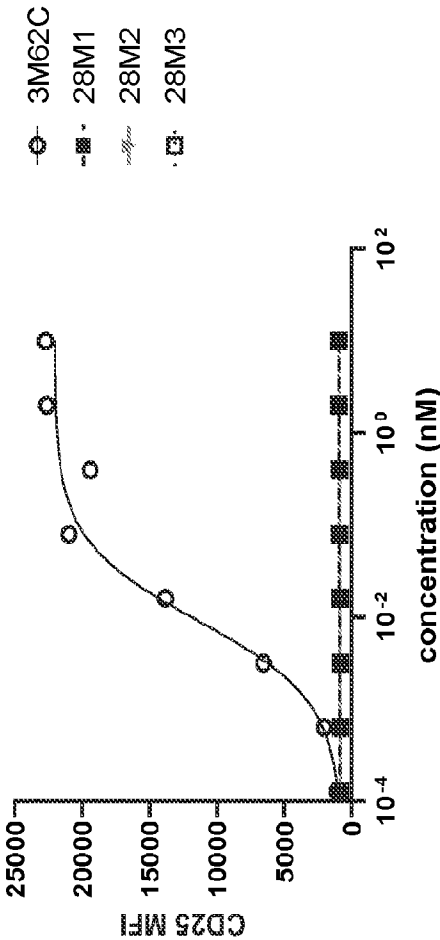


FIG. 30B

Bioactivity of multiple CD3 variants: PBMC killing of ASPC1 cells expressing Muc17

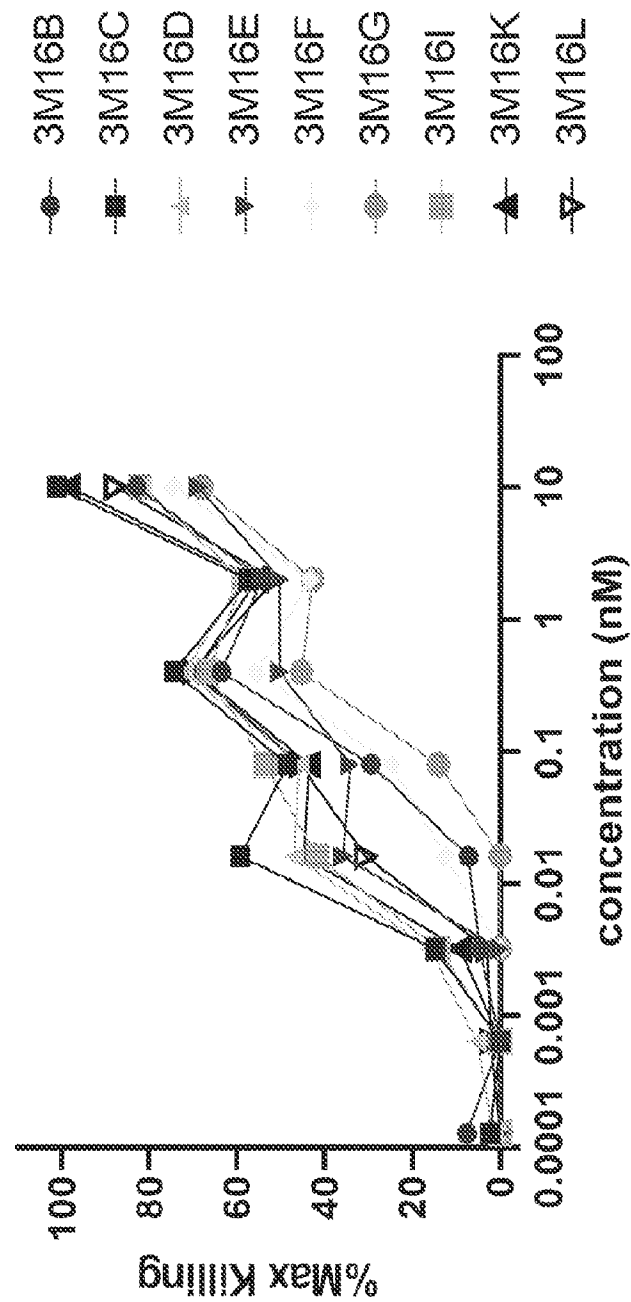


FIG. 31

hu1MU11A and hu1MU32A retain Muc17 binding activity in the Scfv format

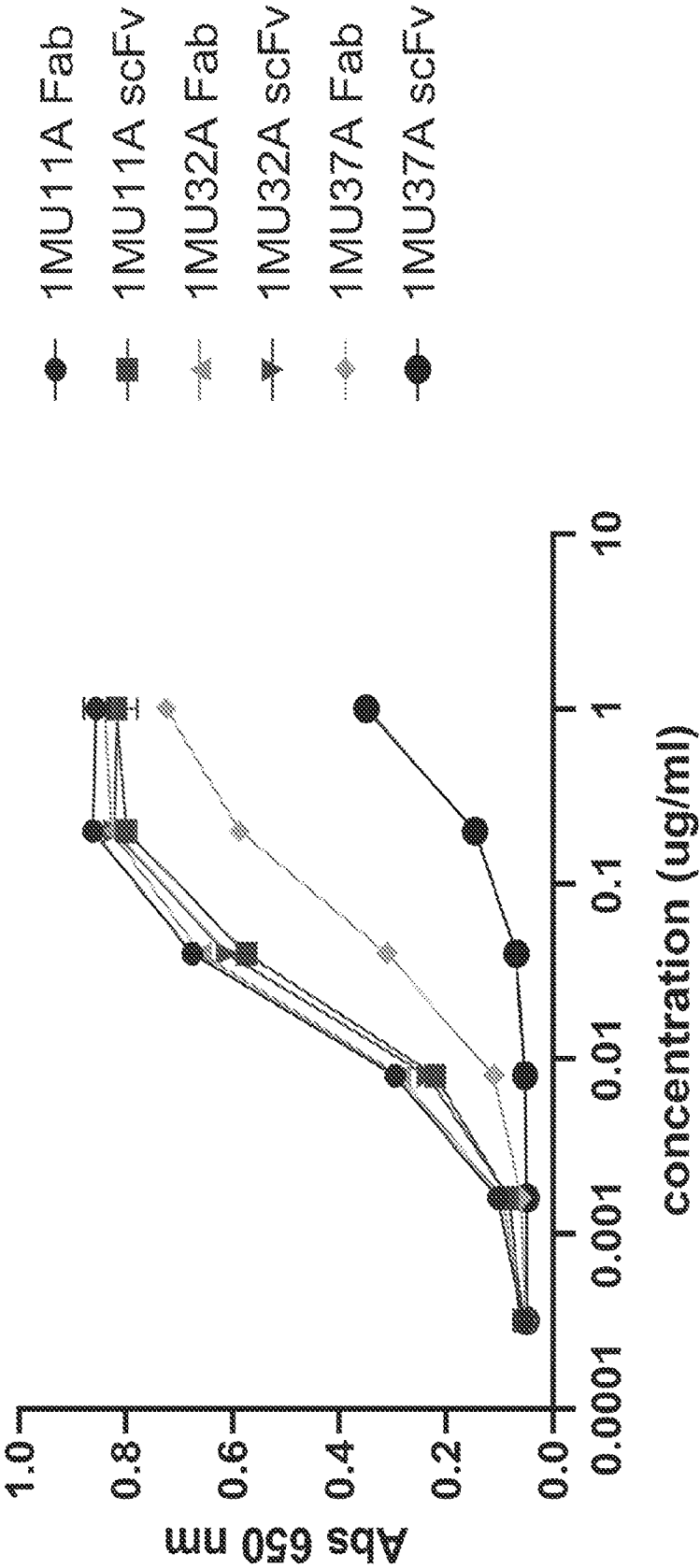


FIG. 32

CD137 Fab x Muc17 scfv bispecific molecules 4M1 increases IFNg secretion by
PBMC when combined with 2pM 3M8B7 benchmark and in the presence of
ASPC1 cells

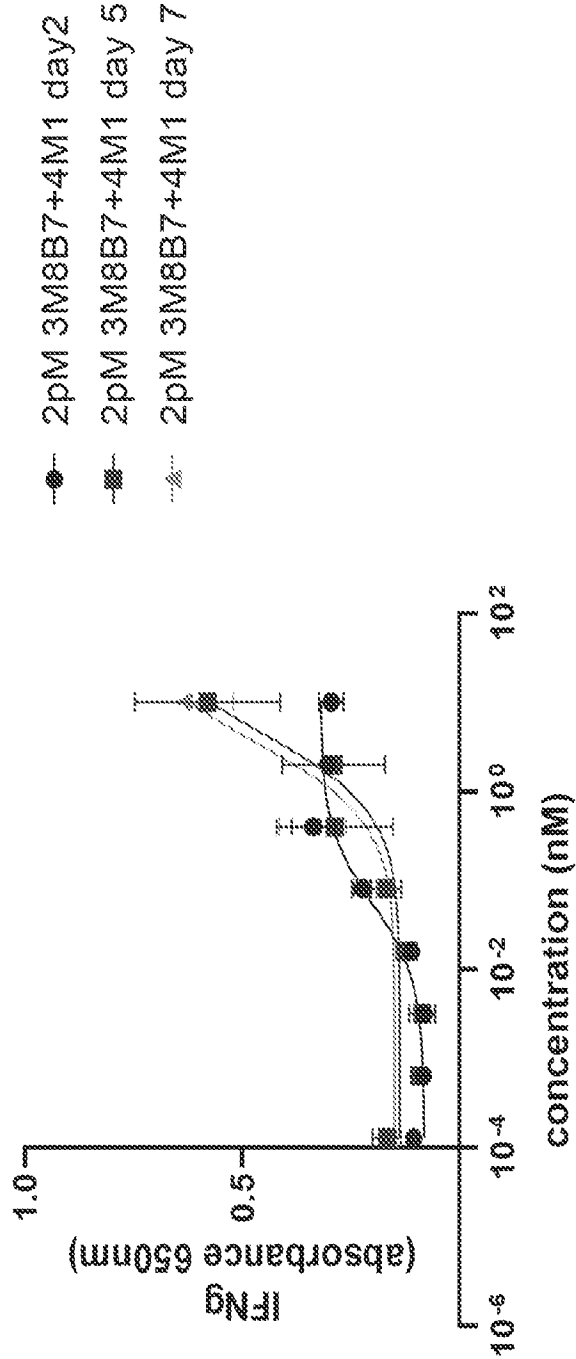


FIG. 33

CD137 Fab x Muc17 scfv bispecific molecules 4M2 increase IFNg secretion by PBMC when combined with 2pM 3M8B7 benchmark and in the presence of ASPC1 cells

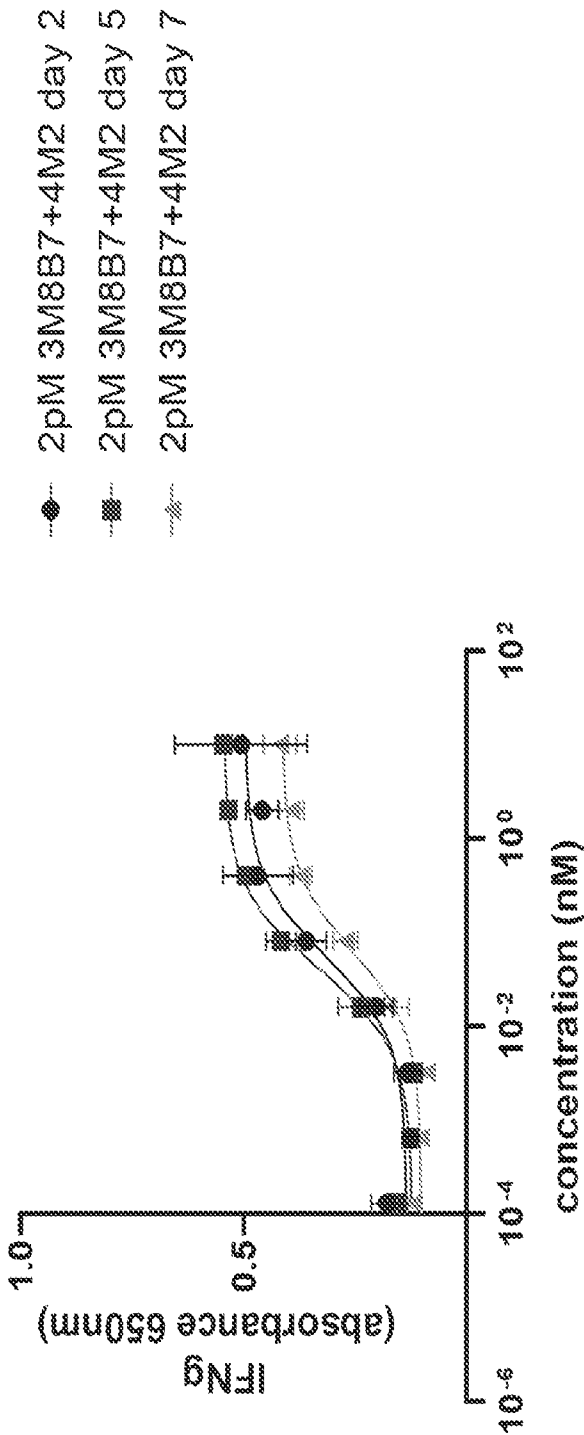


FIG. 34

Muc17xCD137 bispecific 4M2 in combination with 10pM or 20pM CD3 bispecific 3M8B7 activates PBMCs to secrete IFNg in the presence of CHO cells expressing Muc17

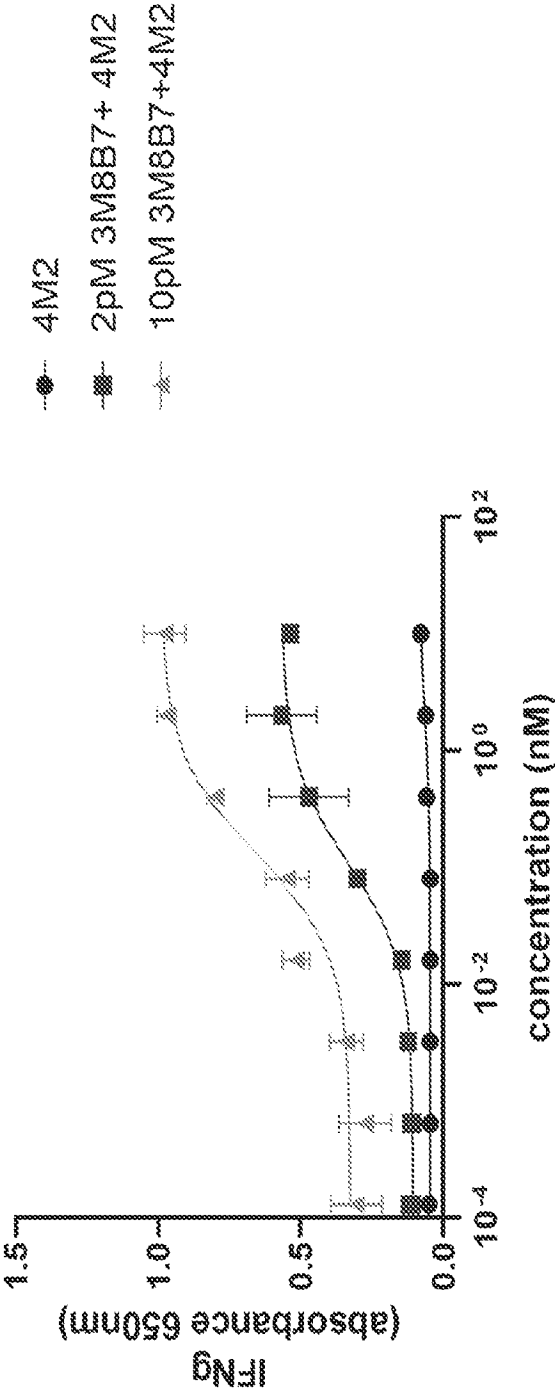


FIG. 35

Muc17xCD137 bispecific 4M7 in combination with 10pM or 20pM CD3
bispecific 3M8B7 activates PBMCs to secrete IFNg in the presence of CHO
cells expressing Muc17

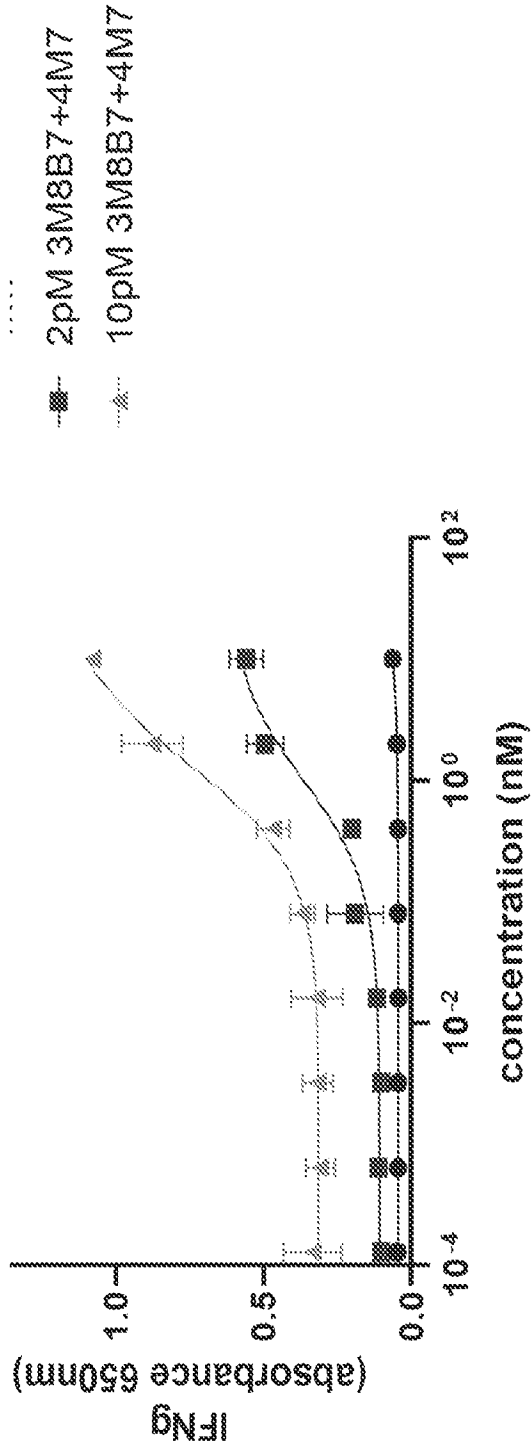


FIG. 36

Muc17xCD137 bispecific 4M8 in combination with 10pM or 20pM CD3
bispecific 3M8B7 activates PBMCs to secrete IFNg in the presence of CHO
cells expressing Muc17

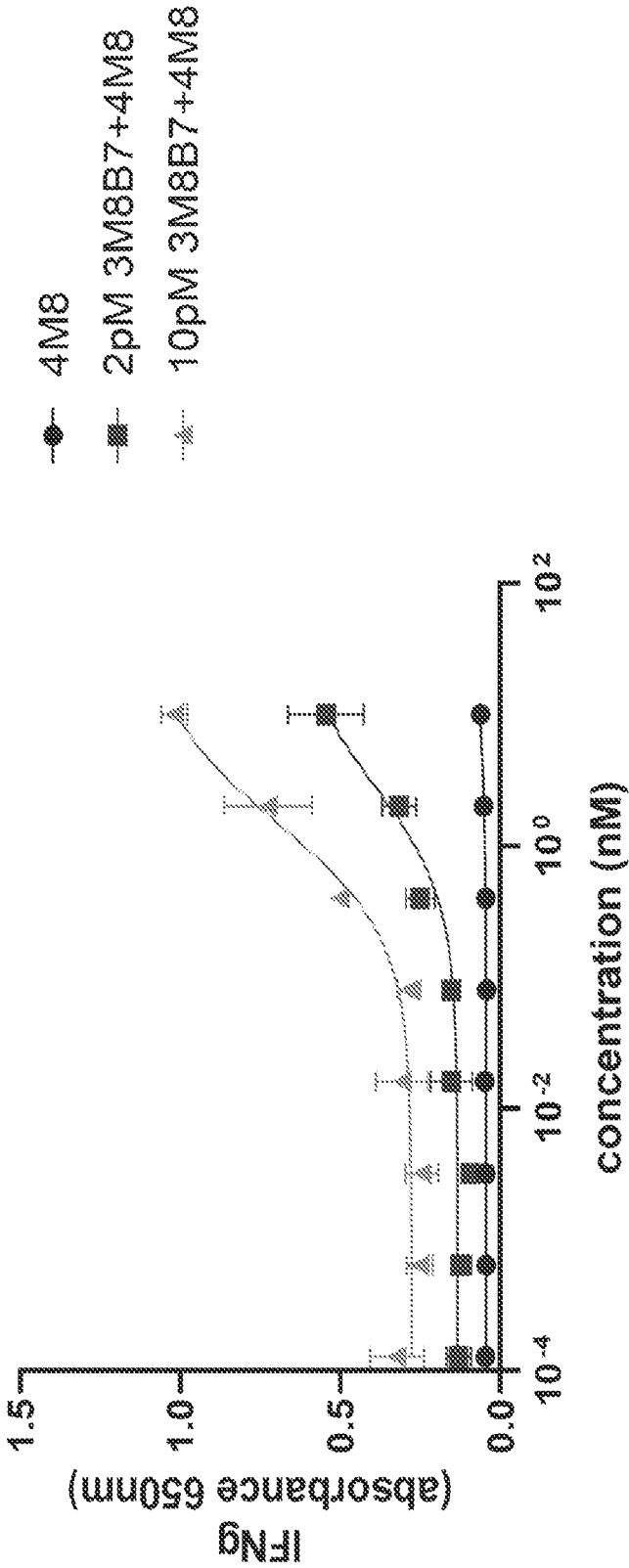


FIG. 37

Cloning Muc17xCD137 and DLL3xCD137 molecules

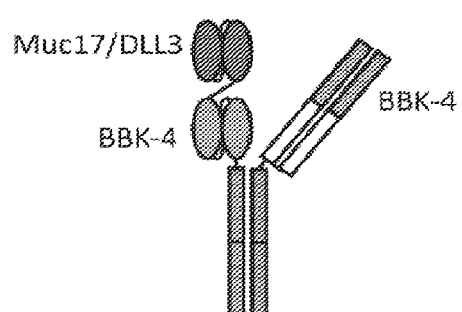


FIG. 38A

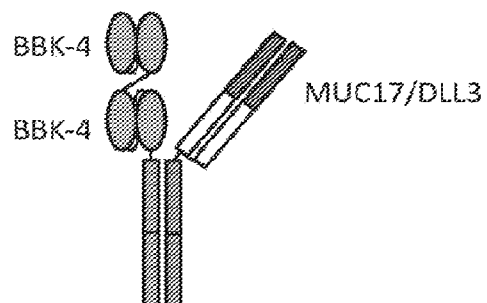


FIG. 38B

Cloning Muc17xCD137 and DLL3xCD137 molecules

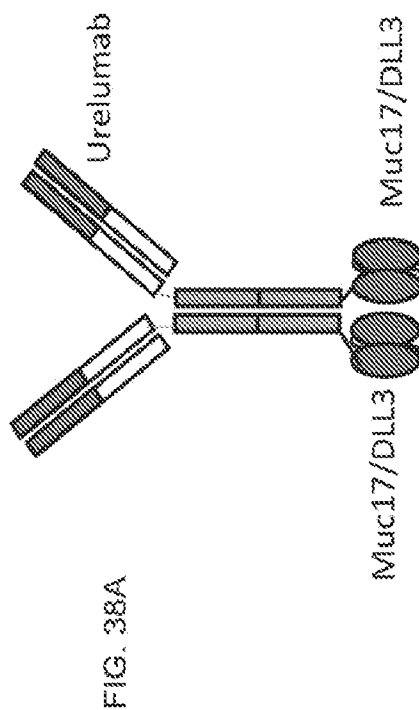


FIG. 39A

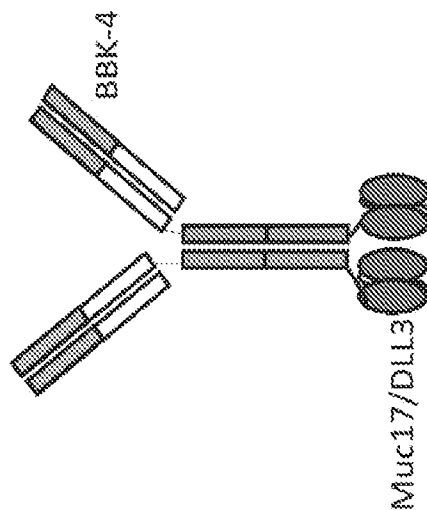


FIG. 39B

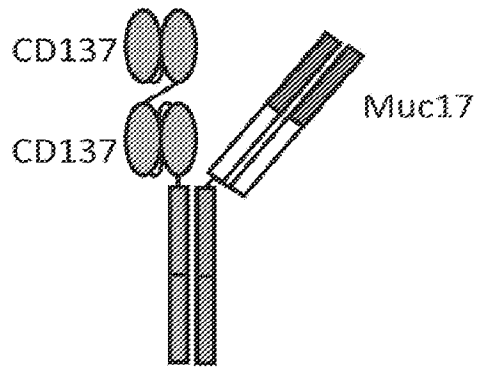


FIG. 39C

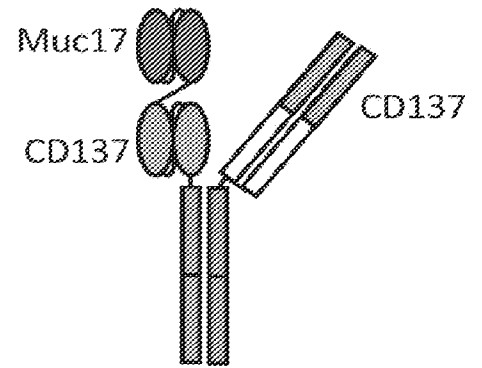


FIG. 39D

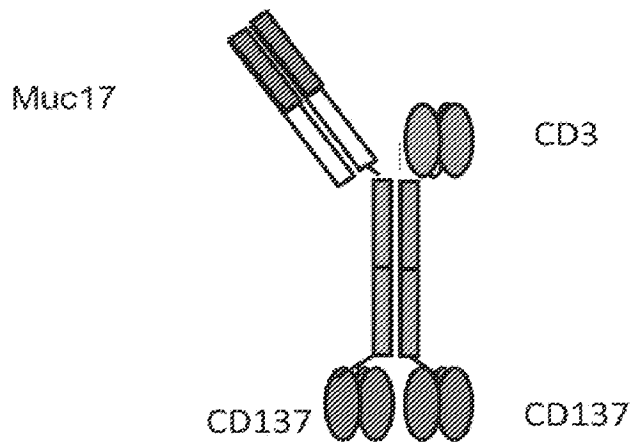


FIG. 39E

Scfv-Fc x Fab-Fc molecules

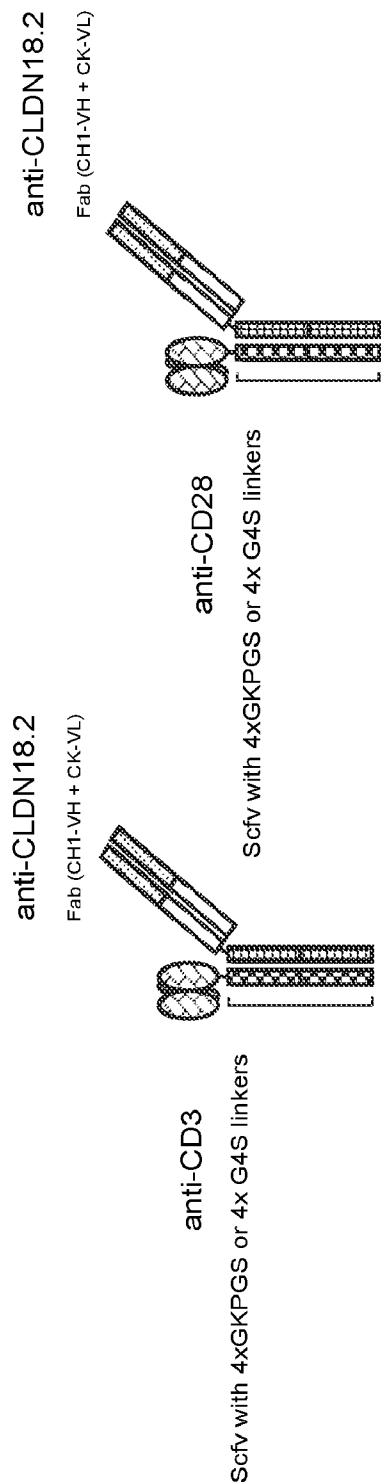


FIG. 40A

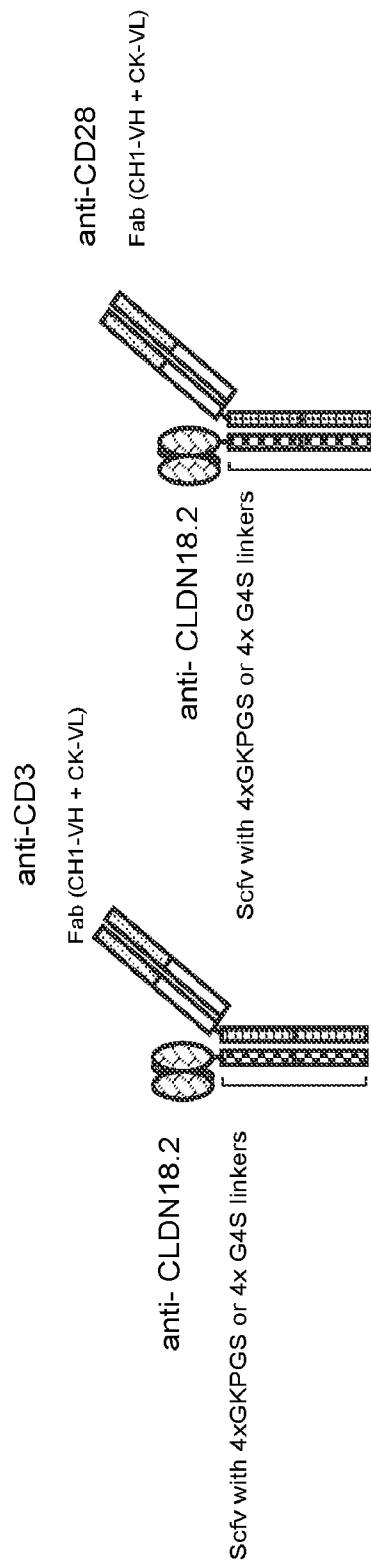


FIG. 40B

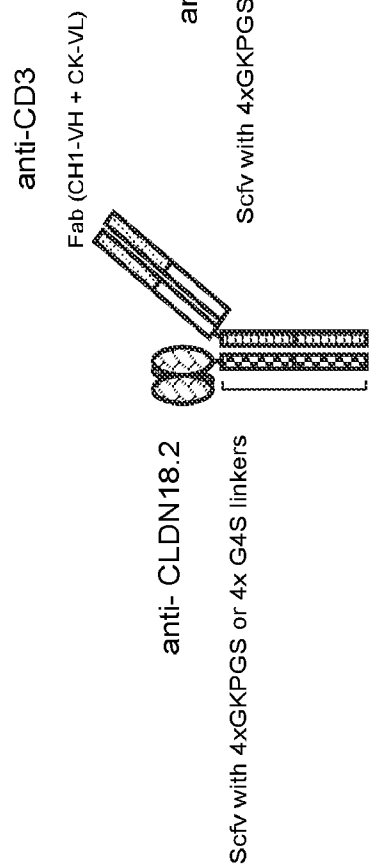


FIG. 40C

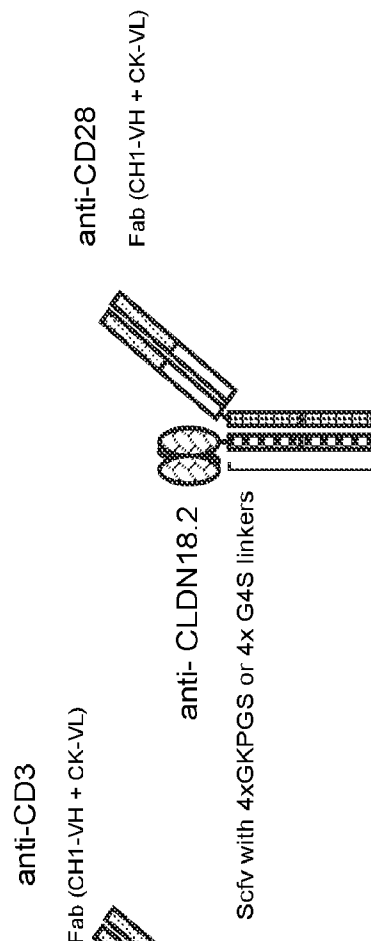


FIG. 40D

Scfv-Fc x Fab-Fc molecules

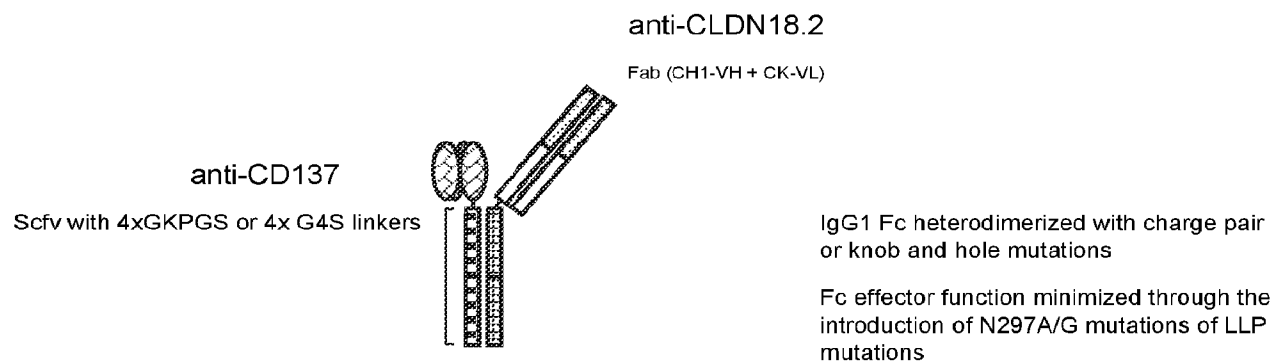


FIG. 40E

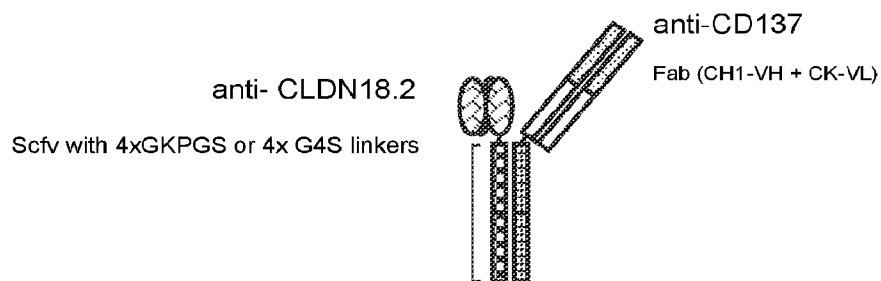


FIG. 40F

Scfv-scFv-Fc x Fc molecules

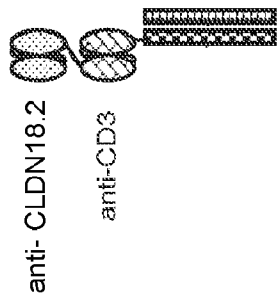


FIG. 41A

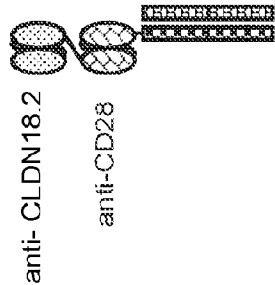


FIG. 41B



FIG. 41C

Scfv-scFv-Fc x Fab-Fc bispecific molecules

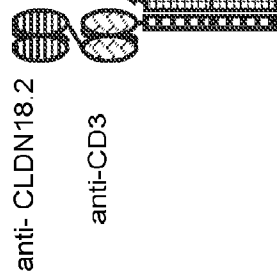


FIG. 41D

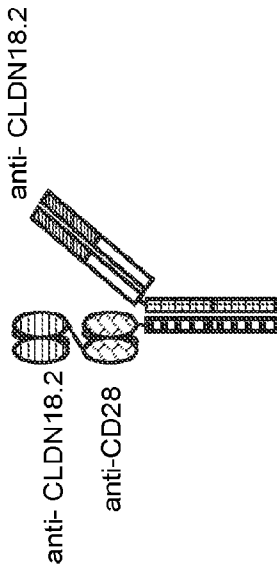


FIG. 41E

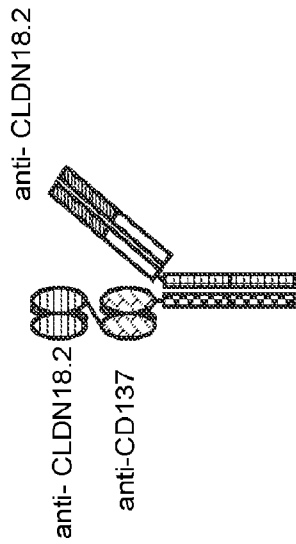


FIG. 41F

Binding of CLDN18.2xCD3 bispecific molecules to CHO cells expressing huCLND18.2

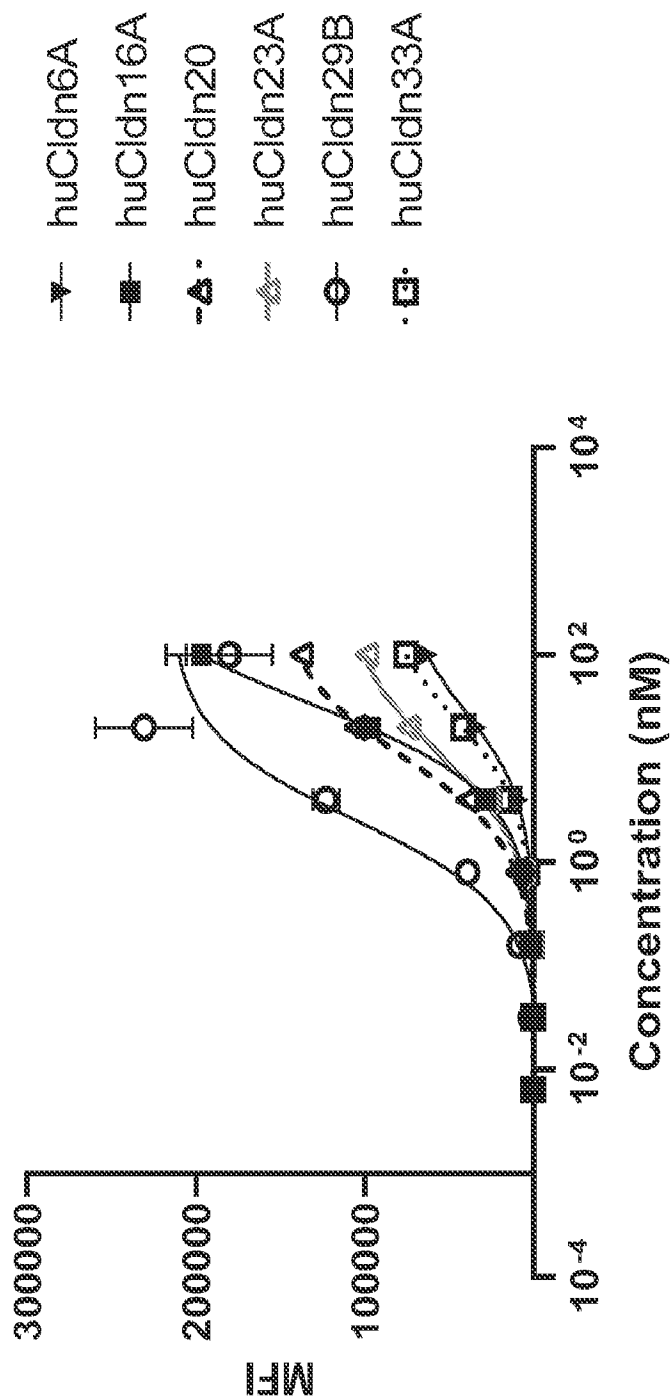


FIG. 42

T cell activation and upregulation of CD25 by
CLDN18.2x CD3 bispecifics in the presence of
CLDN18.2 expressing CHO cells

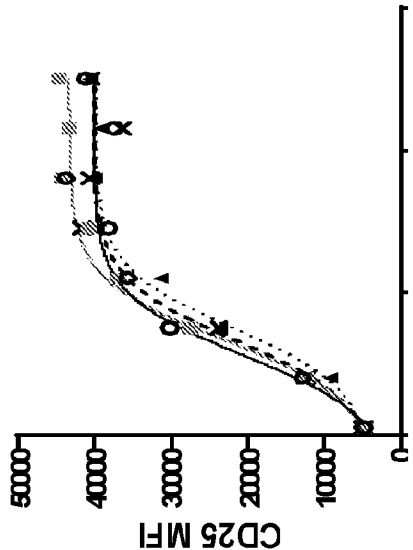


FIG. 43A

Killing of CHO cells expressing huCLDN18.2 by
huPBMCs stimulated by CLDN18.2x CD3 bispecifics

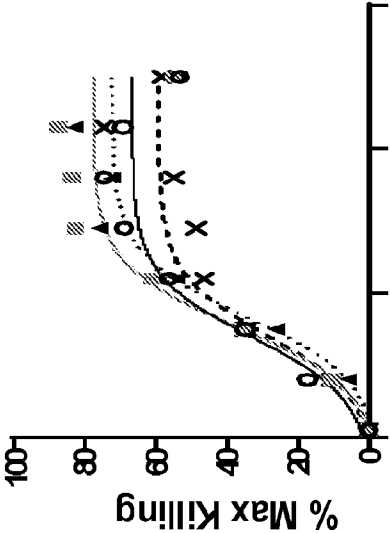


FIG. 43B

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecifics with CD3 variant molecules in the presence of CLDN18.2 expressing CHO cells

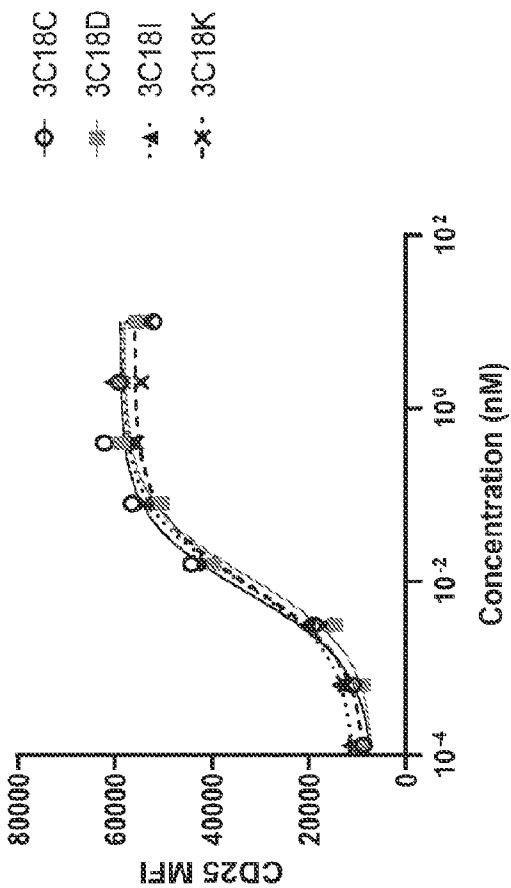


FIG. 44A

Killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecifics with CD3 variant molecules

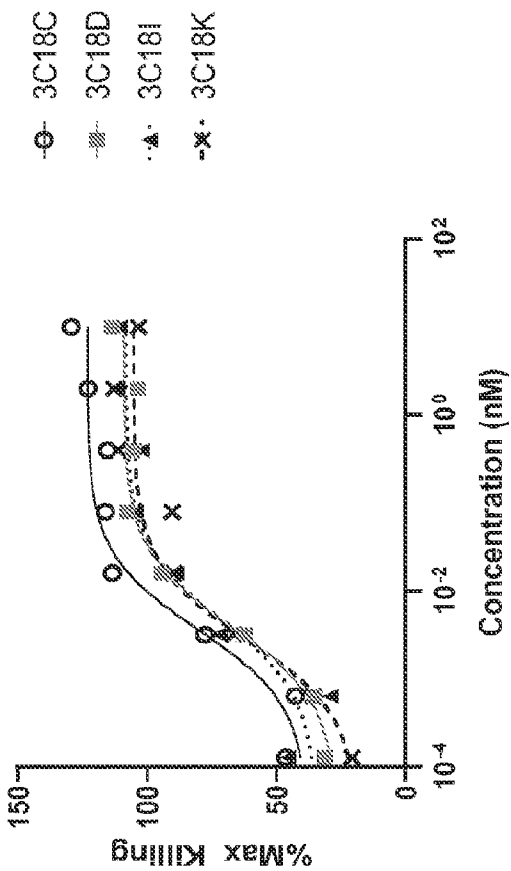


FIG. 44B

T cell activation and upregulation of CD25 by CLDN18.2x CD3 bispecifics with CD3 variant molecules in the presence of CLDN18.2 expressing CHO cells

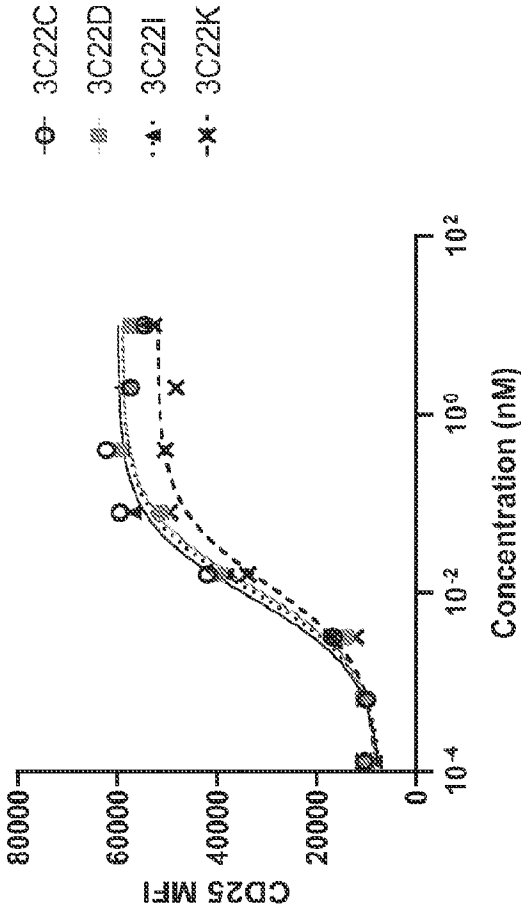


FIG. 45A

Killing of SNU-601 tumor cells by huPBMCs stimulated by CLDN18.2x CD3 bispecifics with CD3 variant molecules

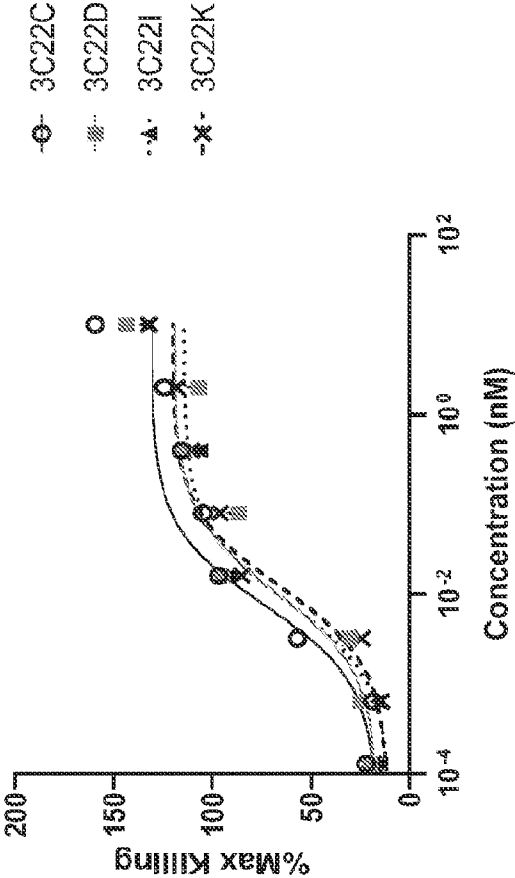


FIG. 45B

Killing of SNU-601 tumor cells by
huPBMCs stimulated by CLDN18.2x CD3
bispecifics with CD3 variant molecules

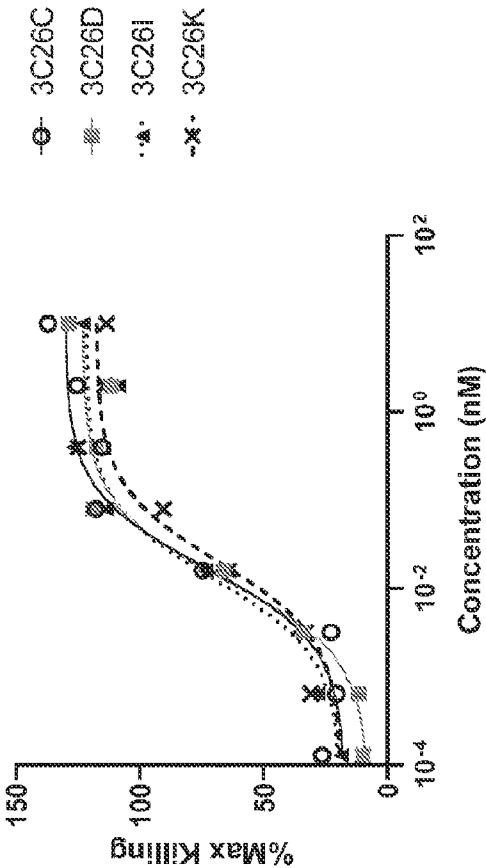


FIG. 46B

T cell activation and upregulation of CD25 by
CLDN18.2x CD3 bispecifics with CD3 variant
molecules in the presence of CLDN18.2 expressing
CHO cells

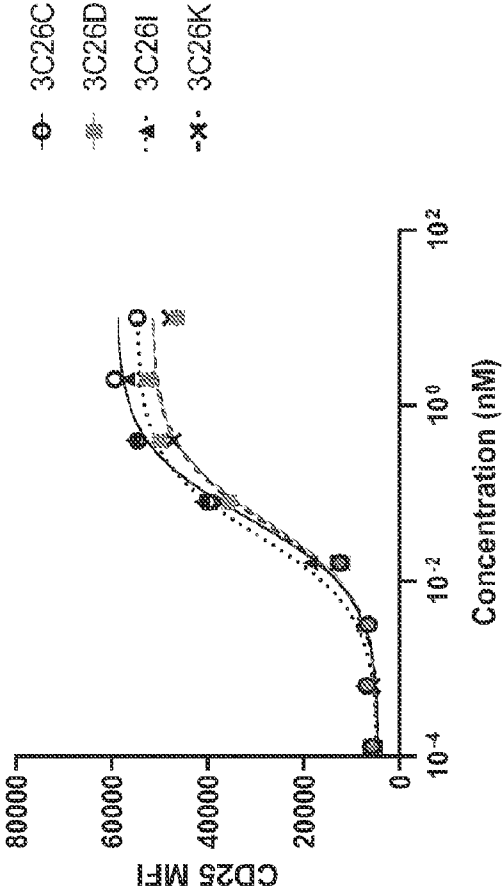


FIG. 46A

CD3xCldn18.2 binding to Cldn18.2-CHO cells

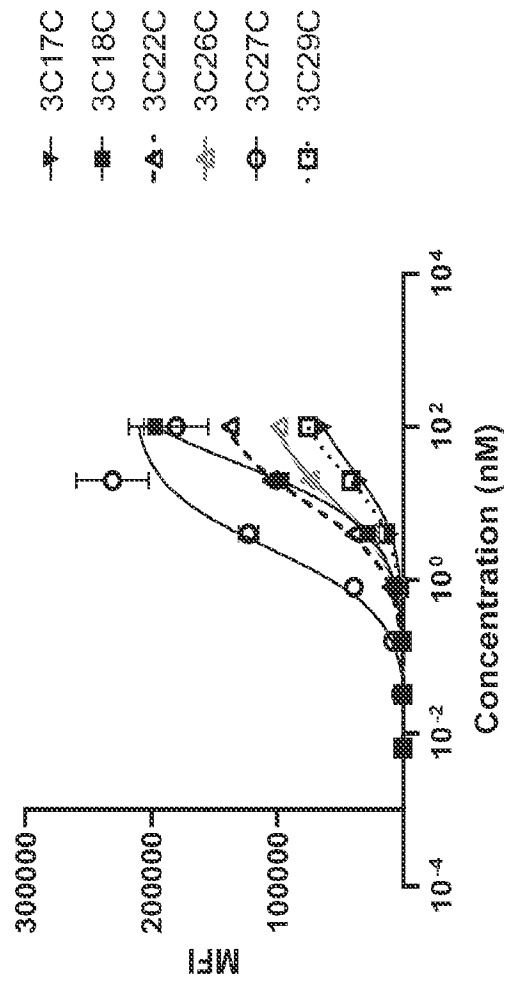


FIG. 47

All 4 CD28xCln18.2 bites in combination with 10pM 3C18C
potently activates PBMCs in the presence of SNU-601 cells

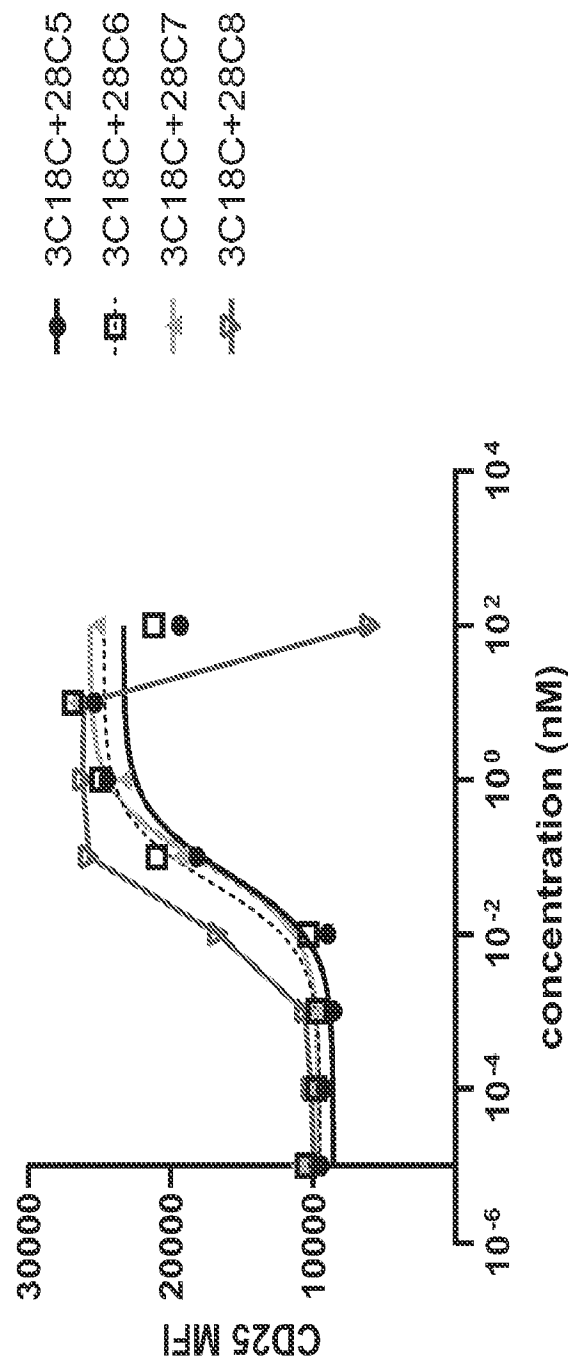


FIG. 48A

All four CD28xCldn18.2 bites in combination with 10pM 3C18C potentially activates PBMCs in the presence of SNU-601 cells

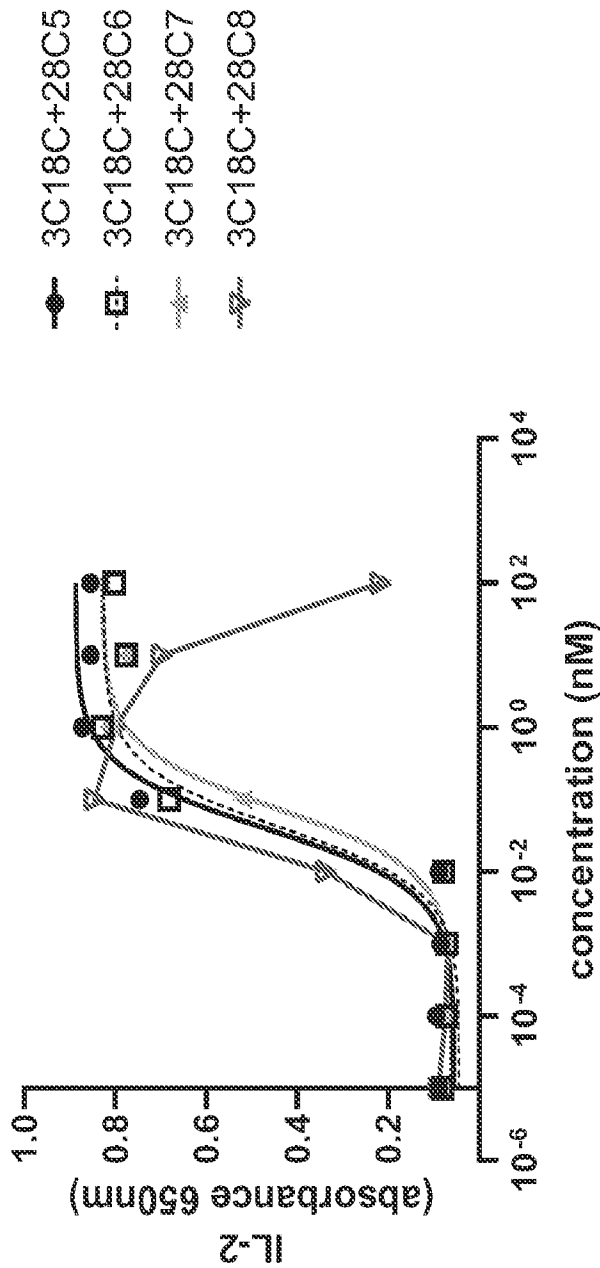


FIG. 48B

All four CD28xCldn18.2 bites in combination with 10pM 3C22C potentially activates PBMCs in the presence of SNU-601 cells

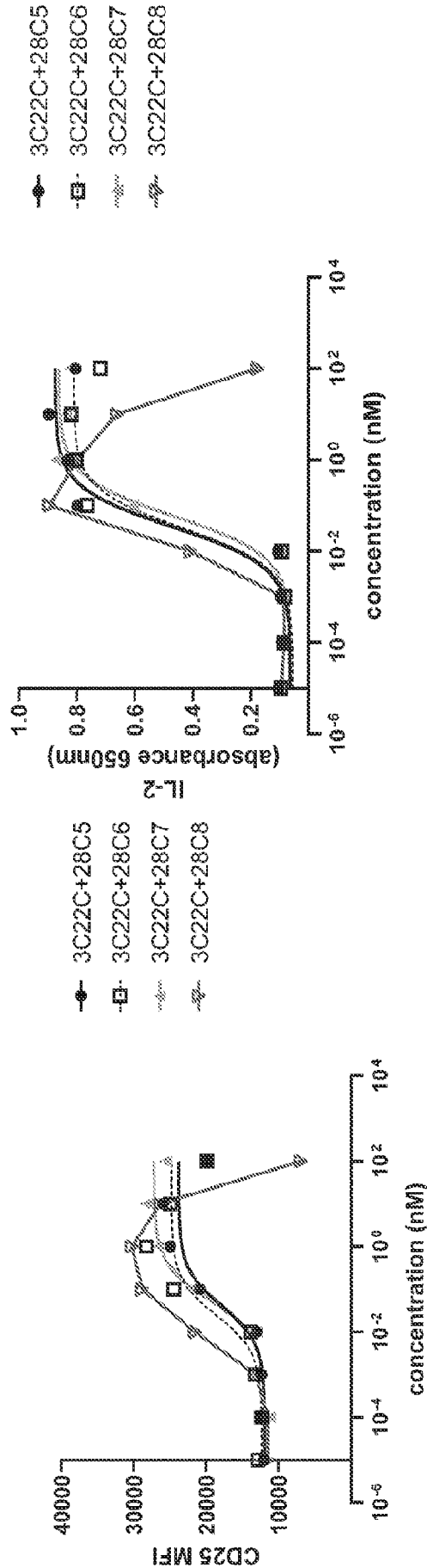


FIG. 49B

FIG. 49A

All four CD28xCldn18.2 bites in combination with 20pM 3C22C potently activates PBMCs in the presence of SNU-601 cells

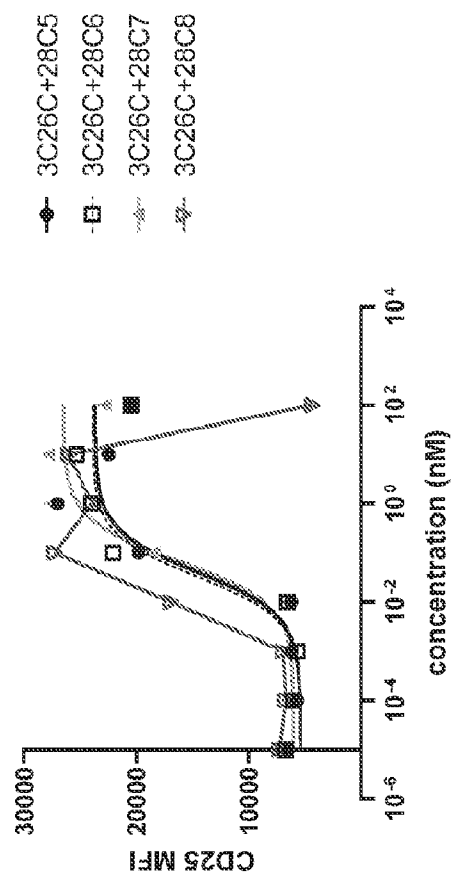


FIG. 50A

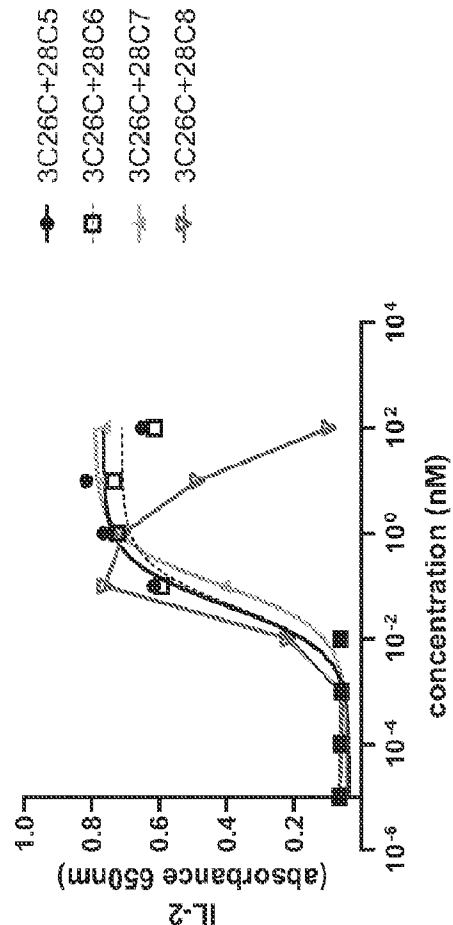


FIG. 50B

All four CD28xCldn18.2 bites in combination with 2pM 3C27C
potently activates PBMCs in the presence of SNU-601 cells

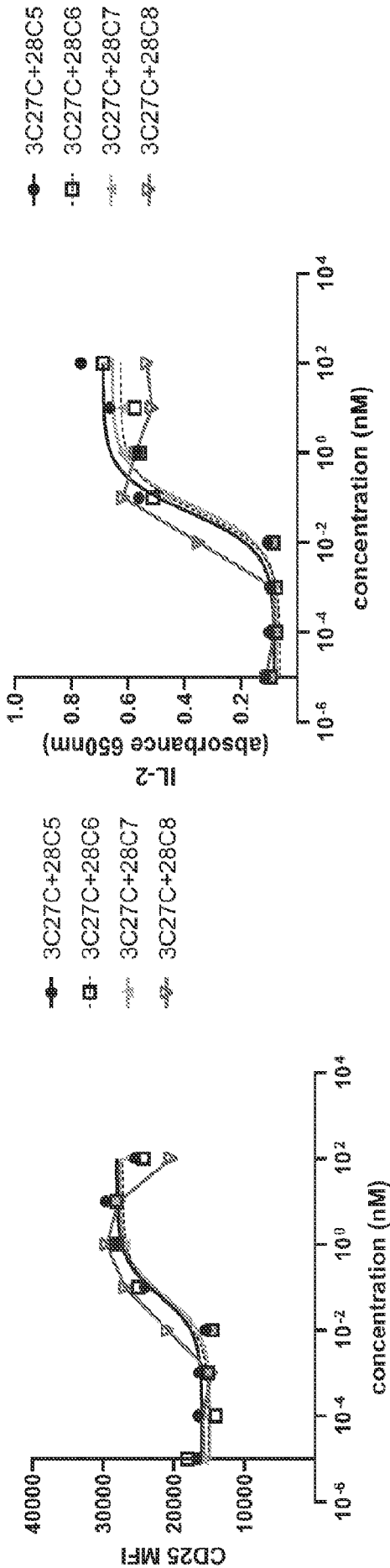
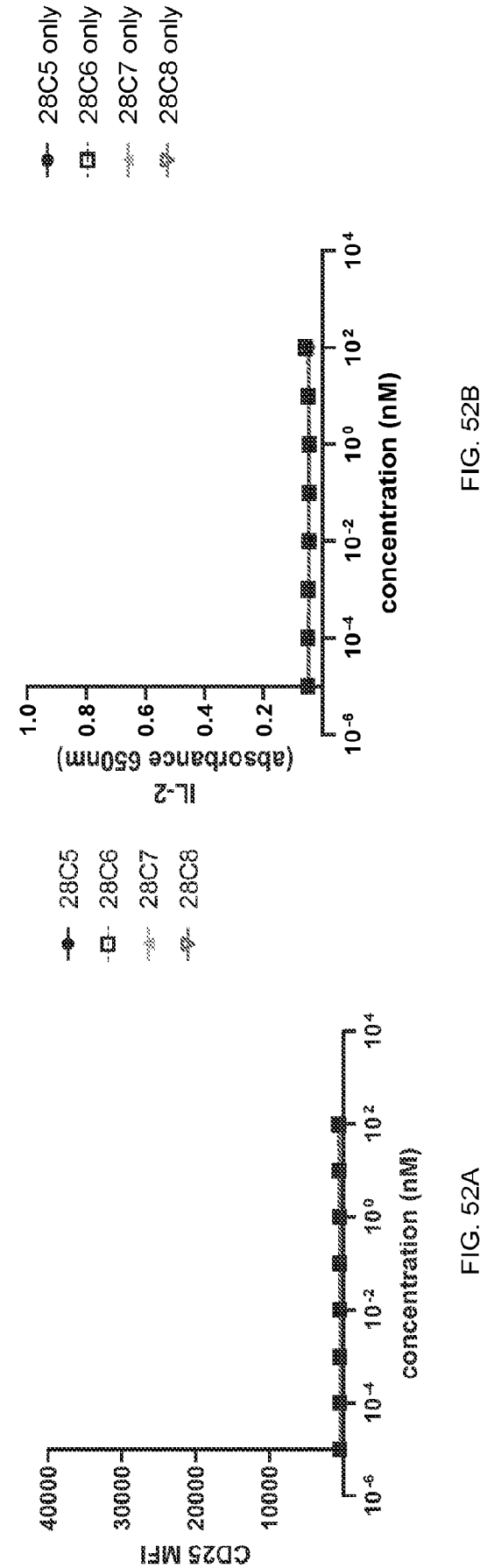


FIG. 51A

FIG. 51B

The four CD28xCldn18.2 bites alone do not activate PBMCs



The four CD3xCldn18.2 bites alone activate PBMCs to express CD25

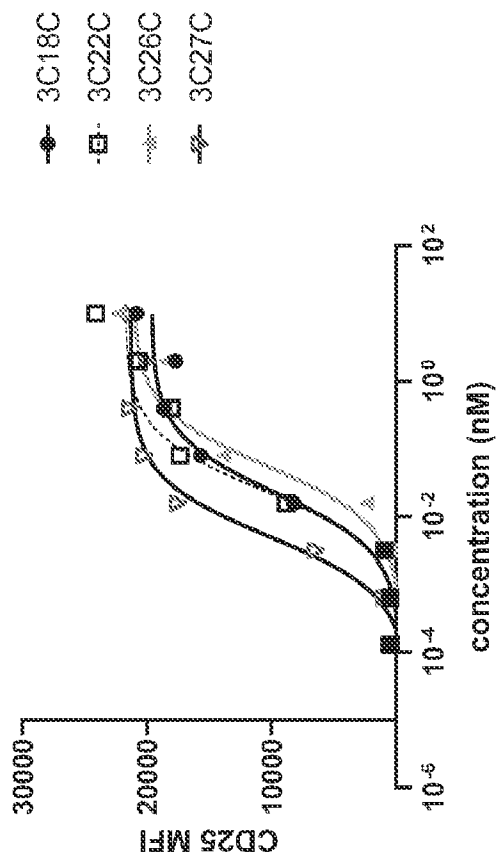


FIG. 53A

The four CD3xCldn18.2 bites alone activate PBMCs to secrete only low levels of IL-2

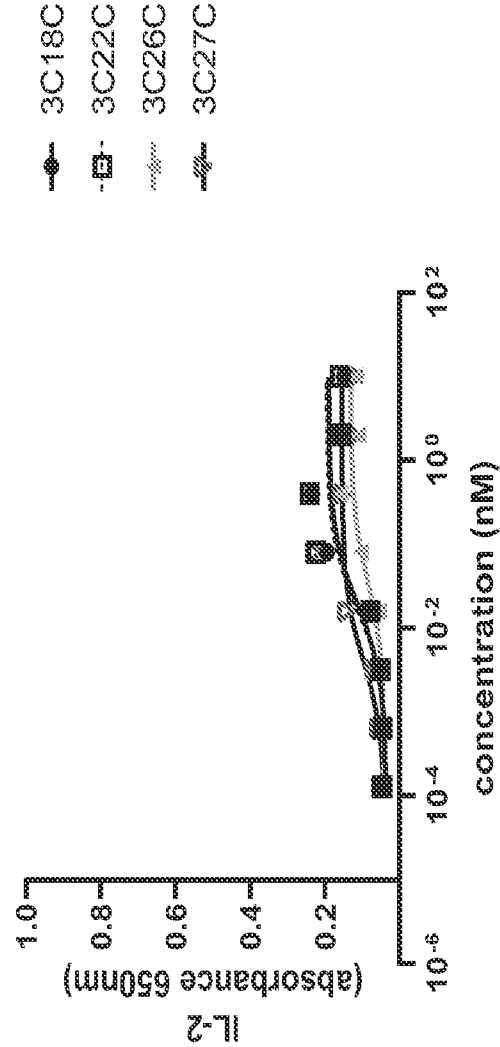


FIG. 53B

CD3xCldn18.2 bispecific 3C22C stimulates PBMC mediated killing of GSU cells more potently than three lots of the benchmark, 3CBM

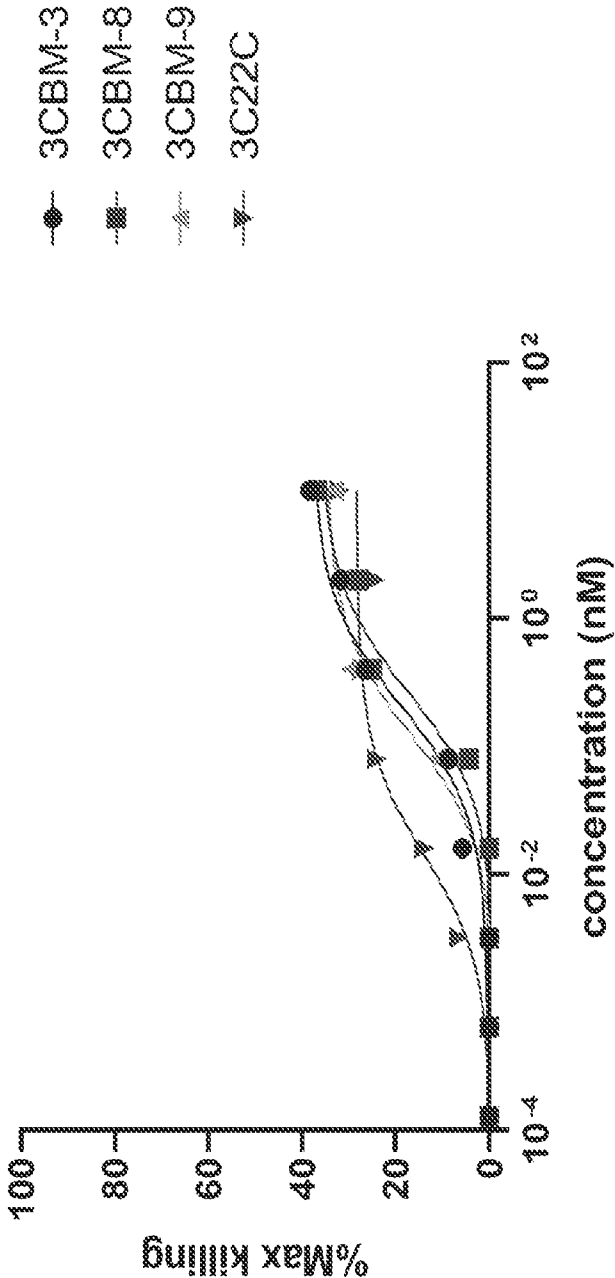


FIG. 54

CD3xCldn18.2 bispecific 3C22C stimulates PBMC to express CD25 in the presence of GSV cells more potently than three lots of the benchmark, 3CBM

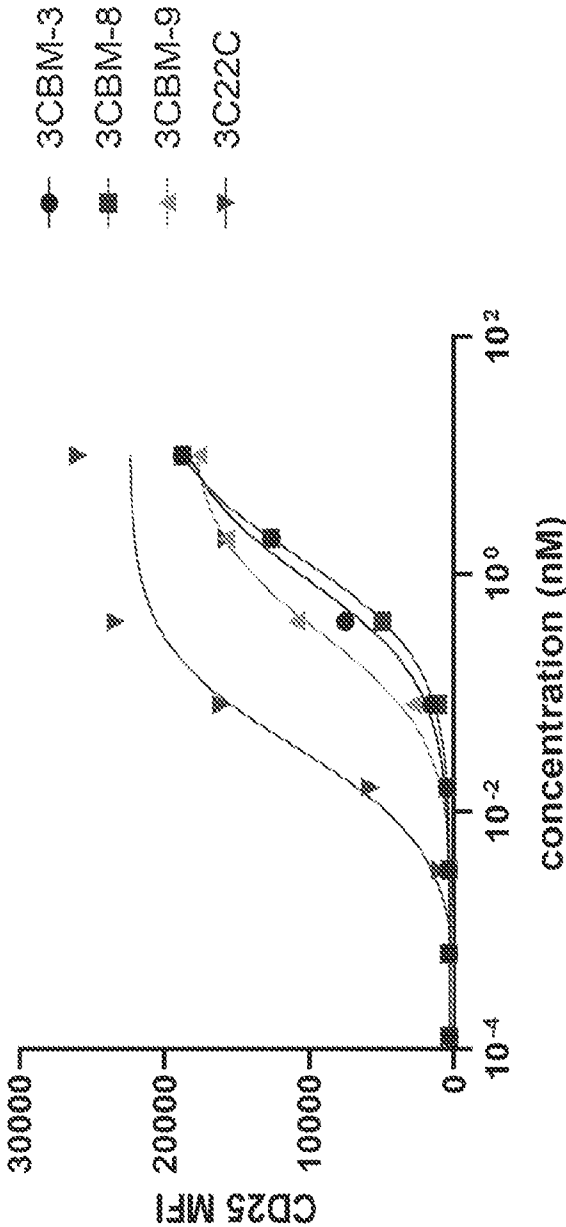


FIG. 55

3C27I is more potent at killing SNU-601 cells than
3C18I, 3C22I, or 3C26I

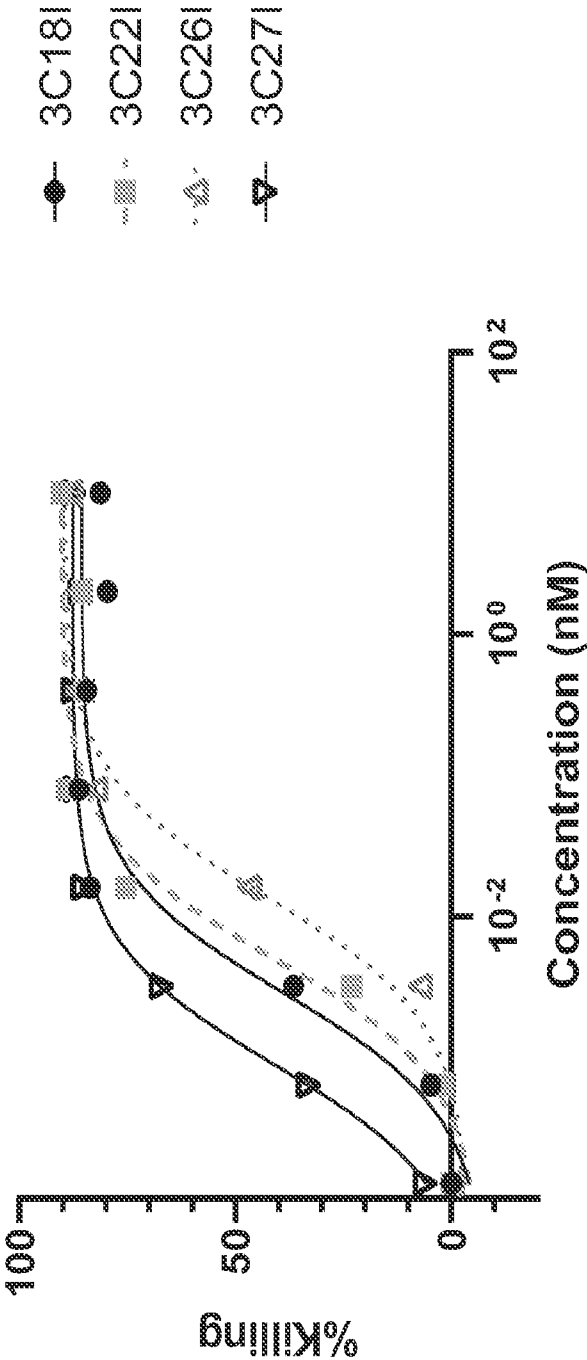


FIG. 56

CD28scFvxCldn18.2Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 bispecific, 3C18C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells

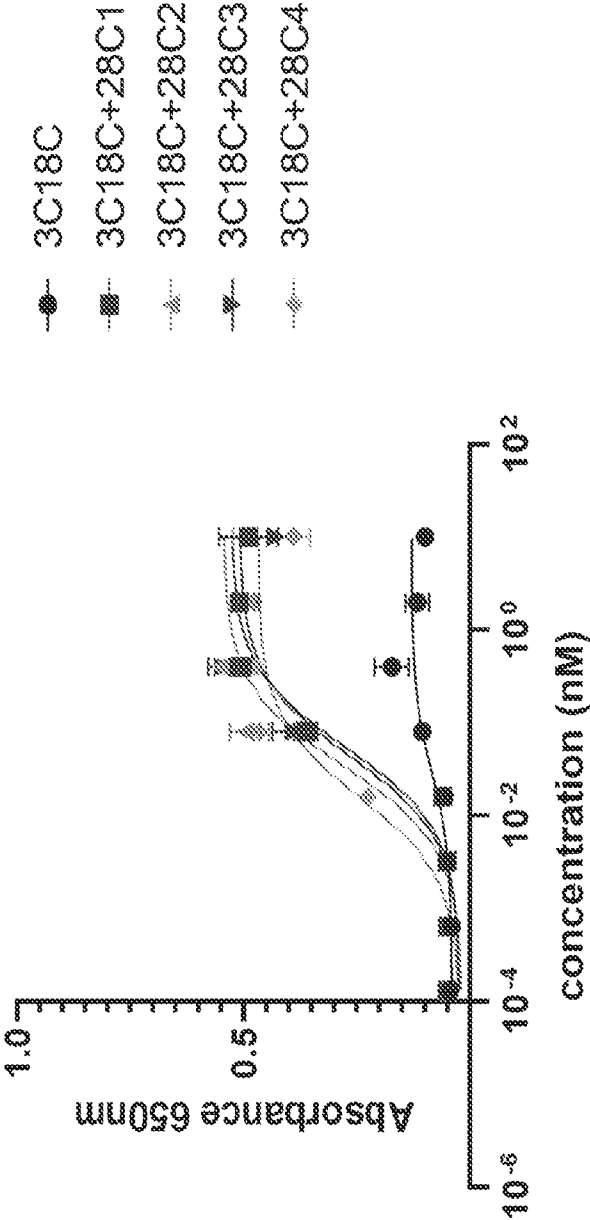


FIG. 57

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 bispecific, 3C22C, activate PBMCs to produce IL-2 when co-cultured with SNU-601 cells

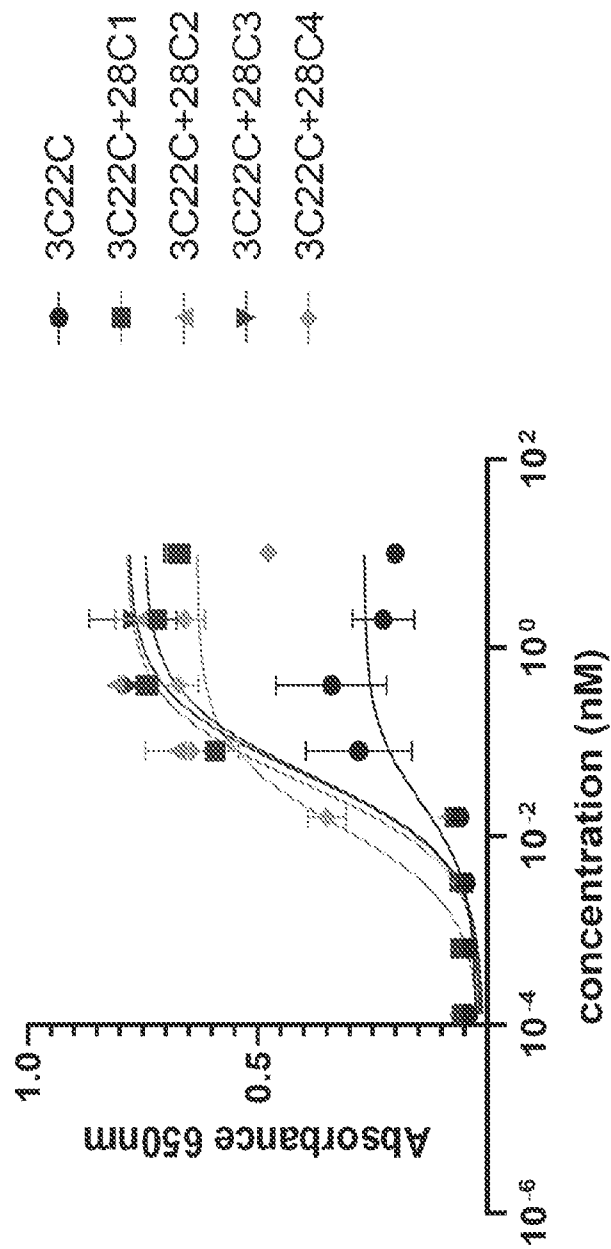


FIG. 58

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 in combination with 10pM CD3xCldn18.2 Bispecific, 3C26C, activate PBMCs to produce IL-2 when co-cultured with SNU-601

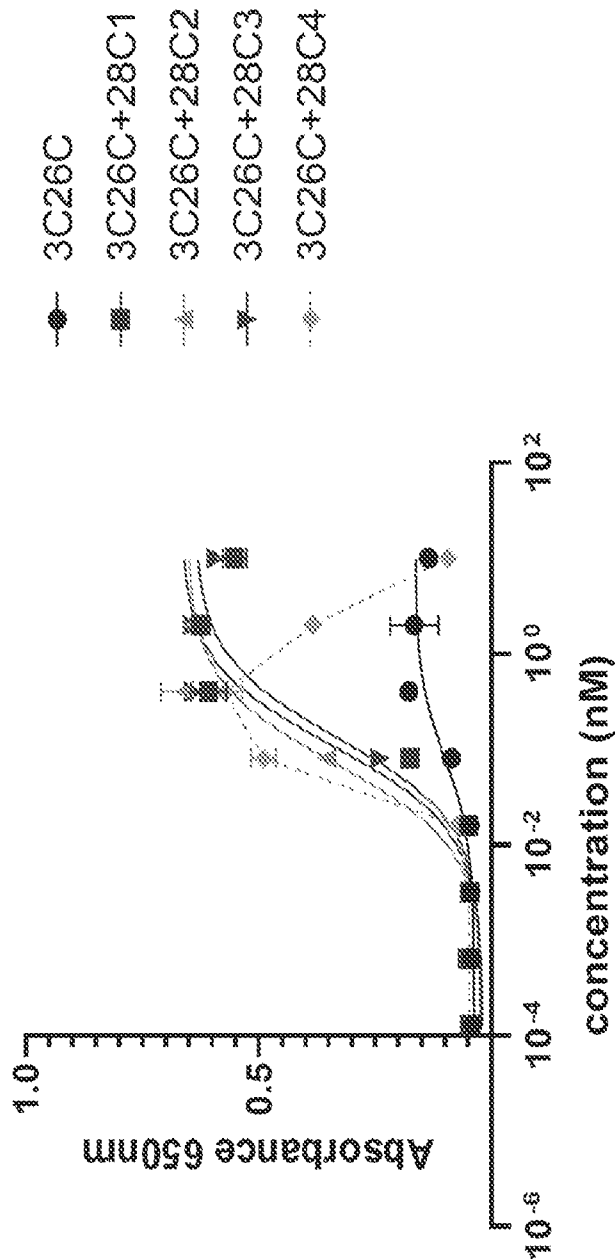


FIG. 59

CD28-scFvxCldn18.2-Fab T cell engagers, 28C1, 28C2, 28C3, and 28C4 alone do not activate PBMCs to express CD25 when co-cultured with SNU-601 cells

Transform X of 02072020 28C1-4 alone CD25MFI

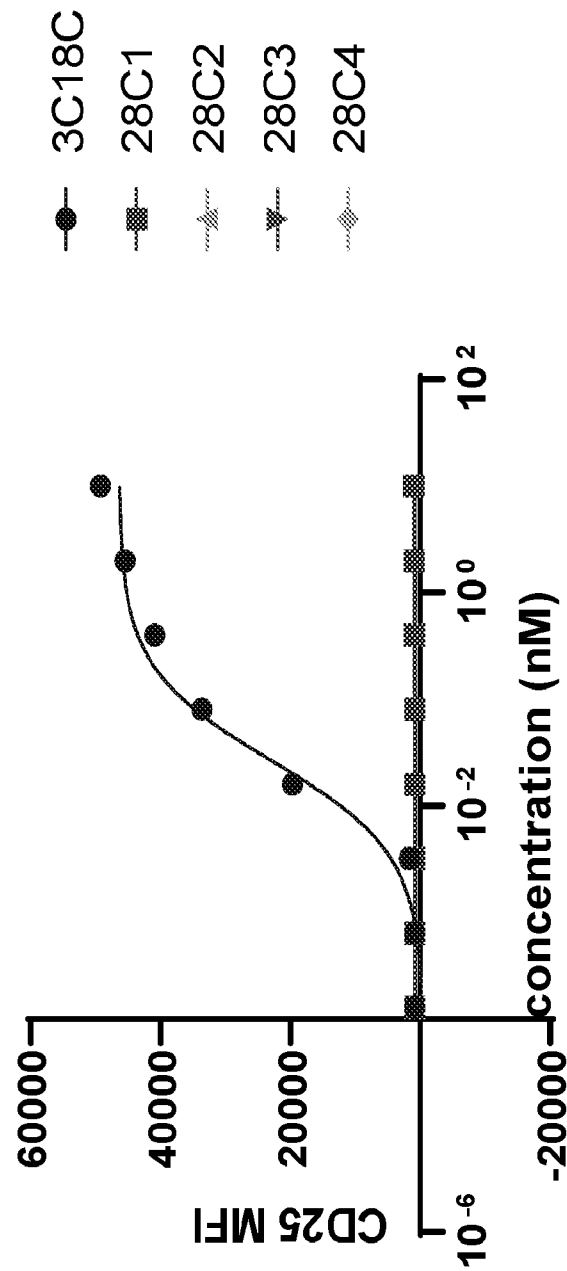


FIG. 60

Cldn18.2xCD28 bispecific molecules 28C7 and 28C10 in combination with 5pM of the CD3 bispecific 3C22I activates T-cells to secrete IL-2

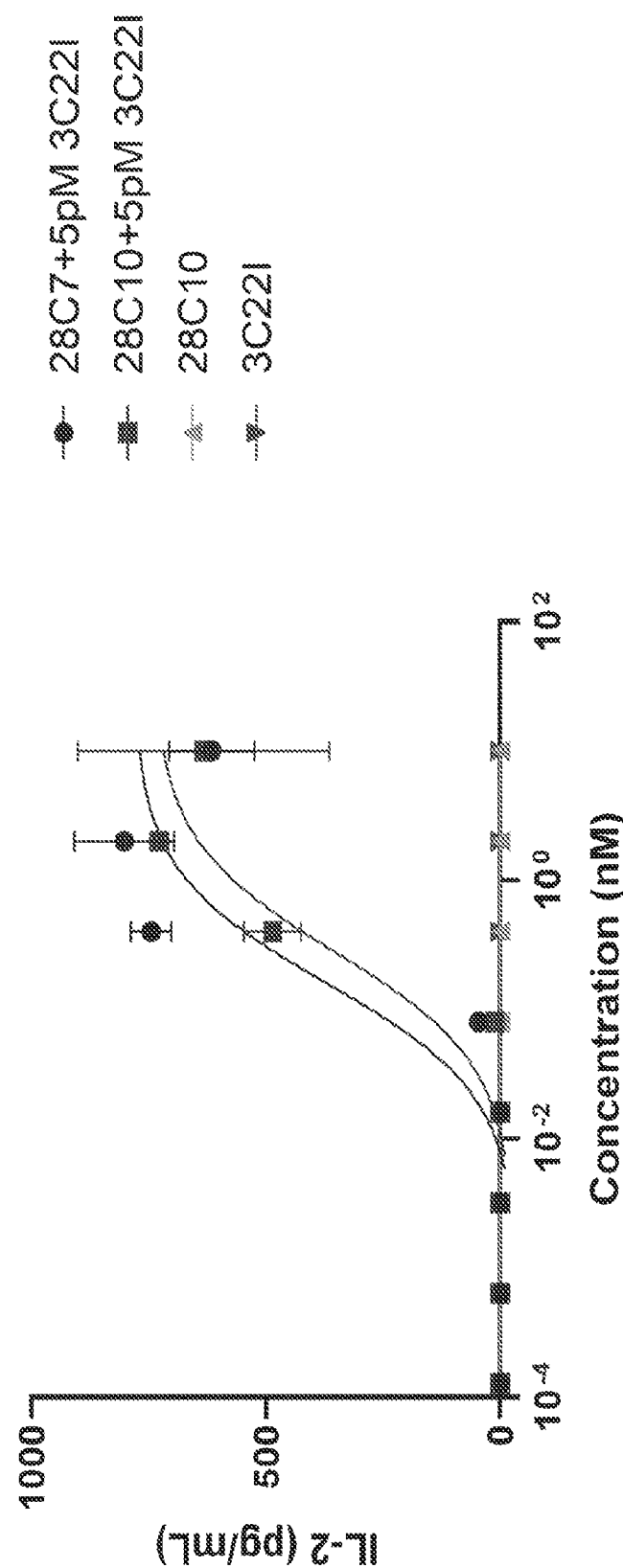


FIG. 61

CLDN18.2 x CD28 bispecifics 28C5, 28C6, 28C7 and 28C8 induced IL-2 secretion by PBMCs when in the presence of CHO cells expressing CLDN18.2 but not with parental CHO cells

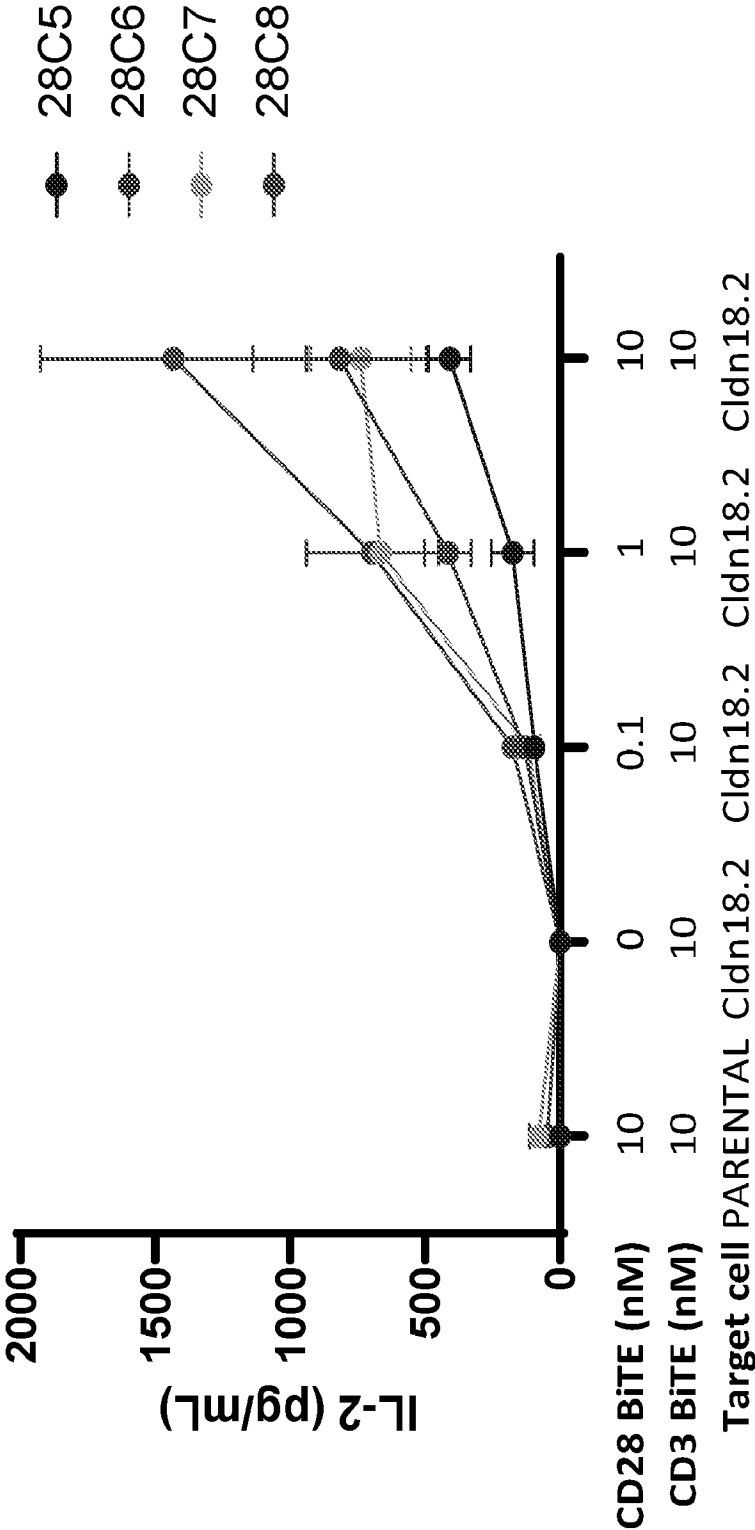


FIG. 62

CD137 x Cldn18.2 bispecific molecule 4C1 in combination with 10pM of the CD3 bispecific 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells

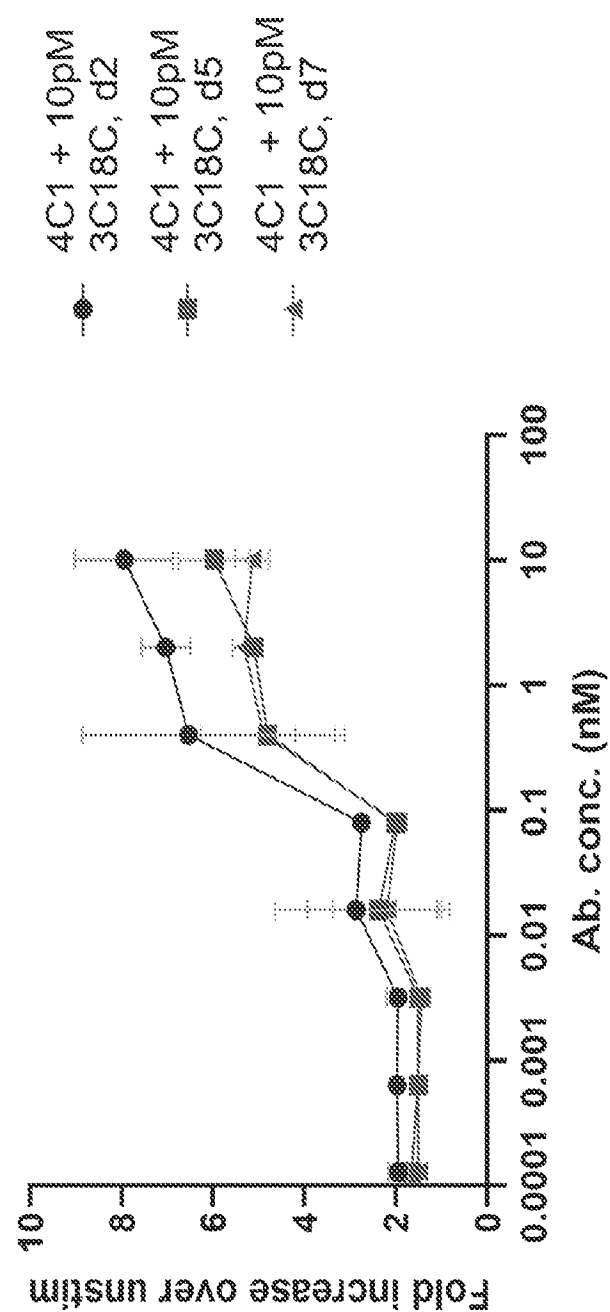


FIG. 63

CD137 x Cldn18.2 bispecific molecule 4C2 in combination with 10pM of the CD3 bispecific 3C18C increase IFNgamma secretion over 3C18 by PBMCs when in the presence of SNU-601 cells

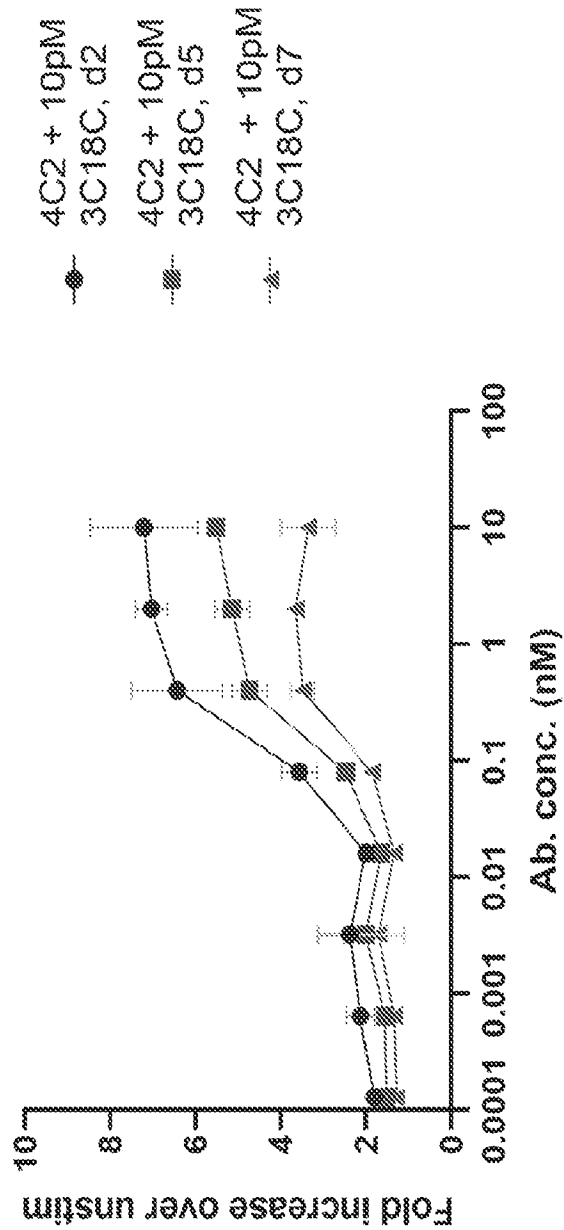


FIG. 64

CD137xCldn18.2 bispecific molecule 4C6 in combination with 3C22I
activate T-cells to secrete IFNg

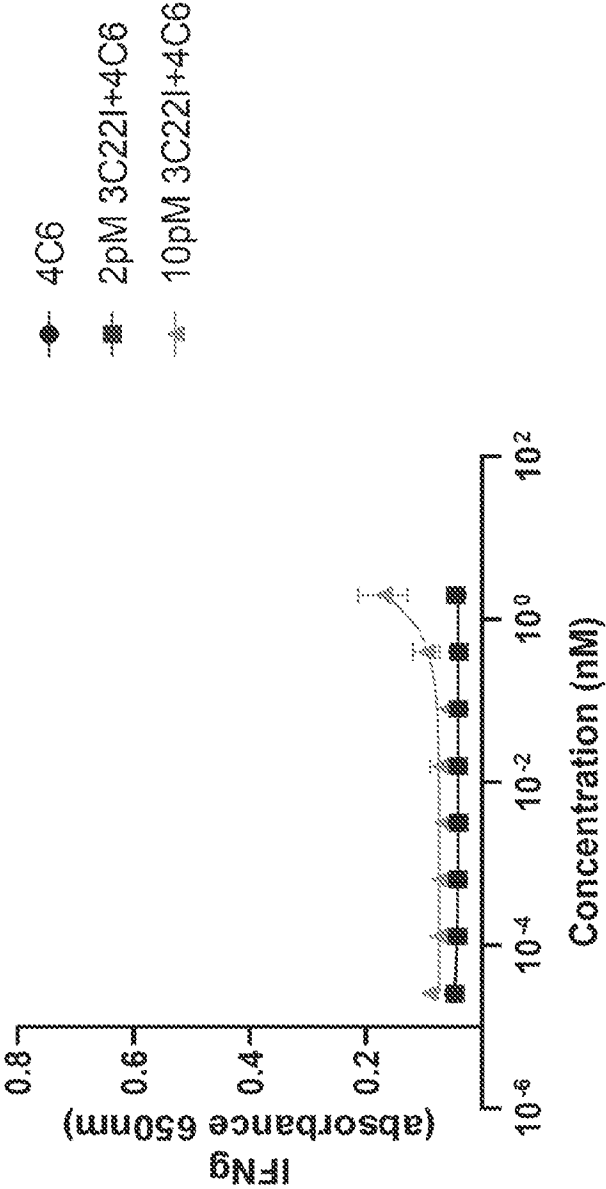


FIG. 65

CD137xCldn18.2 bispecific molecule4C6 in combination with 3C22I
activate T-cells to secrete IFNg

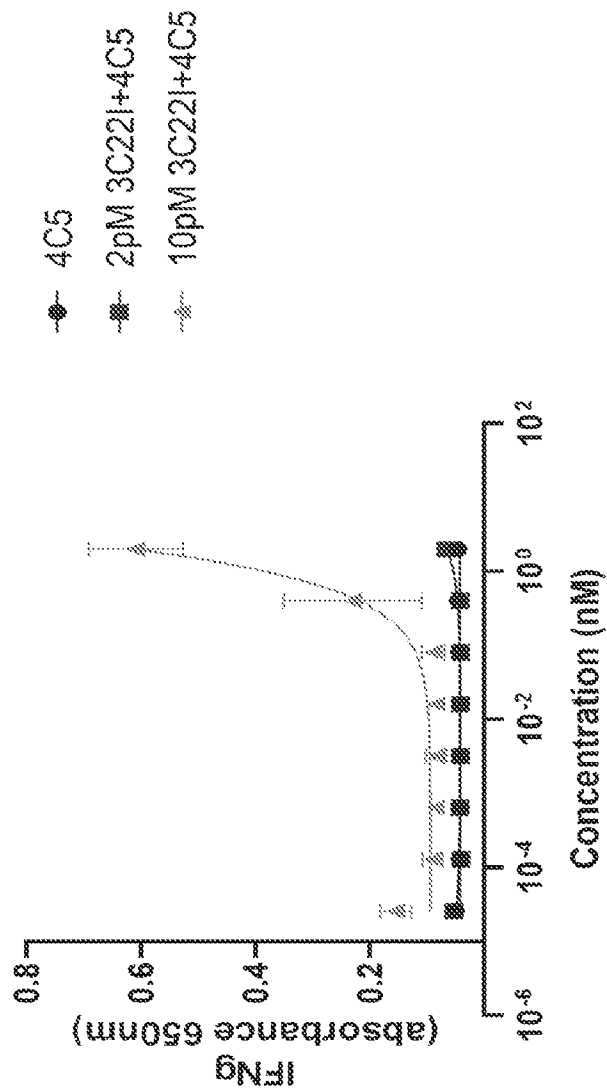


FIG. 66

CD137xCldn18.2 bispecifics 4C1 and 4C5 in combination with 80pM 3C27I increase the activation of CD8 cells in the presence of mitomycin treated CHO cells expressing CLND18.2

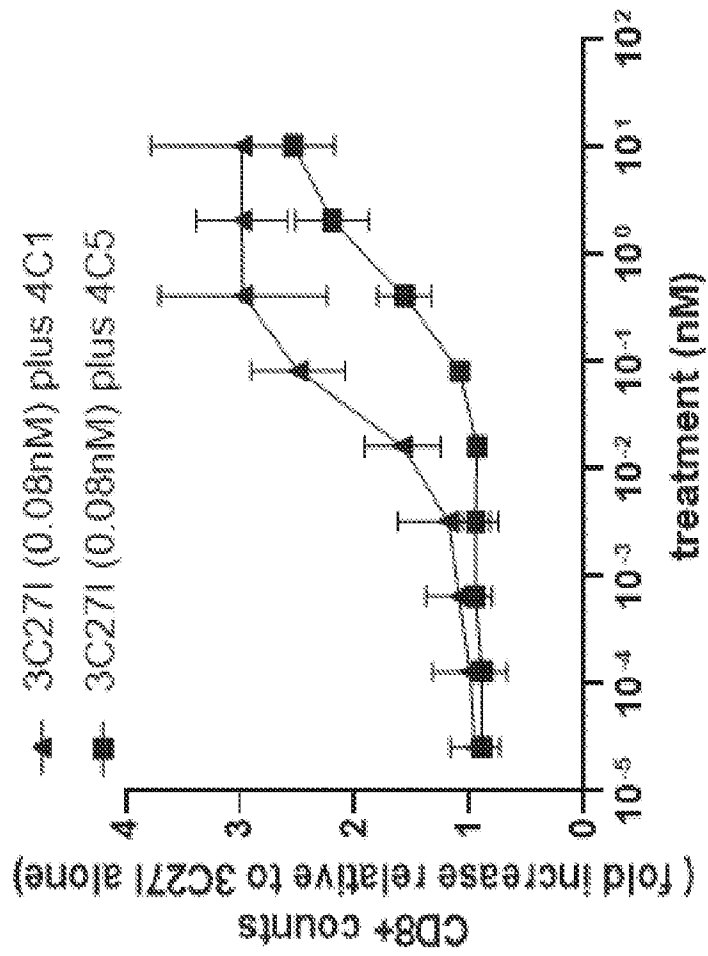


FIG. 67

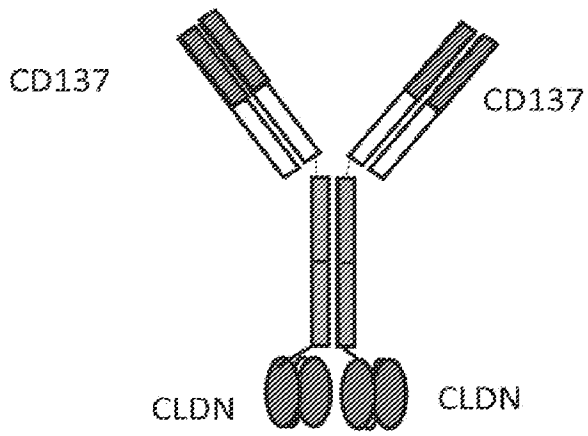


FIG. 68A

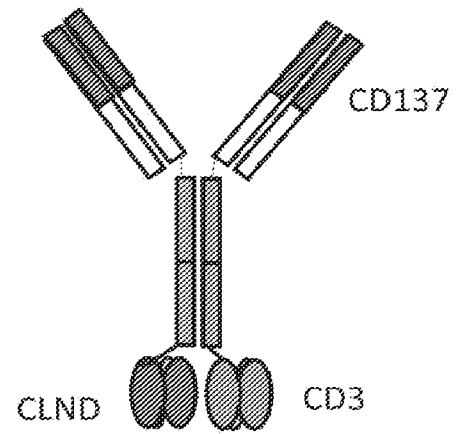


FIG. 68B

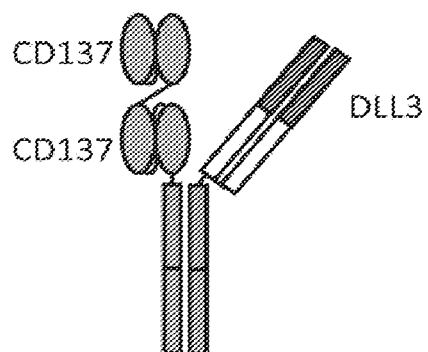


FIG. 69A

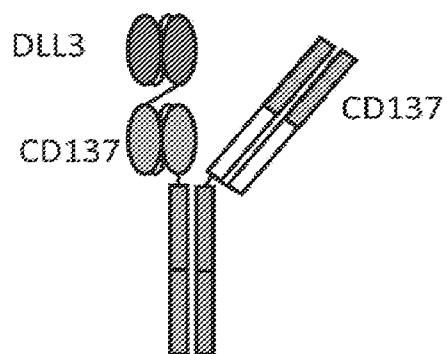


FIG. 69B

SEQUENCE LISTING

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<151> 2020-03-17

<150> 62/981,048

<151> 2020-02-25

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 26
Asp Trp Trp Glu Leu Val Phe Asp Tyr
1 5

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 27

Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr
1 5 10

<210> 28

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 28

Gly Val Trp Asn Tyr Glu Arg Ser Phe Asp Tyr
1 5 10

<210> 29

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 29

Ser Ile Ala Val Thr Gly Phe Tyr Phe Asp Tyr
1 5 10

<210> 30

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 30

Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 31

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 31

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala
1 5 10

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 32

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
1 5 10

<210> 33

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 33

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Ala Lys Thr Phe Leu Tyr
1 5 10 15

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 34

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu Tyr
1 5 10 15

<210> 35

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 35

Arg	Ala	Ser	Glu	Ser	Val	His	Ser	Tyr	Gly	Asn	Ser	Leu	Ile	His
1				5					10				15	

<210> 36

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 36

Arg	Ser	Ser	Lys	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr
1				5					10					15	

<210> 37

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 37

Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asp	Ala	Lys	Thr	Phe	Leu	Asp
1				5					10					15	

<210> 38

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 38

Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asp	Gly	Lys	Thr	Phe	Leu	Asp
1				5					10					15	

<210> 39

<211> 7

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 39
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 40
Ala Ala Ser Asn Arg Tyr Thr
1 5

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 41
Asp Thr Ser Lys Leu Ala Ser
1 5

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 42
Glu Val Ser Asn Arg Ala Ser
1 5

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 43
Glu Val Ser Asn Arg Phe Ser
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Gln Met Ser Asn Leu Ala Ser
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 45
Arg Ala Ser Asn Leu Glu Ser
1 5

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 47
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 48
Ala Gln Asn Leu Glu Leu Pro
1 5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 49
Leu Gln Gly Glu Arg Leu Pro Phe Thr
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 50

Leu Gln Gly Ile His Leu Pro Phe Thr
1 5

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 51

Leu Gln Gly Arg Glu Leu Pro Phe Thr
1 5

<210> 52

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 52

Gln Gln Thr Asn Glu Asp Pro
1 5

<210> 53

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 53

Gln Gln Trp Ser Ser Asn Pro Leu Thr
1 5

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 54

Gln Gln Tyr Asn Asn Tyr Pro Leu Thr
1 5

<210> 55

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 55

Gln Gln Tyr Asn Ser Tyr Pro Phe Thr
1 5

<210> 56

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Gly Ser Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 57

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Gly Ser Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 58

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 59

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 60

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 61

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 61

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 62
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 62
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 63
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 63

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 64

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 64

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Asp Asn Gly Ile Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Val Trp Asn Tyr Glu Arg Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 65

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Tyr Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 66

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 66

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ser Ile Ala Val Thr Gly Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 67

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 67

Gln Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Tyr Val Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Ile Ile Ser Pro Asn Asp Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Val Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Asp Leu Gly Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 68

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 68

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 69

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 70

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 70

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 71
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Tyr Thr Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Asn Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 72
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 72

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 73

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 73

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 74

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 74

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

Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
20 25 30

Ala Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu
35 40 45

Trp Met Gly Tyr Ile Ser Asp Val Gly His Asn Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Phe Leu Lys Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Asp Gln Val Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala
115

<210> 75

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75

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

Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
20 25 30

Ala Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu
35 40 45

Trp Met Gly Tyr Ile Ser Asp Val Gly Ser Asn Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Phe Lys Asn Gln Phe
65 70 75 80

Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Thr Arg Asp Gln Val Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser
115

<210> 76

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 76

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 77

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77

Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Thr Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 78

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 78

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 79
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 80
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 80
Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro Val Thr Val Gly
1 5 10 15

Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn
85 90 95

Leu Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 81

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 81

Asp Ile Val Met Thr Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 82

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 82

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

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 83

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83

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

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 84

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 84

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

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

Asp Ala Lys Thr Phe Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 85

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 85

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

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

Asp Gly Lys Thr Phe Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 86

<211> 112

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 86

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 87

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 87

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 88

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 88

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 89

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 89

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val His Ser Tyr
20 25 30

Gly Asn Ser Leu Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 90

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 90

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Asn Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 91

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 91

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 92
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 92
Gly Phe Thr Phe Ser Ser Phe Gly Met His
1 5 10

<210> 93
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 93
Gly Tyr Ala Phe Ser Asp Tyr Trp Ile Asn
1 5 10

<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 94
Gly Tyr Glu Phe Ser Ser His Trp Met Asn
1 5 10

<210> 95
<211> 10

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 95

Gly	Tyr	Ile	Phe	Ser	Asn	His	Trp	Met	Asn
1				5					10

<210> 96

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 96

Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Leu	Asn
1				5					10

<210> 97

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 97

Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Asn
1				5					10

<210> 98

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 98

Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Asn
1				5					10

<210> 99
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 99
Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 100
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 100
Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Glu Phe Lys
1 5 10 15

Asp

<210> 101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 101
Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 102
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 102
Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe Thr
1 5 10 15

Asp

<210> 103
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 103
Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe Arg
1 5 10 15

Gly

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 104
Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Gly Lys Phe Arg
1 5 10 15

Gly

<210> 105
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 105
Gln Val Tyr Pro Gly Asp Asp Asp Ile Asn Tyr Asn Gly Lys Phe Arg
1 5 10 15

Gly

<210> 106
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 106
Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Thr Val Lys
1 5 10 15

Gly

<210> 107
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 107
His Gly Asn Tyr Val Met Asp Tyr
1 5

<210> 108
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 108

His Gly Asn Tyr Val Met Asp Tyr
1 5

<210> 109

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 109

Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr
1 5 10

<210> 110

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 110

Gln Gly Val Ile Thr Ser Val Gln Glu Phe Ala Tyr
1 5 10

<210> 111

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 111

Trp Gly Tyr Tyr Gly Ser Ser Tyr Phe Ala Tyr
1 5 10

<210> 112

<211> 8

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 112

His Gly Asn Tyr Leu Met Asp Tyr
1 5

<210> 113

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 113

Ser Ala Ser Ser Ser Leu Asn Tyr Ile Tyr
1 5 10

<210> 114

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 114

Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe
1 5 10

<210> 115

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 115

Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr
1 5 10

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 116
Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
1 5 10

<210> 117
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 117
Ser Val Ser Ser Asn Val Asp Tyr Val Phe
1 5 10

<210> 118
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 118
Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala
1 5 10

<210> 119
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 119
Arg Thr Ser Asn Leu Ala Ser
1 5

<210> 120
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 120
Arg Thr Ser Asn Leu Ala Thr
1 5

<210> 121
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 121
Gly Ala Thr Asn Leu Glu Thr
1 5

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 122
Gln Gln Phe His Asp Tyr Pro Arg Thr
1 5

<210> 123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 123

Gln Gln Phe His Ser Tyr Pro Arg Thr
1 5

<210> 124
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 124
Gln Gln Phe Trp Arg Thr Pro Pro Thr
1 5

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 125
Gln Gln Tyr His Ser Tyr Pro Leu Thr
1 5

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 126
Cys Gln Gln Phe Trp Arg Thr Pro Pro Thr
1 5 10

<210> 127
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 127

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 128

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 128

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 129

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 129

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 130

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 130

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 131

<211> 121

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 131

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Glu Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Val Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 132

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 132

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Arg Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 133

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 133

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 134

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 134

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 135

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 135

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 136

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 136

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 137

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 137

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 138

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 138

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Thr Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 139

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 139

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Asp Tyr
20 25 30

Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Val Tyr Pro Gly Asp Asp Asp Ile Asn Tyr Asn Gly Lys Phe
50 55 60

Arg Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 140

<211> 117

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 140

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 141

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 141

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Gly Lys Phe
50 55 60

Arg Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Leu Met Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 142

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 142

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 143

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 143

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 144

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 144

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 145

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 145

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 146

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 146

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Tyr Tyr Gly Ser Ser Tyr Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 147

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 147

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 148

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 148

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Ser Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 149

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 149

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Ser Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 150

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 150

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 151

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 151

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 152

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 152

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 153

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 154

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 154

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Ser Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 155
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 155
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 156
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 156
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Val Ser Ser Asn Val Asp Tyr Val
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Ser Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 157

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 157

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 158
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 158
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Leu Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 159
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 159

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 160

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 160

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 161

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 161

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 162

<211> 106

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 162

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 163

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 163

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 164

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 164

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 165

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 165

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 166

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 166

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 167

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 167

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

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 168

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 168

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

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 169

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 169

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 170

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 170

Gly Phe Thr Phe Ser Ser Phe Gly Met His
1 5 10

<210> 171

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 171

Gly Tyr Ala Phe Asn Asn Tyr Trp Met Asn
1 5 10

<210> 172

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 172

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn
1 5 10

<210> 173

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 173

Gly Tyr Thr Phe Thr Asn Phe Gly Ile Thr
1 5 10

<210> 174

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 174

Gly Tyr Thr Phe Thr Asn Ser Gly Met Asn
1 5 10

<210> 175

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 175

Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn
1				5				10	

<210> 176

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 176

Glu	Ile	Tyr	Pro	Ser	Ser	Gly	Asn	Thr	Phe	Tyr	Asn	Glu	Lys	Phe	Lys
1				5				10						15	

Gly

<210> 177

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 177

Gln	Ile	Ser	Pro	Gly	Asn	Gly	Asn	Ser	Asn	Phe	Asn	Gly	Lys	Phe	Lys
1				5				10						15	

Gly

<210> 178

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 178

Gln Ile Tyr Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe Lys
1 5 10 15

Ala

<210> 179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 179
Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe Arg
1 5 10 15

Gly

<210> 180
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 180
Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe Lys
1 5 10 15

Gly

<210> 181
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 181

Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val Asn
1 5 10 15

Gly

<210> 182
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 182
Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr
1 5 10

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 183
Gly Gly Arg Phe Gly Asn Ala Met Asp Tyr
1 5 10

<210> 184
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 184
Gly Gly Arg Tyr Gly Asn Ala Met Asp Tyr
1 5 10

<210> 185
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 185

Leu Arg Tyr Gly Asn Ser Phe Asp Tyr
1 5

<210> 186

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 186

Tyr Phe Tyr Gly Asn Ser Phe Val Tyr
1 5

<210> 187

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 187

Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr
1 5

<210> 188

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 188

Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
1 5 10 15

Thr

<210> 189
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 189
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Arg Asn Tyr Leu
1 5 10 15

Thr

<210> 190
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 190
Arg Ser Ser Gln Ser Leu Phe Ser Ser Gly Asn Gln Lys Asn Tyr Leu
1 5 10 15

Thr

<210> 191
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 191
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 192
<211> 9

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 192

Gln Asn Ala Tyr Phe Tyr Pro Tyr Thr
1 5

<210> 193

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 193

Gln Asn Asp Tyr Tyr Tyr Pro Leu Thr
1 5

<210> 194

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 194

Gln Asn Asn Tyr Phe Tyr Pro Leu Thr
1 5

<210> 195

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 195

Gln Asn Asn Tyr Asn Phe Pro Leu Thr
1 5

<210> 196
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 196
Gln Asn Asn Tyr Tyr Tyr Pro Leu Thr
1 5

<210> 197
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 197
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Tyr Gly Asn Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 198
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 198
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val
 50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Leu Arg Tyr Gly Asn Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 199
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 199

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe
50 55 60

Arg Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 200

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 200

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Tyr Pro Ser Ser Gly Asn Thr Phe Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Ala Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 201

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 201

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Tyr Pro Ser Ser Gly Asn Thr Phe Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 202

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 202

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 203

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 203

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Phe Tyr Gly Asn Ser Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 204

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 204

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Ser Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Tyr Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 205

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 205

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Ala Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Phe Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 206

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 206

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Ala Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Phe Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 207
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 207
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 208
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 208

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Asn Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 209

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 209

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 210

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 210

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Arg Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 211

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 211

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

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Phe Ser Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 212

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 212

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

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Phe Ser Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 213

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 213

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

Glu Arg Ala Thr Met Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 214

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 214

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 215

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 215

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Phe Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 216
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 216
Ser Gly Gly Gly Gly Ser
1 5

<210> 217
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 217
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 218
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 218
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 219

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 219

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 220

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 220

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 221

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 221

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 222
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 222

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 223

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 223

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 224

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 224

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 225

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 225

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 226

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 226

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 227

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 227

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 228

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 228

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 229

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 229

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 230

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 230

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 231

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 231

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 232

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 232

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 233

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 233

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 234
<211> 232
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 234

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 235

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 235

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 236

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 236

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 237

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 237

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 238

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 238

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 239

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 239

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 240

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 240

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 241

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 241

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 242

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 242

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 243

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 243

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 244

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 244

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 245

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 245

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 246

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 246

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 247

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 247

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 248

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 248

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Lys Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 249

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 249

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 250

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 250

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 251

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 251

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 252

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 252

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 253

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 253

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 254

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 254

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 255
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 255

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 256
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 256

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 257

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 257

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 258

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 258

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 259

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 259

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Tyr Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 260

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 260

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met
20 25 30

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 261

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 261

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly
35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 262

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 262

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 263

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 263

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 264

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 264

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 265

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 265

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 266

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 266

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 267

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 267

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 268

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 268

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 269

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 269

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 270

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 270

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 271

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 271

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe
100 105 110

Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 272

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 272

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Tyr Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
130 135 140

Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
145 150 155 160

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr
165 170 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg
180 185 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg
195 200 205

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly
210 215 220

Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
225 230 235 240

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 273

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 273

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met
20 25 30

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser
115 120 125

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln
130 135 140

Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
145 150 155 160

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
165 170 175

Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu
180 185 190

Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser
195 200 205

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln
210 215 220

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His
225 230 235 240

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser
245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
325 330 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
370 375 380

Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val
385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
420 425 430

Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
435 440 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465 470 475 480

Ser Pro Gly Lys

<210> 274

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 274

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Gly Ser Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 275

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 275

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Gly Ser Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 276

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 276

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 277

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 277

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 278

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 278

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 279

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 279

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 280

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 280

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 281

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 281

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 282

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 282

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Asp Asn Gly Ile Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Val Trp Asn Tyr Glu Arg Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 283

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 283

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Tyr Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 284

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 284

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ser Ile Ala Val Thr Gly Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 285

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 285

Gln Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Tyr Val Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Ile Ile Ser Pro Asn Asp Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Val Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Asp Leu Gly Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 286

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 286

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 287

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 287

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 288

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 288

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 289

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 289

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Tyr Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 290

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 290

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Tyr Thr Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Asn Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 291

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 291

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 292

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 292

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 293

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 293

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

Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
20 25 30

Ala Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu
35 40 45

Trp Met Gly Tyr Ile Ser Asp Val Gly His Asn Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Phe Leu Lys Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Asp Gln Val Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 294

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 294

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

Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
20 25 30

Ala Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu
35 40 45

Trp Met Gly Tyr Ile Ser Asp Val Gly Ser Asn Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Phe Lys Asn Gln Phe
65 70 75 80

Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Thr Arg Asp Gln Val Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 295

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 295

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 296
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 296
Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Thr Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 297

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 297

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 298

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 298

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 299

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 299

Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro Val Thr Val Gly
1 5 10 15

Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn
85 90 95

Leu Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 300

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 300

Asp Ile Val Met Thr Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 301

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 301

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

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 302

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 302

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

Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 303

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 303

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

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

Asp Ala Lys Thr Phe Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 304

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 304

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

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

Asp Gly Lys Thr Phe Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 305
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 305
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 306

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 306

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Ala Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Arg Glu Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Ser Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
180 185 190

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
210 215 220

Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 307

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 307

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 308

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 308

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Glu Arg Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Ser Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
180 185 190

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
210 215 220

Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 309

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 309

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 310

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 310

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

Ser Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
180 185 190

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
210 215 220

Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 311

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 311

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val His Ser Tyr
20 25 30

Gly Asn Ser Leu Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 312

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 312

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Asn Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 313
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 313
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 314
<211> 1
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 314
Gly
1

<210> 315
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 315
Gly Ser
1

<210> 316
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 316
Gly Ser Ser
1

<210> 317
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 317
Gly Ser Ser Ser Gly
1 5

<210> 318
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 318
Gly Gly Gly Gly Ser
1 5

<210> 319
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 319
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 320
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 320

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 321
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 321
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 322
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 322
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 323
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 323
Pro Gly Gly Gly Gly Ser Pro
1 5

<210> 324
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 324
Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro Gly Gly Gly
1 5 10 15

Gly Ser Pro

<210> 325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 325
Gly Glu Pro Gly Ser Gly Glu
1 5

<210> 326
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 326
Gly Glu Pro Gly Ser Gly Glu Gly Glu Pro Gly Ser Gly Glu
1 5 10

<210> 327
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 327

Gly Glu Pro Gly Ser Gly Glu Gly Glu Pro Gly Ser Gly Glu Glu Gly
1 5 10 15

Glu Pro Gly Ser Gly Glu
20

<210> 328

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 328

Glu Gly Glu Pro Gly Ser Gly Glu Glu Gly Glu Pro Gly Ser Gly Glu
1 5 10 15

Glu Gly Glu Pro Gly Ser Gly Glu Glu Gly Glu Pro Gly Ser Gly Glu
20 25 30

<210> 329

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 329

Gly Lys Pro Gly Ser
1 5

<210> 330

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 330

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
1 5 10

<210> 331
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 331
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
1 5 10 15

<210> 332
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 332
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
1 5 10 15

Lys Pro Gly Ser
20

<210> 333
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 333
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
1 5 10 15

Lys Pro Gly Ser Gly Lys Pro Gly Ser
20 25

<210> 334
<211> 5

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 334
Ser Ser Ser Ser Gly
1 5

<210> 335
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 335
Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
1 5 10

<210> 336
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 336
Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
1 5 10 15

<210> 337
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 337
Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
1 5 10 15

Ser Ser Ser Gly
20

<210> 338
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 338
Gly Arg Pro Gly Ser Gly Pro Gly Ser Gly Arg Pro Gly Ser Gly Arg
1 5 10 15

Pro Gly Ser

<210> 339
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 339
Gly Arg Pro Gly Ser Gly Pro Gly Ser Gly Arg Pro Gly Ser Gly Arg
1 5 10 15

Pro Gly Ser Gly Arg Gly Pro Ser
20

<210> 340
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 340
Gly Lys Pro Gly Ser Gly Arg Pro Gly Ser Gly Lys Gly Pro Ser Gly
1 5 10 15

Arg Pro Gly Ser
20

<210> 341

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 341

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Tyr Thr Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Asn Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Ser Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
245 250 255

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
260 265 270

Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
275 280 285

Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
290 295 300

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
305 310 315 320

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
325 330 335

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser
340 345 350

Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
355 360 365

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
370 375 380

Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu
385 390 395 400

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
405 410 415

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
420 425 430

Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
450 455 460

Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
465 470 475 480

Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu
485 490 495

Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
500 505 510

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
565 570 575

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
595 600 605

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys
625 630 635 640

Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe
675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 342

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 342

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Ser Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
245 250 255

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
260 265 270

Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
275 280 285

Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
290 295 300

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
305 310 315 320

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
325 330 335

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser
340 345 350

Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
355 360 365

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
370 375 380

Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu
385 390 395 400

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
405 410 415

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
420 425 430

Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
450 455 460

Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
465 470 475 480

Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu
485 490 495

Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
500 505 510

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
565 570 575

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
595 600 605

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys
625 630 635 640

Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe
675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 343

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 343

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
325 330 335

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val
420 425 430

Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn
435 440 445

Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala
465 470 475 480

Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His
500 505 510

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
515 520 525

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
530 535 540

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
545 550 555 560

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
565 570 575

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
580 585 590

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
595 600 605

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
610 615 620

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
625 630 635 640

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
645 650 655

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
660 665 670

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
675 680 685

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
690 695 700

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
705 710 715 720

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 344

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 344

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Cys Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
325 330 335

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val
420 425 430

Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn
435 440 445

Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala
465 470 475 480

Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His
500 505 510

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
515 520 525

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
530 535 540

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
545 550 555 560

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
565 570 575

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
580 585 590

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
595 600 605

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
610 615 620

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
625 630 635 640

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
645 650 655

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
660 665 670

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
675 680 685

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
690 695 700

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
705 710 715 720

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 345

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 345

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Pro Leu Ile Tyr Ser Thr Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235 240

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
245 250 255

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
260 265 270

Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
275 280 285

Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
290 295 300

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
305 310 315 320

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
325 330 335

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asp Ser
340 345 350

Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
355 360 365

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
370 375 380

Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu
385 390 395 400

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
405 410 415

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
420 425 430

Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
450 455 460

Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
465 470 475 480

Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu
485 490 495

Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
500 505 510

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
565 570 575

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
595 600 605

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys
625 630 635 640

Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe
675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 346
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 346
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
325 330 335

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val
420 425 430

Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn
435 440 445

Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala
465 470 475 480

Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His
500 505 510

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
515 520 525

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
530 535 540

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
545 550 555 560

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
565 570 575

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
580 585 590

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
595 600 605

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
610 615 620

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
625 630 635 640

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
645 650 655

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
660 665 670

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
675 680 685

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
690 695 700

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
705 710 715 720

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 347

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 347

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
325 330 335

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val
420 425 430

Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn
435 440 445

Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala
465 470 475 480

Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His
500 505 510

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
515 520 525

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
530 535 540

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
545 550 555 560

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
565 570 575

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
580 585 590

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
595 600 605

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
610 615 620

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
625 630 635 640

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
645 650 655

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
660 665 670

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
675 680 685

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
690 695 700

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
705 710 715 720

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 348

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 348

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
325 330 335

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asp Ser Tyr Val Ser Trp Phe Asn Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val
420 425 430

Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn
435 440 445

Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala
465 470 475 480

Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His
500 505 510

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
515 520 525

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
530 535 540

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
545 550 555 560

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
565 570 575

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
580 585 590

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
595 600 605

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
610 615 620

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
625 630 635 640

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
645 650 655

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
660 665 670

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
675 680 685

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
690 695 700

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
705 710 715 720

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 349

<211> 733

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 349

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Cys Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Leu Thr Gln Ser Pro
130 135 140

Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met Phe Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Pro Trp Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Phe His Asp Tyr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
325 330 335

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg
435 440 445

Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Asp Tyr
465 470 475 480

Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
500 505 510

Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
565 570 575

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys
610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
625 630 635 640

Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly
675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 350

<211> 733

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 350

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Leu Thr Gln Ser Pro
130 135 140

Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met Phe Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Pro Trp Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Phe His Asp Tyr Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
325 330 335

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg
435 440 445

Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Asp Tyr
465 470 475 480

Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
500 505 510

Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
565 570 575

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys
610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
625 630 635 640

Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly
675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 351
<211> 984
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 351

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

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

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Lys Lys Tyr Ser Thr Val Trp Ser Tyr Phe Asp Asn Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu Thr Gln Pro Ser Ser
130 135 140

Val Ser Val Pro Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp
145 150 155 160

Lys Leu Gly Asp Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Val Leu Val Ile Tyr Gln Asp Arg Lys Arg Pro Ser Gly Val
180 185 190

Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
210 215 220

Trp Gly Ser Ser Thr Ala Val Phe Gly Cys Gly Thr Lys Leu Thr Val
225 230 235 240

Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 352

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 352

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Gly Ile Trp Ser Glu Gly Ser Asn Lys Tyr Tyr Ala Asp Ala Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Thr Tyr Thr Thr Gly Trp Ser Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Glu Leu Thr Gln Pro Pro
130 135 140

Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly
145 150 155 160

Asp Lys Leu Gly Asp Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Ser Gly
165 170 175

Gln Ser Pro Val Leu Val Ile Tyr Gln Asp Ala Lys Arg Pro Ser Gly
180 185 190

Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu
195 200 205

Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln
210 215 220

Ala Phe His Gln Ser Thr Trp Val Phe Gly Cys Gly Thr Gln Leu Thr
225 230 235 240

Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 353

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 353

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 354

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 354

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val
245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser
290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
325 330 335

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
340 345 350

Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly Gln
355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
465 470 475 480

Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys

<210> 355

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 355

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 356

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 356

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 357

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 357

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 358

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 358

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly

<210> 359

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 359

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Ser Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 360

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 360

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Phe Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly Lys

<210> 361

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 361

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
370 375 380

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val
385 390 395 400

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
405 410 415

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala
420 425 430

Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly
435 440 445

Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu
465 470 475 480

Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp
500 505 510

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
515 520 525

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
530 535 540

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
545 550 555 560

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
565 570 575

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
580 585 590

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
595 600 605

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
610 615 620

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
625 630 635 640

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
645 650 655

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
660 665 670

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
675 680 685

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
690 695 700

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
705 710 715 720

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
725 730 735

Gly

<210> 362

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 362

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val
245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser
290 295 300

Lys Ile Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
325 330 335

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
340 345 350

Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln
355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
465 470 475 480

Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys

<210> 363

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 363

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val
245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser
290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
325 330 335

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
340 345 350

Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln
355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
465 470 475 480

Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys

<210> 364

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 364

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val
245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser
290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
325 330 335

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
340 345 350

Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Glu Tyr Trp Gly Gln
355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
465 470 475 480

Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys

<210> 365

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 365

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Asn Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val
245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser
290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
325 330 335

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
340 345 350

Gly Asn Phe Gly Asp Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln
355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gln Ala Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
465 470 475 480

Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
500 505 510

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
515 520 525

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
530 535 540

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
545 550 555 560

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
565 570 575

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Lys

<210> 366

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 366

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
115 120 125

Lys Pro Gly Ser Gly Lys Pro Gly Ser Ile Gln Leu Thr Gln Ser Pro
130 135 140

Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met Phe Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Pro Trp Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Phe His Asp Tyr Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
370 375 380

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
420 425 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 367

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 367

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 368
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 368
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Tyr Tyr Gly Ser Ser Tyr Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 369

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 369

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 370

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 370

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 371

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 371

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 372

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 372

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Glu Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Val Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 373

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 373

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Arg Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 374

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 374

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 375

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 375

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 376

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 376

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 377

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 377

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 378

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 378

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 379

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 379

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 380

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 380

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Ile Ile Thr Ser Val Gln Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 381

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 381

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 382

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 382

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 383

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 383

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Ser Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 384

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 384

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Ser Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 385

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 385

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Phe Trp Arg Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 386

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 386

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 387

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 387

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 388

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 388

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 389

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 389

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 390

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 390

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 391

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 391

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 392

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 392

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 393

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 393

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 394
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 394
Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 395

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 395

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Gln Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 396

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 396

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 397

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 397

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 398

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 398

Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Phe
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe His Asp Tyr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 399

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 399

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

Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Ile Tyr
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg
35 40 45

Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Leu Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 400

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 400

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Arg Gly
35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 401

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 401

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Tyr Gly Asn Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 402

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 402

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Tyr Gly Asn Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 403

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 403

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe
50 55 60

Arg Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 404

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 404

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Tyr Pro Ser Ser Gly Asn Thr Phe Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Ala Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 405

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 405

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Tyr Pro Ser Ser Gly Asn Thr Phe Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 406
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 406
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 407

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 407

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Phe Tyr Gly Asn Ser Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 408

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 408

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Ser Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Tyr Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 409

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 409

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Ala Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Phe Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 410

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 410

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Ala Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Phe Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 411

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 411

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 412

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 412

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 413
<211> 220
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 413

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Phe Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 414

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 414

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Asn Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 415

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 415

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asn Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 416

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 416

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Arg Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 417

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 417

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

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Phe Ser Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 418

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 418

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

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Phe Ser Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Tyr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 419

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 419

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

Glu Arg Ala Thr Met Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Ala Tyr Phe Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 420
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 420
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Cys Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 421

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 421

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 422

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 422

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 423

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 423

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 424

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 424

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 425

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 425

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Cys Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 426

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 426

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 427

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 427

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Cys Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 428

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 428

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 429

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 429

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 430

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 430

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 431

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 431

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Tyr Thr Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Asn Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Ser Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
245 250 255

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260 265 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275 280 285

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
290 295 300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305 310 315 320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
325 330 335

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
340 345 350

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
355 360 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
370 375 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405 410 415

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
420 425 430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460

Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 432

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 432

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
245 250 255

Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe
260 265 270

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
275 280 285

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305 310 315 320

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
325 330 335

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
340 345 350

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
355 360 365

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
370 375 380

Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385 390 395 400

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
405 410 415

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser
420 425 430

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
435 440 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
450 455 460

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 433

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 433

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Pro Leu Ile Tyr Ser Thr Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235 240

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
245 250 255

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260 265 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275 280 285

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
290 295 300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305 310 315 320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
325 330 335

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
340 345 350

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
355 360 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
370 375 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405 410 415

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
420 425 430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460

Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 434

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 434

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Thr Asp Tyr Ile Phe Ser Asn Tyr
20 25 30

Tyr Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Thr Gly Asn Thr Val Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Asp Tyr Ala Leu Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
145 150 155 160

Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
210 215 220

Asn Ser Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
245 250 255

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260 265 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275 280 285

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
290 295 300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305 310 315 320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
325 330 335

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
340 345 350

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
355 360 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
370 375 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405 410 415

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
420 425 430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460

Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 435

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 435

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Ile
35 40 45

Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Cys
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 436

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 436

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys His Ala Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser
180 185 190

Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 437
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 437

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 438

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 438

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 439

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 439

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 440

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 440

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

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 441

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 441

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
180 185 190

Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
210 215 220

Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 442

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 442

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
130 135 140

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
145 150 155 160

Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr
180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys Arg Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 443
<211> 492
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 443

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala
145 150 155 160

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
165 170 175

Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
180 185 190

Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly
195 200 205

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
210 215 220

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
225 230 235 240

Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr Phe Gly Gly Gly Thr Lys
245 250 255

Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
290 295 300

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
370 375 380

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
385 390 395 400

Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
420 425 430

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser
435 440 445

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
450 455 460

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 444

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 444

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Lys Pro
100 105 110

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser
130 135 140

Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly
145 150 155 160

Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp
165 170 175

Ile Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu
180 185 190

Glu Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
195 200 205

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
210 215 220

Ala Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp
225 230 235 240

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 445

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 445

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
130 135 140

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
145 150 155 160

Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr
180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr Phe Ser Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys Arg Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 446

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 446

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys

<210> 447

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 447

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys

<210> 448

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 448

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met
65 70 75 80

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys

<210> 449

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 449

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Cys Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
180 185 190

Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
210 215 220

Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 450

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 450

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Cys Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
180 185 190

Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
210 215 220

Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 451

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 451

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 452

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 452

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 453

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 453

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 454
<211> 479
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 454

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Thr Asn Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Leu Thr Gly Thr Trp Gly Gln Gly Thr Met Val Thr Val
 100 105 110

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
 115 120 125

Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser
 130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
 165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser
180 185 190

Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
210 215 220

Val Tyr Tyr Cys Leu Gln Tyr Asp Arg Tyr Pro Phe Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 455

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 455

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Thr Gly Thr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Asp Ile Ile Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Glu Leu Leu Ile Tyr Tyr Ala Ser
180 185 190

Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
210 215 220

Val Tyr Tyr Cys Leu Gln Tyr Asp Arg Tyr Pro Phe Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 456

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 456

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Thr Gly Thr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser
180 185 190

Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
210 215 220

Val Tyr Tyr Cys Leu Gln Tyr Asp Arg Tyr Pro Phe Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 457

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 457

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Met Glu Trp Val
35 40 45

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

Thr Asn Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Leu Thr Gly Thr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Asp Ile Ile Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Glu Leu Leu Ile Tyr Tyr Ala Ser
180 185 190

Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
210 215 220

Val Tyr Tyr Cys Leu Gln Tyr Asp Arg Tyr Pro Phe Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 458

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 458

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Met Glu Trp Val
35 40 45

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

Thr Asn Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Leu Thr Gly Thr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser
180 185 190

Thr Arg Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
210 215 220

Val Tyr Tyr Cys Leu Gln Tyr Asp Arg Tyr Pro Phe Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 459
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 459
Gln Val Lys Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Val Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Asp Ser His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 460

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 460

Gln Val Lys Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Val Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 461

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 461

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met Glu Ile Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
35 40 45

Ile Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Asn Glu Lys
50 55 60

Phe Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala
65 70 75 80

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Phe Lys Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro
115 120 125

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met
130 135 140

Thr Gln Ser Pro Ala Phe Leu Ser Val Thr Pro Gly Glu Lys Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asp Tyr Leu His Trp Tyr
165 170 175

Gln Gln Lys Pro Asp Gln Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser
180 185 190

Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala
210 215 220

Thr Tyr Tyr Cys Gln Asp Gly His Ser Trp Pro Pro Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 462

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 462

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asn Gly His Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Asp Ser His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 463

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 463

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asn Gly His Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 464

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 464

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly His Thr Lys Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Asp Ser His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 465

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 465

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly His Thr Lys Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 466

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 466

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly
115 120 125

Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile
130 135 140

Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg
145 150 155 160

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
180 185 190

Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe
225 230 235 240

Gly Cys Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys
245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 467

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 467

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Phe Phe Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
115 120 125

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
145 150 155 160

Cys Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu
165 170 175

Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
180 185 190

Glu Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly Glu Arg Leu Pro Phe Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Lys

<210> 468

<211> 728

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 468

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Asp Ile Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Arg Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Val Leu Tyr Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Arg Tyr
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln
245 250 255

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr Trp Met His Trp Val Arg
275 280 285

Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Glu Ile Asn Pro Gly
290 295 300

Asn Gly His Thr Asn Tyr Ser Gln Lys Phe Gln Gly Arg Val Thr Ile
305 310 315 320

Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
325 330 335

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Phe Thr Thr
340 345 350

Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
355 360 365

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
370 375 380

Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln Ser Pro Pro Thr Leu
385 390 395 400

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
405 410 415

Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser
420 425 430

Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
450 455 460

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Asp Gly
465 470 475 480

His Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490 495

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
565 570 575

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
660 665 670

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys
725

<210> 469

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 469

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val
210 215 220

Tyr Tyr Cys Gln Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr Trp Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Glu Ile Asn
290 295 300

Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe Gln Gly Arg Val
305 310 315 320

Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Phe
340 345 350

Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
355 360 365

Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro
370 375 380

Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln Ser Pro Pro
385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala
405 410 415

Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Gln Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly
435 440 445

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
465 470 475 480

Asp Gly His Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
500 505 510

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
515 520 525

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
530 535 540

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
545 550 555 560

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
565 570 575

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
580 585 590

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
595 600 605

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
610 615 620

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
625 630 635 640

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
645 650 655

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
660 665 670

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
675 680 685

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
690 695 700

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
705 710 715 720

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730

<210> 470

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 470

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
450 455 460

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
465 470 475 480

Gly Tyr Thr Phe Thr Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro
485 490 495

Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Tyr Asn Asp Ile
500 505 510

Thr Ile Tyr Asn Gln Lys Phe Gln Gly Arg Val Thr Met Thr Val Asp
515 520 525

Arg Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Val Leu Tyr Asp Gly
545 550 555 560

Tyr Tyr Glu Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
580 585 590

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
595 600 605

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
610 615 620

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
625 630 635 640

Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
660 665 670

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
675 680 685

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
690 695

<210> 471

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 471

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser
450 455 460

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
465 470 475 480

Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe Met Asn Trp Val Arg Gln
485 490 495

Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Tyr Asn
500 505 510

Asp Ile Thr Ile Tyr Asn Gln Lys Phe Gln Gly Arg Val Thr Met Thr
515 520 525

Val Asp Arg Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg
530 535 540

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Val Leu Tyr
545 550 555 560

Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
580 585 590

Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser
595 600 605

Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly
610 615 620

Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
625 630 635 640

Leu Ile Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe
645 650 655

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
660 665 670

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr
675 680 685

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
690 695 700

<210> 472

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 472

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Gly Asn Gly His Thr Asn Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Val Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
450 455 460

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
465 470 475 480

Gly Tyr Thr Phe Thr Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro
485 490 495

Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Tyr Asn Asp Ile
500 505 510

Thr Ile Tyr Asn Gln Lys Phe Gln Gly Arg Val Thr Met Thr Val Asp
515 520 525

Arg Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Val Leu Tyr Asp Gly
545 550 555 560

Tyr Tyr Glu Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
580 585 590

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
595 600 605

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
610 615 620

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
625 630 635 640

Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
660 665 670

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
675 680 685

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
690 695

<210> 473

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 473

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser
450 455 460

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
465 470 475 480

Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe Met Asn Trp Val Arg Gln
485 490 495

Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Tyr Asn
500 505 510

Asp Ile Thr Ile Tyr Asn Gln Lys Phe Gln Gly Arg Val Thr Met Thr
515 520 525

Val Asp Arg Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg
530 535 540

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Val Leu Tyr
545 550 555 560

Asp Gly Tyr Tyr Glu Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
580 585 590

Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser
595 600 605

Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly
610 615 620

Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
625 630 635 640

Leu Ile Tyr Ala Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe
645 650 655

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
660 665 670

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Tyr
675 680 685

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
690 695 700

<210> 474

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 474

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Glu Phe Ser Ser His
20 25 30

Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Cys Leu Glu Trp Met
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
115 120 125

Lys Pro Gly Ser Gly Lys Pro Gly Ser Ile Gln Leu Thr Gln Ser Pro
130 135 140

Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met Phe Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Pro Trp Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Phe His Asp Tyr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys
370 375 380

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
420 425 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 475

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 475

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Tyr Pro Ser Ser Gly Asn Thr Phe Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Gly Pro Leu Arg Ser Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys
115 120 125

Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val
130 135 140

Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala
145 150 155 160

Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Phe Ser Ser Gly Asn Gln
165 170 175

Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
180 185 190

Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
195 200 205

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
210 215 220

Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Tyr
225 230 235 240

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro
245 250 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
325 330 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn
385 390 395 400

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430

Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
450 455 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465 470 475 480

Ser Leu Ser Pro Gly Lys
485

<210> 476

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 476

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Gly Asn Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Tyr Gly Asn Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
115 120 125

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln
130 135 140

Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145 150 155 160

Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr
165 170 175

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
180 185 190

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
210 215 220

Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn Asn Tyr Tyr Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys

<210> 477

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 477

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Ser Pro Gly Asn Gly Asn Ser Asn Phe Asn Gly Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Arg Tyr Gly Asn Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr
130 135 140

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
145 150 155 160

Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Arg Asn
165 170 175

Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
180 185 190

Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
210 215 220

Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn Ala Tyr Phe Tyr Pro
225 230 235 240

Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser
245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
325 330 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
370 375 380

Val Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val
385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
420 425 430

Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
435 440 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465 470 475 480

Ser Pro Gly Lys

<210> 478

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 478

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Phe Ala Glu Glu Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
115 120 125

Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Val Met Thr Gln
130 135 140

Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
145 150 155 160

Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr
165 170 175

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
180 185 190

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
210 215 220

Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn Asn Tyr Phe Tyr Pro Leu
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys

<210> 479

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 479

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asn Gly His Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Phe Thr Thr Ala Arg Ala Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys Tyr Ala Ser Gln
180 185 190

Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Asp Ser His Ser Phe Pro Pro Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Cys Arg Lys Lys Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475