(12) STANDARD PATENT (11) Application No. **AU 2017341936 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Modular tetravalent bispecific antibody platform

(51) International Patent Classification(s)
C07K 16/28 (2006.01) ***C07K 16/46*** (2006.01)

(21) Application No: **2017341936** (22) Date of Filing: **2017.10.16**

(87) WIPO No: **WO18/071913**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/408,271	**2016.10.14**	**US**

(43) Publication Date: **2018.04.19**
(44) Accepted Journal Date: **2024.10.31**

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(56) Related Art
WO 2013/096346 A1
MÃ LLER ET AL: "A dimeric bispecific miniantibody combines two specificities with avidity.", FEBS LETTERS, vol. 432, no. 1-2, 1 July 1998 (1998-07-01), pages 45 - 49, XP055058073, ISSN: 0014-5793, DOI: 10.1016/S0014-5793(98)00829-1
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Pohl, Stefanie Claudia, et al. "A cassette vector system for the rapid cloning and production of bispecific tetravalent antibodies." Antibodies vol 1(1), 2012, pg. 19-38.
US 8084026 B2

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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
19 April 2018 (19.04.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/071913 A3

(51) International Patent Classification:
C07K 16/28 (2006.01) *C07K 16/46* (2006.01)

(21) International Application Number:
PCT/US2017/056814

(22) International Filing Date:
16 October 2017 (16.10.2017)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/408,271 14 October 2016 (14.10.2016) US

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

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

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

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

(54) Title: MODULAR TETRAVALENT BISPECIFIC ANTIBODY PLATFORM

(57) Abstract: The present invention relates to a tetrameric bispecific antibody molecule, as well as a method for producing the same, its use and a nucleic acid molecule encoding the tetrameric bispecific antibody molecule.

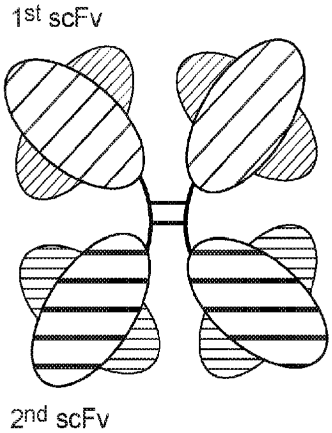


Figure 1

[Continued on next page]

(88) Date of publication of the international search report:
24 May 2018 (24.05.2018)

MODULAR TETRAMERIC BISPECIFIC ANTIBODY PLATFORM

RELATED APPLICATIONS

[0001] This application claims benefit of, and priority to, U.S.S.N. 62/408,271 filed on October 14, 2016 the contents of which is hereby incorporated by reference its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates generally to tetrameric bispecific antibody molecules, methods and systems of producing same.

GOVERNMENT INTEREST

[0003] This invention was made with government support under [ ] awarded by the []. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0004] Bispecific antibodies (BsAb) are antibodies or antibody-like molecules having two different binding specificities. BsAbs have broad applications in biomedicine, especially in immunotherapy for tumors. Presently, a focus of immunotherapy research is on how to utilize cell-mediated cytotoxicity of BsAb to kill tumor cells. A BsAb can be designed to target a tumor cell and an effector cell simultaneously, while triggering the effector cell's destruction of the tumor cell.

[0005] BsAb can be prepared by methods such as chemical engineering, cell engineering and genetic engineering. An advantage of genetic engineering is that the antibodies can be easily modified, which renders design and production of many different forms of bispecific antibody fragments, including diabodies, tandem ScFv, and single-chain diabodies, as well as derivatives thereof. Since those BsAbs do not have an IgG Fc domain, their small size enhances their penetration into tumors, but they have significantly shorter half-life in vivo and also lack the ADCC effect that is associated with the constant region of the antibody.

[0006] To improve the stability and therapeutic potential, recombinant genetic modifications were made in the heavy chains to facilitate their heterodimerization and to produce greater yields of Fc-containing IgG-like bispecific antibodies. Several rational design strategies have been used to engineer antibody CH3 chains for heterodimerization, namely disulfide bonds, salt bridges, knobs-into-holes. The bases for creating knob and hole in the juxtaposed positions is that the knob and hole interaction will favor heterodimer formation, whereas the knob-knob and the hole-hole interaction will prevent homodimers formation due to the deletion of favorable interactions. While this knob-into-holes approach solves the heavy chain homodimerization problem, it did not address the issues regarding mispairing between the light chain and heavy chains from two different antibodies. Although it is possible to identify identical light chains for two different antibodies, the possibility of BsAb construction using two antibody sequences that can share the common light chain is very limited.

[0007] There is a need to provide better BsAbs that are easier to prepare, have better clinical stability and efficacy and/or reduced systematic toxicity.

SUMMARY OF THE INVENTION

[0008] The present invention provides tBsAbs that are easier to prepare, have better clinical stability and efficacy, and/or reduced systematic toxicity.

[0009] One aspect of the present invention relates to a tetravalent antibody molecule. The tetravalent antibody may be a dimer of a bispecific scFv fragment including a first binding site for a first antigen, a second binding site for a second antigen. The two binding sites may be joined together via a linker domain. In embodiments, the scFv fragment is a tandem scFv, the linker domain includes an immunoglobulin hinge region (e.g., an IgG1, an IgG2, an IgG3, and an IgG4 hinge region) amino acid sequence. In embodiments, the immunoglobulin hinge region amino acid sequence may flanked by a flexible linker amino acid sequence, e.g., having the amino acid sequence $(GGGS)_{X1\text{-}6}$, $(GGGGS)_{X1\text{-}6}$, and GSAGSAAGSGEF. In embodiments, the linker domain includes at least a portion of an immunoglobulin Fc domain, e.g., an IgG1, an IgG2, an IgG3, and an IgG4 Fc domain. The at least a portion of the immunoglobulin Fc domain may be a CH2 domain. The Fc domain may be linked to the C-terminus of an immunoglobulin hinge region (e.g., an IgG1, an IgG2, an IgG3, and an IgG4 hinge region) amino acid sequence. The linker domain may include a flexible linker amino acid sequence (e.g., $(GGGS)_{X1\text{-}6}$, $(GGGGS)_{X1\text{-}6}$, and GSAGSAAGSGEF) at one terminus or at both termini.

[00010] Another aspect, the present invention relates to nucleic acid construct. The construct may include nucleic acid molecules encoding: a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to a first antigen; a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to a second antigen; and a linker domain. In embodiments, the linker domain is an immunoglobulin hinge region (e.g., an IgG1, an IgG2, an IgG3, and an IgG4 hinge region) amino acid sequence. In embodiments, the linker domain is at least a portion of an immunoglobulin Fc domain, e.g., an IgG1, an IgG2, an IgG3, and an IgG4 Fc domain. The at least a portion of the immunoglobulin Fc domain may be a CH2 domain. The Fc domain may be linked to the C-terminus of an immunoglobulin hinge region (e.g., an IgG1, an IgG2, an IgG3, and an IgG4 hinge region) amino acid sequence. The linker domain may include a flexible linker amino acid sequence (e.g., (GGGS)X1-6, (GGGGS)X1-6, and GSAGSAAGSGEF) at one terminus or at both termini.

[00011] Yet another aspect of the present invention is a vector including the nucleic acid construct of the above aspect.

[00012] Another aspect of the present invention is a host cell (e.g., a T-cell, a B-cell, a follicular T-cell, and an NK-cell) which includes the vector of the above aspect.

[00013] An aspect of the present invention is a chimeric antigen receptor (CAR). The CAR may include an intracellular signaling domain, a transmembrane domain and an extracellular domain including the tetravalent antibody molecule of any of the above aspects or embodiments. In embodiments, the transmembrane domain further includes a stalk region positioned between the extracellular domain and the transmembrane domain and/or the transmembrane domain comprises CD28. In embodiments, the CAR further includes one or more additional costimulatory molecules (e.g., CD28, 4-1BB, ICOS, and OX40) positioned between the transmembrane domain and the intracellular signaling domain, e.g., a CD3 zeta chain.

[00014] Yet another aspect of the present invention is a genetically engineered cell. The genetically engineered cell may express and bear on its cell surface membrane the chimeric antigen receptor of an above aspect or embodiment. In embodiments, the cell is a T-cell (e.g., CD4+ and/or CD8+) or an NK cell. The cell may comprise a mixed population of CD4+ and CD8 cells+.

[00015] An aspect of the present invention is method for treating a disease or disorder. The method may include administering the tetravalent antibody molecule of an above aspect or embodiment. In embodiments, the disease or disorder is a CNS-related disease or disorder, e.g., a CNS cancer or a neurodegenerative disease. The CNS cancer may be a Glioblastoma (GBM). The neurodegenerative disease may be Amyotrophic Lateral Sclerosis, Parkinson's Disease, Alzheimer's Disease, or Huntington's Disease. In embodiments, the tetravalent antibody molecule recognizes and/or is bound by a CNS transport receptor, e.g., a transferrin receptor (TfR), VCAM-1, CD98hc, and an insulin receptor. In this aspect and any above aspect or embodiment, the tetravalent antibody molecule augments transport across the blood brain barrier.

[00016] Any of the above aspects or embodiments may be combined with any other aspect or embodiment.

[00017] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are expressly incorporated by reference in their entirety. In cases of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples described herein are illustrative only and are not intended to be limiting.

[00018] Other features and advantages of the invention will be apparent from and encompassed by the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[00019] Figure 1 is an illustration showing the design and formation of a tetrameric bispecific antibody (tBsAb).

[00020] Figure 2 is a schematic representation of the pcDNA3.1\1 scFv-hinge –scFv expression vector.

[00021] Figure 3A is an SDS gel showing a synthetic tetramer linker that was digested using NotI and BsiWI and then inserted into tetramer expressing vector. Figure 3B is an SDS gel showing the purification of a tBsAb according to the invention.

[00022] Figure 4A is an illustration showing the method for detection of antibody binding affinity of a tBsAb. Figure 4B to Figure 4C are graphs showing data when plates were coated with CCR4-Fc (B) or with PD-L1-Fc (C) and then incubated with tetravalent bispecific (anti-CCR4 and anti-PD-L1) and control antibodies. The result showed this tetravalent antibody could bind to both CCR4-Fc and PD-L1-Fc in a dose dependent manner.

[00023] Figure 5 is a graph showing that anti-CAIX-PD-L1 bispecific mAb binds to CAIX-Fc fusion protein.

[00024] Figure 6 is a graph showing that anti-CAIX-PD-L1 bispecific mAb binds to PD-L1-Fc fusion protein.

[00025] Figure 7A is an illustration of how linker lengths can be changed to optimize bispecific mAb binding. Figure 7B is a schematic of a tBsAb sequence.

[00026] Figure 8 A. αGITR-αPD-L1 tBsAb engagement. The tBsAb binds to the GITR protein on T cells and PD-L1 protein on tumor cells. B. Schematic representation of the tBsAb format which is achieved through interchain disulfide bond formation between cysteine residues of the hinge region.

[00027] Figure 9 A. Basic structure of the two scFvs linked to form the tBsAb. Figure 9 B. Bispecific dimeric taFv directed against GITR and PD-L1. Each V_H and V_L pair is connected by a linker of 15 residues to form scFv. Two scFv are connected by a linker-hinge-linker (55 residues). The hinge region has two cysteine residues allowing the pairing of two taFv through disulfide bridges under oxidative conditions.

[00028] Figure 10 A. Basic structure of the tandem scFv. Figure 10 B. Trifunctional tBsAb directed against GITR and PD-L1 with an additional CH2 domain. Each V_H and V_L pair is connected by linker of 15 residues. Two scFv are connected by a linker-hinge-CH2-linker domain. The hinge region has two cysteine residues allowing the pairing of two tandem scFv through disulfide bridges under oxidative conditions. The N-terminal end of the CH2 domain can bind Fc-γ or C1q. The resulting format is a trifunctional tBsAb.

[00029] Figure 11 Mechanism of action of αGITR-αPD-L1 tBsAb. Figure 11 A. Tumor cells overexpress the PD-L1 protein. The PD-1/PD-L1 interaction inhibits an effective T cell activation and promotes immune suppression and adaptive immune resistance. Figure 11 B. The αGITR-αPD-L1 tBsAb may enhance immune response. The αPD-L1 arm blocks PD-1/PD-L1 pathway and may therefore inhibit T cell exhaustion and abrogate T reg suppression. The αGITR arm acts as an agonist on the co-stimulator GITR receptor, resulting in upregulation of GITR expression enhancing T cell activation and proliferation.

[00030] Figure 12 Schematic representation of the αGITR-αPD-L1 cloning process. The donor vector and the pcDNA 3.4 expression vector were digested with SfiI and NotI restriction enzymes. The V_HGITR-V_LGITR gene was isolated and subsequently ligated to each other. The final plasmid resulted in the αGITR-αPD-L1 clone.

[00031] Figure 13 Schematic representation of the control plasmid (1) cloning process. The pcDNA3.1 vector and the expression vector pcDNA 3.4 were digested with SfiI and NotI restriction enzymes. The V_HF10-V_LF10 gene was isolated and subsequently ligated to the pcDNA 3.4 expression vector. The final plasmid resulted in the αGITR-αPD-L1 clone.

[00032] Figure 14 Schematic representation of the control plasmids (2) and (3) cloning process. The isolated F10 V_H and V_L DNA and the recipient vector pcDNA 3.4 were digested with BsiWI and BamHI restriction enzymes and subsequently ligated to each other. The final plasmid resulted in the final αGITR1-αPD-L1 and αGITR10-αPD-L1 clone.

[00033] Figure 15 Schematic representation of the cloning strategy for the αGITR-αPD-L1 with CH2 construct. The HindIII restriction site was introduced into the pcDNA 3.4 expression vector by site directed mutagenesis. The isolated CH2 fragment and the expression vector were subsequently digested and ligated to each other to finalize the construct αGITR-αPD-L1 with CH2.

[00034] Figure 16 Restriction enzyme analysis (REA) of recipient pcDNA 3.4 vector, six V_HGITR-V_LGITR inserts and one V_HF10-V_LF10 insert. Shown is an ethidium bromide stained 1% agarose gel of DNA electrophoresed in TAE buffer. All plasmids were digested with SfiI and NotI restriction enzymes. Lane 1: shown is a 7.5 kb digested recipient pcDNA 3.4 vector. The lower band between 500 and 1000 bp is a previously-used scFv insert (from the Marasco Laboratory). Lanes 2-6: Lower bands represent the 800bp V_HGITR-linker-V_LGITR inserts. The larger bands clustered at 8kb are the double digested descendent vectors. Lane 7: The 800bp V_HF10-linker-V_LF10 inserts is visualized in the lower band clustered between 500 and 1000 bp. The lane “bp” represents the 1kb DNA ladder (NEB).

[00035] Figure 17 REA of V_HF10-linker-V_LF10 cDNA and recipient pcDNA 3.4 expression (containing V_HGITR1-V_LGITR1 or V_HGITR10-V_LGITR10, respectively). Shown is an ethidium bromide stained 1% agarose gel of DNA electrophoresed in TAE buffer. The recipient expression vectors and the insert were digested with BsiWI and

BamHI restriction enzymes. Lane1: shown is a single band clustered at 800bp, representing the V_HF10-linker-V_LF10 (scFv) fragment isolated by PCR. Lanes 2 and 3: The upper two bands visualize the pcDNA 3.4 expression vectors containing V_HGITR1-V_LGITR1 (lane 2) and V_HGITR10-V_LGITR10 (lane 3). Both comprise 7500 bp and can be detected at the correct level of the ladder. The lower bands in lanes 2 and 3 clustered between 500 and 1000 bp represent the digested V_HPD-L1-V_LPD-L1 fragment separated from its vector. The lane "bp" corresponds to the 1kb DNA ladder (NEB).

[00036] Figure 18 Analysis of purified tBsAbs by SDS-PAGE. Shown is a Coomassie blue stained SDS gel of protein electrophoresed in MES buffer. 3-5 μg of protein sample was loaded and separated on the gel under (A) reducing and (B) non-reducing conditions. Lanes 1-8: Under non-reducing conditions, the SDS PAGE revealed two major bands of each protein. The higher bands have an apparent molecular weight between 80kDa and 115 kDa and the lower molecular weight bands between 70 and 80kDa. In the non-reduced SDS-gel analysis, some weak but high molecular weight bands (>180 kDa) can be observed. The SDS-gel analysis under reducing conditions (10% DTT; 70°C for 10 minutes) displays only one band with an apparent molecular weight between 70 and 80 kDa. Lane 9: Under non-reducing conditions, a single band is shown with an apparent molecular weight slightly over 140 kDa. The visualization of two bands under reducing conditions emphasizes the correct expression of αGITR IgG that display separated heavy and light chains (50 kDa and 25 kDa). The lanes kDa represent the benchmark pre-stained protein ladder (Invitrogen) under the corresponding conditions (4-12% gel concentration run in MES buffer).

[00037] Figure 19 ELISA absorbance values of αGITR-αPD-L1 tBsAbs, F10-αPD-L1 tBsAb and αPD-L1 mAb tested against passively immobilized PD-L1 antigen. A concentration range of each αGITR-αPD-L1 (0.0001 mg/mL – 1 mg/mL; horizontal axis) was subjected to ELISA on PD-L1 antigen. The results show the mean and standard deviation of the absorbance at 450 nm (vertical axis). Each sample was run in triplicates at every concentration. The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00038] Figure 20 Cell-based ELISA testing αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies binding against GITR+ expressing CF2 cells fixed with acetone-methanol. The

F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:3 dilutions ranging from 3.3 mg/mL to 0.0046 mg/mL. All antibodies were tested against 1000 GITR+CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00039] Figure 21 Cell based ELISA testing αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies binding against GITR+ expressing CF2 cells fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:3 dilutions ranging from 3.3 mg/mL to 0.0046 mg/mL. All antibodies were tested against 1000 GITR+CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00040] Figure 22 Cell-based ELISA testing αGITR10-αPD-L1 and commercial αGITR10 mAb antibodies binding against GITR+ expressing CF2 cells fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:2 dilutions ranging from 5 mg/mL to 0.078 mg/mL. All antibodies were tested against 10,000 GITR+CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00041] Figure 23 A. Flow cytometric analysis of fluorescent-activated αGITR10-αPD-L1 tBsAb (anti-His Alexa 488 (APC) conjugated) tested with GITR+CF2 cells. Figure 23 B. Flow cytometric analysis of fluorescent-activated αGITR10 IgG Ab (anti human IgG Fc (FITC conjugated) tested with GITR+CF2 cells. Horizontal lines indicate the intensity signal of fluorescence and the vertical axis indicates the cell counts. Each individual picture represents different concentration of αGITR10-αPD-L1 with constant cell number.

[00042] Figure 24 A. Flow cytometric analysis of fluorescent-activated αGITR1-αPD-L1 tBsAb (anti-His Alexa 488 (APC) conjugated) tested with GITR+CF2 cells. Figure 24 B. Flow cytometric analysis of fluorescent-activated αGITR10 IgG Ab (anti human IgG Fc

(FITC conjugated) tested with GITR+CF2 cells. Horizontal lines indicate the intensity signal of fluorescence and the vertical axis indicates the cell counts. Each individual picture represents different concentration of αGITR10-αPD-L1 (Figure 24 A) and αGITR10 IgG (Figure 24 B) with constant cell number.

[00043] Figure 25 Restriction enzyme analysis (REA) of 16 clones. Shown is an ethidium bromide stained 1% agarose gel of DNA electrophoresed in TAE buffer. All plasmids were digested with HindIII and BamHI restriction enzymes. Two bands are shown in lane No.10: The band clustered between 6kb and 8kb represents the digested recipient pcDNA 3.4 vector (7.5 kb). The lower band between 500 and 1000 bp indicates a close approximation to the expected theoretical size of 800bp of the fragment isolated with HindIII and BamHI restriction enzymes. The lane "bp" represents the 1kb DNA ladder.

[00044] Figure 26 REA of clone 10 (GITR10-PDL1 with HindIII) and GITR10-PDL1 (without HindIII restriction site). Shown is an ethidium bromide stained 1% agarose gel of DNA electrophoresed in TAE buffer. Both plasmids were digested with only HindIII (lane 1), only NotI (lane 2) and with HindIII and NotI simultaneously (lane 3). The digestions of clone No.10 with a single enzyme (lanes 1 & 2) resulted one band clustered around 8000 bp. The digestion of clone No. 10 with both enzymes (lane 3) resulted in the generation of two fragments, of which the smaller-sized band is clustered below 500bp. The digestion of αGITR10-αPD-L1with only HindIII restriction site (lane 1), revealed a supercoiled plasmid DNA.

[00045] Figure 27 Restriction enzyme digestion analysis of vector GITR10-PDL1 (containing HindIII restriction site) and CH2 fragment. Shown is an ethidium bromide stained 1% agarose gel of DNA electrophoresed in TAE buffer. Lane 1: single digestion of the αGITR-αPD-L1 with HindIII. Lane 2: The CH2 fragment digested with HindIII resulted in a band clustered below the 500 bp mark of the ladder. The lane "bp" corresponds to the 1kb DNA ladder.

[00046] Figure 28 Analysis of purified αGITR10-αPD-L1 with CH2 BsAb by SDS-PAGE. Shown is a Coomassie blue stained SDS gel of protein electrophoresed in MES buffer. 3-5 μg of protein sample was loaded and separated on the gel under (R) reducing and (NR) non-reducing conditions. Under non-reducing conditions, the SDS PAGE revealed two major bands of each protein. The higher band has an apparent molecular of around 140kDa and the lower hand has a molecular weight of 80kDa, correlating with the theoretical size of dimeric (150kDa) and monomeric (75kDa) BsAbs. The SDS-gel analysis under reducing conditions (10% DTT; 70°C for 10 minutes) displays only one band with an apparent molecular weight between around 80 kDa and reinforces the correct expression of tBsAb that can be reduced by its disulfide bridges in the hinge region. The lane "kDa" represents the benchmark pre-stained protein ladder (Invitrogen) under the corresponding conditions (4-12% gel concentration run in MES buffer).

[00047] Figure 29 Cell-based ELISA testing αGITR10-αPD-L1 with CH2 and αGITR10 IgG antibodies binding against GITR+ expressing CF2 cells fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:2 dilutions ranging from 5 mg/mL to 0.16 mg/mL. All antibodies were tested against 10,000 GITR+CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00048] Figure 30 ADCC activity of αGITR10-αPD-L1 with CH2 antibody. The ADCC activity of αGITR10-αPD-L1 with CH2 and was measured at varying concentrations. All antibodies were serially diluted (1:2), starting the highest concentration at 20 mg/mL until 0.02 mg/mL and tested against 20,000 GITR+CF2 cells per well. The ratio of effector cells (GITR+CF2) to target cells (Wils-2) was 5:1. The αGITR IgG represents the positive control and F10-αPD-L1 the negative control. The vertical axis represents the raw value of luciferase activity in the effector cell quantified with luminescence readout. Each sample was run in triplicate at every concentration; the mean standard deviation is indicated in brackets. The background of GITR+CF2 cells in RPMI medium was subtracted from the obtained values.

[00049] Figure 31 αGITR10-αPD-L1 with CH2 antibody mediated CDC activity via mouse complement. Percentage of GITR+CF2 cell lysis obtained with serial dilutions of αGITR10-αPD-L1 tBsAb and the controls αGITR mAb (positive), αGITR10-αPD-L1 (negative) determined by the CDC assay. All antibodies were serially diluted (1:10), starting the highest concentration at 20 mg/mL until 0.2 mg/mL and tested against 10,000 GITR+CF2 cells per well. The vertical axis represents the percentage of lysis. It is calculated as ratio of obtained sample signal to the signal intensity from fully lysed GITR+

CF2 cells. Each sample was run in triplicate at every concentration; the mean standard deviation is indicated in brackets. The background of GITR+CF2 cells in RPMI medium was subtracted from the obtained values. Each bar represents the simple average obtained from triplicate samples (standard deviations indicated by brackets).

[00050] Figure 32 Cell-based ELISA testing αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies binding against CF2 cells (without GITR expression) fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:3 dilutions ranging from 3.3 mg/mL to 0.0046 mg/mL. All antibodies were tested against 1000 GITR-CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00051] Figure 33 Cell-based ELISA testing αGITR10-αPD-L1 and αGITR10 IgG antibodies binding against CF2 cells (without GITR expression) fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:2 dilutions ranging from 5 mg/mL to 0.078 mg/mL. All antibodies were tested against 10,000 GITR-CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00052] Figure 34 Cell-based ELISA testing αGITR10-αPD-L1 with CH2 and αGITR10 IG antibodies binding against GITR- CF2 cells fixed with 8% paraformaldehyde. The F10-αPD-L1 antibody represents the negative control. All antibodies were tested using a range of serial 1:2 dilutions ranging from 5 mg/mL to 0.16 mg/mL. All antibodies were tested against 10,000 GITR+CF2 cells per well. Each bar represents an average obtained from triplicate samples (deviations indicated by bars). The raw signal intensity was corrected for the background signal by subtracting the mean signal of wells incubated in the absence of the primary antibody from the wells where primary antibody was added.

[00053] Figure 35 Control set-up for Flow cytometric analysis of fluorescent-activated αGITR1-αPD-L1 antibody. Lanes 1 to 6 show the controls set up for GITR+ CF2 cells. Lanes 7 to 9 refer to the controls set up for GITR- CF2 cells.

DETAILED DESCRIPTION OF THE INVENTION

[00054] The invention relates to bispecific antibody contains two binding sites for each receptor (*i.e.* a tetravalent bispecific antibody or “tBsAb”), systems and methods of producing same.

[00055] The clinical development of bispecific antibodies (BsAb) as therapeutics has been hampered by the difficulty in preparing the materials in sufficient quantity and quality by traditional methods. In recent years, a variety of recombinant methods have been developed for efficient production of BsAb, both as antibody fragments and as full-length IgG-like molecules. These recombinant antibody molecules possess dual antigen-binding capability with, in most cases, monovalency to each of their target antigens. The present invention provides an efficient approach for the production of a novel tetravalent BsAb (tBsAb), with two antigen-binding sites to each of its target antigens, genetically engineering a scFV bispecific antibody and fusing the two together.

[00056] Compared to the bispecific/divalent antibody, the tBsAb binds more efficiently to both of its target antigens and is more efficacious in blocking ligand binding to the receptors. Additionally, expression of the tBsAb in mammalian cells yielded higher level of production and better antibody activity. Importantly, the tBsAbs’ exhibit higher stability and longer half-life compared to monovalent bispecific antibodies. One drawback of monovalent bispecific antibodies is their small size and therefor short serum half-life requiring administration in continuous low doses for several weeks. In contrast, the longer half-life of the tBsAbs of the invention solves this problem and therefore more suitable for clinical applications. This design and expression for tBsAb should be applicable to any pair of antigen specificities.

[00057] Preferably, the tBsAb is specific for BMCA, CAIX, CCR4, PD-L1, PD-L2, PD1, Glucocorticoid-Induced Tumor Necrosis Factor Receptors (GITR), Severe acute respiratory syndrome (SARS), influenza, flavivirus or Middle East Respiratory Syndrome (MERS).

[00058] Exemplary antibodies useful in constructing the tBsAb according to the invention includes antibodies disclosed in for example: WO/2005/060520 , WO/2006/089141, WO/2007/065027, WO/2009/086514, WO/2009/079259, WO/2011/153380, WO/2014/055897, WO 2015/143194, WO 2015/164865, WO 2013/166500, WO 2014/144061, WO 2016/057488, WO 2016/054638, WO/2016/164835, PCT/US2016/026232, PCT/US2017/050093, PCT/US2017/050327 and PCT/US2017/043504 the contents of which are hereby incorporated by reference in their entireties.

[00059] PDL1 (68)

[00060] Exemplary anti-PDL1 antibodies include antibodies having a VH nucleotide sequence having SEQ ID NO: 1485 and a VL nucleotide sequence having SEQ ID NO: 1487; a VH nucleotide sequence having SEQ ID NO: 1485 and a VL nucleotide sequence having SEQ ID NO: 1487; a VH nucleotide sequence having SEQ ID NO: 1489 and a VL nucleotide sequence having SEQ ID NO: 1491; a VH nucleotide sequence having SEQ ID NO: 1493 and a VL nucleotide sequence having SEQ ID NO: 1495; a VH nucleotide sequence having SEQ ID NO: 1497 and a VL nucleotide sequence having SEQ ID NO: 1499; a VH nucleotide sequence having SEQ ID NO: 1501 and a VL nucleotide sequence having SEQ ID NO: 1503; a VH nucleotide sequence having SEQ ID NO: 1505 and a VL nucleotide sequence having SEQ ID NO: 1507; a VH nucleotide sequence having SEQ ID NO: 1509 and a VL nucleotide sequence having SEQ ID NO: 1511; a VH nucleotide sequence having SEQ ID NO: 1513 and a VL nucleotide sequence having SEQ ID NO: 1515; a VH nucleotide sequence having SEQ ID NO: 1517 and a VL nucleotide sequence having SEQ ID NO: 1519; a VH nucleotide sequence having SEQ ID NO: 1521 and a VL nucleotide sequence having SEQ ID NO: 1523; a VH nucleotide sequence having SEQ ID NO: 1525 and a VL nucleotide sequence having SEQ ID NO: 1527; a VH nucleotide sequence having SEQ ID NO: 1529 and a VL nucleotide sequence having SEQ ID NO: 1531; a VH nucleotide sequence having SEQ ID NO: 1533 and a VL nucleotide sequence having SEQ ID NO: 1535; a VH nucleotide sequence having SEQ ID NO: 1537 and a VL nucleotide sequence having SEQ ID NO: 1539.

[00061] Exemplary anti-PDL1 antibodies include antibodies having a VH amino acid sequence having SEQ ID NO: 970 and a VL amino acid sequence having SEQ ID NO: 971; a VH amino acid having SEQ ID NO: 1486 and a VL polypeptide sequence having SEQ ID NO: 1488 a VH amino acid having SEQ ID NO: 1490 and a VL polypeptide sequence having SEQ ID NO: 1492 a VH amino acid having SEQ ID NO: 1494 and a VL polypeptide sequence having SEQ ID NO: 1496 a VH amino acid having SEQ ID NO: 1498 and a VL polypeptide sequence having SEQ ID NO: 1500 a VH amino acid having SEQ ID NO: 1502 and a VL polypeptide sequence having SEQ ID NO: 1504 a VH amino acid having SEQ ID NO: 1506 and a VL polypeptide sequence having SEQ ID NO: 1508 a VH amino acid having SEQ ID NO: 1510 and a VL polypeptide sequence having SEQ ID NO: 1512 a VH amino acid having SEQ ID NO: 1514 and a VL polypeptide sequence having SEQ ID NO: 1516 a VH amino acid having SEQ ID NO: 1518 and a VL polypeptide sequence having SEQ ID NO: 1520 a VH amino acid having SEQ ID NO: 1522 and a VL polypeptide sequence having SEQ ID NO: 1524 a VH amino acid having SEQ ID NO: 1526 and a VL polypeptide sequence having SEQ ID NO: 1528 a VH amino acid having SEQ ID NO: 1530 and a VL polypeptide sequence having SEQ ID NO: 1532 a VH amino acid having SEQ ID NO: 1534 and a VL polypeptide sequence having SEQ ID NO: 1536 a VH amino acid having SEQ ID NO: 1538 and a VL polypeptide sequence having SEQ ID NO: 1540.

[00062] In other embodiments the anti-PDL1 antibodies have a heavy chain with three CDRs including the amino acid sequences SEQ ID NO: 1541, 1554, 1569 respectively and a light chain with three CDRs including the amino acid sequences 1584, 1599, 1610 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 1543, 1556, 1571 and a light chain with three CDRs comprising the amino acid sequences 1586, 1600, 1612; or a heavy chain with three CDRs comprising the amino acid sequences 1544, 1557, 1572 and a light chain with three CDRs comprising the amino acid sequences 1587, 1601, 1613; or a heavy chain with three CDRs comprising the amino acid sequences 1545, 1558, 1573 and a light chain with three CDRs comprising the amino acid sequences 1588, 1602, 1614; or a heavy chain with three CDRs comprising the amino acid sequences 1546, 1559, 1574 and a light chain with three CDRs comprising the amino acid sequences 1589, 1603, 1615; or a heavy chain with three CDRs comprising the amino acid sequences 1547, 1560, 1575 and a light chain with three CDRs comprising the amino acid sequences 1590, 1604, 1616; or a heavy chain with three CDRs comprising the amino acid sequences 1548, 1561, 1576 and a light chain with three CDRs comprising the amino acid sequences 1591, 1605, 1617; or a heavy chain with three CDRs comprising the amino acid sequences 1541, 1562, 1577 and a light chain with three CDRs comprising the amino acid sequences 1592, 1599, 1618; or a heavy chain with three CDRs comprising the amino acid sequences 1549, 1563, 1578 and a light chain with three CDRs comprising the amino acid sequences 1593, 1606, 1619; or a heavy chain with three CDRs comprising the amino acid sequences 1550, 1564, 1579 and a light chain with three CDRs comprising the amino acid sequences 1594, 1607, 1620; or a heavy chain with three CDRs comprising the amino acid sequences 1551, 1565, 1580 and a light chain with three CDRs comprising the amino acid sequences 1595, 1599, 1621; or a heavy chain with three CDRs comprising the amino acid sequences 1542, 1566, 1581 and a light chain with three CDRs comprising the amino acid sequences 1596, 1599, 1622; or a heavy chain with three CDRs comprising the amino acid sequences 1552, 1567, 1582 and a light chain with three CDRs comprising the amino acid sequences 1597, 1608, 1623; or a heavy chain with three CDRs comprising the amino acid sequences 1553, 1568, 1583 and a light chain with three CDRs comprising the amino acid sequences 1598, 1609 1624.

[00063] SARS (26)

[00064] Exemplary SARS neutralizing antibodies include antibodies having a VH nucleotide sequence having SEQ ID NO: 1626 and a VL nucleotide sequence having SEQ ID NO: 1628; a VH nucleotide sequence having SEQ ID NO: 1630 and a VL nucleotide sequence having SEQ ID NO: 1639; a VH nucleotide sequence having SEQ ID NO: 1634 and a VL nucleotide sequence having SEQ ID NO: 1640; a VH nucleotide sequence having SEQ ID NO: 1632 and a VL nucleotide sequence having SEQ ID NO: 1641; a VH nucleotide sequence having SEQ ID NO: 1633 and a VL nucleotide sequence having SEQ ID NO: 1642; a VH nucleotide sequence having SEQ ID NO: 1634 and a VL nucleotide sequence having SEQ ID NO: 1643; a VH nucleotide sequence having SEQ ID NO: 1635 and a VL nucleotide sequence having SEQ ID NO: 1644; a VH nucleotide sequence having SEQ ID NO: 1636 and a VL nucleotide sequence having SEQ ID NO: 1645; a VH nucleotide sequence having SEQ ID NO: 1637 and a VL nucleotide sequence having SEQ ID NO: 1646

[00065] CXCR4 (33)

[00066] Exemplary anti-CXCR4 antibody include antibodies having a VH amino acid sequence having SEQ ID NO: 771 and a VL amino acid sequence having SEQ ID NO: 779; a VH amino acid sequence having SEQ ID NO: 772 and a VL amino acid sequence having SEQ ID NO: 780; a VH amino acid sequence having SEQ ID NO: 773 and a VL amino acid sequence having SEQ ID NO: 781; a VH amino acid sequence having SEQ ID NO: 774 and a VL amino acid sequence having SEQ ID NO: 782; a VH amino acid sequence having SEQ ID NO: 775 and a VL amino acid sequence having SEQ ID NO: 783; a VH amino acid sequence having SEQ ID NO: 776 and a VL amino acid sequence having SEQ ID NO: 784; a VH amino acid sequence having SEQ ID NO: 777 and a VL amino acid sequence having SEQ ID NO: 785; or a VH amino acid sequence having SEQ ID NO: 778 and a VL amino acid sequence having SEQ ID NO: 786.

[00067] In other embodiments the anti-CXCR4 antibodies have a heavy chain with three CDRs including the amino acid sequences SEQ ID NO: 803, 804, 805 respectively and a light chain with three CDRs including the amino acid sequences 806, 807, 808 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 809, 810, 811, respectively and a light chain with three CDRs comprising the amino acid sequences 812, 813, 814, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 815, 816, 817 respectively and a light chain with three CDRs comprising the amino acid sequences 818, 819, 820 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 827, 828, 829 respectively and a light chain with three CDRs comprising the amino acid sequences 830, 831, 832 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 833, 834, 835, respectively and a light chain with three CDRs comprising the amino acid sequences 836, 837, 838, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 839, 840, 841 respectively and a light chain with three CDRs comprising the amino acid sequences 842, 843, 844 respectively.

[00068] CARBONIC ANHYDRASE IX (40)

[00069] Exemplary anti-CA IX antibodies include antibodies having a VH amino acid sequence having SEQ ID NO: 845 and a VL amino acid sequence having SEQ ID NO: 846; a VH amino acid sequence having SEQ ID NO: 847 and a VL amino acid sequence having SEQ ID NO: 868; a VH amino acid sequence having SEQ ID NO: 848 and a VL amino acid sequence having SEQ ID NO: 869; a VH amino acid sequence having SEQ ID NO: 849 and a VL amino acid sequence having SEQ ID NO: 870; a VH amino acid sequence having SEQ ID NO: 850 and a VL amino acid sequence having SEQ ID NO: 871; a VH amino acid sequence having SEQ ID NO: 851 and a VL amino acid sequence having SEQ ID NO: 872; a VH amino acid sequence having SEQ ID NO: 852 and a VL amino acid sequence having

SEQ ID NO: 873; a VH amino acid sequence having SEQ ID NO: 853 and a VL amino acid sequence having SEQ ID NO: 874; a VH amino acid sequence having SEQ ID NO: 854 and a VL amino acid sequence having SEQ ID NO: 875; a VH amino acid sequence having SEQ ID NO: 855 and a VL amino acid sequence having SEQ ID NO: 876; a VH amino acid sequence having SEQ ID NO: 856 and a VL amino acid sequence having SEQ ID NO: 877; a VH amino acid sequence having SEQ ID NO: 857 and a VL amino acid sequence having SEQ ID NO: 878; a VH amino acid sequence having SEQ ID NO: 858 and a VL amino acid sequence having SEQ ID NO: 879; a VH amino acid sequence having SEQ ID NO: 859 and a VL amino acid sequence having SEQ ID NO: 880; a VH amino acid sequence having SEQ ID NO: 860 and a VL amino acid sequence having SEQ ID NO: 881; a VH amino acid sequence having SEQ ID NO: 861 and a VL amino acid sequence having SEQ ID NO: 882 a VH amino acid sequence having SEQ ID NO: 862 and a VL amino acid sequence having SEQ ID NO: 883; a VH amino acid sequence having SEQ ID NO: 863 and a VL amino acid sequence having SEQ ID NO: 884; a VH amino acid sequence having SEQ ID NO: 864 and a VL amino acid sequence having SEQ ID NO: 885; a VH amino acid sequence having SEQ ID NO: 865 and a VL amino acid sequence having SEQ ID NO: 886; a VH amino acid sequence having SEQ ID NO: 866 and a VL amino acid sequence having SEQ ID NO: 887; a VH amino acid sequence having SEQ ID NO: 867 and a VL amino acid sequence having SEQ ID NO: 888.

[00070] In other embodiments the anti-CA IX antibodies have a heavy chain with three CDRs including the amino acid sequences SEQ ID NO: 803, 804, 805 respectively and a light chain with three CDRs including the amino acid sequences 806, 807, 808 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 905, 906, 952 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 935, 943, 953 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 935, 906, 954 or a heavy chain with three CDRs comprising the amino acid sequences 910, 916, 923 and a light chain with three CDRs comprising the amino acid sequences 936, 944, 955 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 936, 944, 956 or a heavy chain with three CDRs comprising the amino acid sequences 911, 917, 924 and a light chain with three CDRs comprising the amino acid sequences 937, 945, 957 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 935, 946, 958 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 938, 946, 959 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 905, 946, 960 or a heavy chain with three CDRs comprising the amino acid sequences 899, 918, 925 and a light chain with three CDRs comprising the amino acid sequences 937, 947, 955 or a heavy chain with three CDRs comprising the amino acid sequences 899, 918, 926 and a light chain with three CDRs comprising the amino acid sequences 937, 945, 957 or a heavy chain with three CDRs comprising the amino acid sequences 912, 919, 927 and a light chain with three CDRs comprising the amino acid sequences 937, 943, 961 or a heavy chain with three CDRs comprising the amino acid sequences 899, 918, 928 and a light chain with three CDRs comprising the amino acid sequences 937, 906, 960 or a heavy chain with three CDRs comprising the amino acid sequences 899, 918, 928 and a light chain with three CDRs comprising the amino acid sequences 937, 906, 960 or a heavy chain with three CDRs comprising the amino acid sequences 913, 920, 929 and a light chain with three CDRs comprising the amino acid sequences 939, 948, 962 or a heavy chain with three CDRs comprising the amino acid sequences 899, 918, 930 and a light chain with three CDRs comprising the amino acid sequences 935, 944, 955 or a heavy chain with three CDRs comprising the amino acid sequences 899, 921, 931 and a light chain with three CDRs comprising the amino acid sequences 935, 944, 955 or a heavy chain with three CDRs comprising the amino acid sequences 912, 919 ,932 and a light chain with three CDRs comprising the amino acid sequences 940, 949, 963 or a heavy chain with three CDRs comprising the amino acid sequences 899, 915, 909 and a light chain with three CDRs comprising the amino acid sequences 935, 943, 960 or a heavy chain with three CDRs comprising the amino acid sequences 914, 922, 933 and a light chain with three CDRs comprising the amino acid sequences 941, 950, 964 or a heavy chain with three CDRs comprising the amino acid sequences 912, 918, 934 and a light chain with three CDRs comprising the amino acid sequences 942, 951, 965.

[00071] **CC-CHEMOKINE RECEPTOR 4 (CCR4) (048)**

[00072] Exemplary CC-chemokine receptor 4 (CCR4) antibodies include antibodies having a VH nucleotide sequence having SEQ ID NO: 969 and a VL nucleotide sequence having SEQ ID NO: 971; a VH nucleotide sequence having SEQ ID NO: 969 and a VL nucleotide sequence having SEQ ID NO: 972.

[00073] Exemplary CCR4 antibodies include antibodies having a VH amino acid sequence having SEQ ID NO: 970 and a VL amino acid sequence having SEQ ID NO: 971.

[00074] In other embodiments the CCR4 antibodies have a heavy chain with three CDRs including the amino acid sequences SEQ ID NO: 973, 974, 975 respectively and a light chain with three CDRs including the amino acid sequences 976, 977, 978 respectively.

[00075] **MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS (MERS-COV). (85)**

[00076] Exemplary anti-Middle East Respiratory Syndrome coronavirus (MERS-CoV) antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 677and a VL nucleotide sequence having SEQ ID NO:679; a VH nucleotide sequence having SEQ ID NO: 681and a VL nucleotide sequence having SEQ ID NO:683; a VH nucleotide sequence having SEQ ID NO: 685and a VL nucleotide sequence having SEQ ID NO:687; a VH nucleotide sequence having SEQ ID NO: 689and a VL nucleotide sequence having SEQ ID NO:692; a VH nucleotide sequence having SEQ ID NO: 693and a VL nucleotide sequence having SEQ ID NO:695; a VH nucleotide sequence having SEQ ID NO: 697and a VL nucleotide sequence having SEQ ID NO:699; and a VH nucleotide sequence having SEQ ID NO: 701and a VL nucleotide sequence having SEQ ID NO:703.

[00077] Exemplary anti-Middle East Respiratory Syndrome coronavirus (MERS-CoV) antibody include antibodies having a VH amino acid sequence SEQ ID NO: 678 and a VL amino acid sequence having SEQ ID NO: 680; a VH amino acid sequence SEQ ID NO: 682 and a VL amino acid sequence having SEQ ID NO: 684; a VH amino acid sequence SEQ ID NO: 686 and a VL amino acid sequence having SEQ ID NO: 688; a VH amino acid sequence SEQ ID NO: 690 and a VL amino acid sequence having SEQ ID NO: 692; a VH amino acid sequence SEQ ID NO: 694 and a VL amino acid sequence having SEQ ID NO: 696; a VH amino acid sequence SEQ ID NO: 698 and a VL amino acid sequence having SEQ ID NO: 700; and a VH amino acid sequence SEQ ID NO: 702 and a VL amino acid sequence having SEQ ID NO: 704.

[00078] In other embodiments the anti-Middle East Respiratory Syndrome coronavirus (MERS-CoV) antibody has a heavy chain with three CDRs including the amino acid sequences of 705, 706, and 707 and a light chain with three CDRs including the amino acid sequences 722, 723, and 724; a heavy chain with three CDRs including the amino acid sequences of 708, 709, and 710 and a light chain with three CDRs including the amino acid sequences 725, 726, and 727; a heavy chain with three CDRs including the amino acid sequences of 711, 712, and 713 and a light chain with three CDRs including the amino acid sequences 728, 729, and 730; a heavy chain with three CDRs including the amino acid sequences of 711, 735, and 715 and a light chain with three CDRs including the amino acid sequences 731, 732, and 733; a heavy chain with three CDRs including the amino acid sequences of 711, 735, and 716 and a light chain with three CDRs including the amino acid sequences 737, 738, and 739; a heavy chain with three CDRs including the amino acid sequences of 717, 718, and 719 and a light chain with three CDRs including the amino acid sequences 736, 742, and 743; and a heavy chain with three CDRs including the amino acid sequences of 714, 720, and 721 and a light chain with three CDRs including the amino acid sequences 740, 729, and 741.

[00079] **GITR (93)**

[00080] Exemplary anti-human GITR antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 1361 and a VL nucleotide sequence having SEQ ID NO: 1363; a VH nucleotide sequence having SEQ ID NO: 1365 and a VL nucleotide sequence having SEQ ID NO:1367; a VH nucleotide sequence having SEQ ID NO: 1369 and a VL nucleotide sequence having SEQ ID NO: 1371; a VH nucleotide sequence having SEQ ID NO: 1381 and a VL nucleotide sequence having SEQ ID NO: 1375; a VH nucleotide sequence having SEQ ID NO: 1377 and a VL nucleotide sequence having SEQ ID NO: 1379; a VH nucleotide sequence having SEQ ID NO: 1381 and a VL nucleotide sequence having SEQ ID NO: 1383; a VH nucleotide sequence having SEQ ID NO: 1385 and a VL nucleotide sequence having SEQ ID NO: 1387; a VH nucleotide sequence having SEQ ID NO: 1389 and a VL nucleotide sequence having SEQ ID NO:1391; a VH nucleotide sequence having SEQ ID NO: 1393 and a VL nucleotide sequence having SEQ ID NO: 1395; a VH nucleotide sequence having SEQ ID NO: 1397 and a VL nucleotide sequence having SEQ ID NO: 1398; or a VH nucleotide sequence having SEQ ID NO: 1401and a VL nucleotide sequence having SEQ ID NO: 1403.

[00081] Exemplary anti-human GITR antibody include antibodies having a VH amino acid sequence having SEQ ID NO: 1362 and a VL amino acid sequence having SEQ ID NO: 1364; a VH amino acid having SEQ ID NO: 1366 and a VL polypeptide sequence having SEQ ID NO:1368; a VH amino acid sequence having SEQ ID NO: 1371 and a VL amino acid sequence having SEQ ID NO: 1372; a VH amino acid sequence having SEQ ID NO: 1382 and a VL amino acid sequence having SEQ ID NO: 1376; a VH nucleotide sequence having SEQ ID NO: 1378 and a VL nucleotide sequence having SEQ ID NO: 1380; a VH amino acid having SEQ ID NO: 1382 and a VL polypeptide sequence having SEQ ID NO: 1384; a VH amino acid sequence having SEQ ID NO: 1386 and a VL amino acid sequence having SEQ ID NO: 1388; a VH amino acid sequence having SEQ ID NO: 1390 and a VL amino acid sequence having SEQ ID NO: 1392; a VH amino acid having SEQ ID NO: 1394 and a VL polypeptide sequence having SEQ ID NO: 1396; a VH amino acid sequence having SEQ ID NO: 1399 and a VL amino acid sequence having SEQ ID NO: 1400; or a VH amino acid sequence having SEQ ID NO: 1402 and a VL amino acid sequence having SEQ ID NO: 1404.

[00082] In other embodiments the anti-human GITR antibody has a heavy chain with three CDRs including the amino acid sequences 1405, 1406, and 1407 and a light chain with three CDRs including the amino acid sequences1408, 1409, and 1410 respectively; a heavy chain with three CDRs including the amino acid sequences 1411, 1412, and 1413 and a light chain with three CDRs including the amino acid sequences1414, 1415, and 1416 respectively; a heavy chain with three CDRs including the amino acid sequences 1417, 1418, and 1419 and a light chain with three CDRs including the amino acid sequences1420, 1421, and 1422 respectively; a heavy chain with three CDRs including the amino acid sequences 1423, 1424, and 1425 and a light chain with three CDRs including the amino acid sequences1426, 1427, and 1428 respectively; a heavy chain with three CDRs including the amino acid sequences 1429, 1430, and 1431 and a light chain with three CDRs including the amino acid sequences1432, 1433, and 1434 respectively; a heavy chain with three CDRs including the amino acid sequences 1435, 1436, and 1437 and a light chain with three CDRs including the amino acid sequences1438, 1439, and 1440 respectively; a heavy chain with three CDRs including the amino acid sequences 1441, 1442, and 1443 and a light chain with three CDRs including the amino acid sequences1444, 1445, and 1446 respectively; a heavy chain with three CDRs including the amino acid sequences 1447, 1448, and 1449 and a light chain with three CDRs including the amino acid sequences1450, 1451, and 1452 respectively; a heavy chain with three CDRs including the amino acid sequences 1453, 1454, and 1455 and a light chain with three CDRs including the amino acid sequences1456, 1457, and 1458 respectively; a heavy chain with three CDRs including the amino acid sequences 1459, 1460, and 1461 and a light chain with three CDRs including the amino acid sequences1462, 1463, and 1464 respectively; or a heavy chain with three CDRs including the amino acid sequences 1465, 1466, and 1467 and a light chain with three CDRs including the amino acid sequences1468, 1469, and 1470 respectively.

[00083] FLAVIVIRUS (73)

[00084] Exemplary anti-West Nile virus envelope protein E (WNE) antibody include antibodies having a VH nucleotide sequence having a VH amino acid sequence having SEQ ID NO: 1224 and a VL amino acid sequence having SEQ ID NO: 1226.

[00085] Exemplary anti-West Nile virus envelope protein E (WNE) antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 1225 and a VL nucleotide sequence having SEQ ID NO: 1227.

[00086] In other embodiments the anti-West Nile virus envelope protein E (WNE) antibody has a heavy chain with three CDRs including the amino acid sequences 1244, 1245, and 1246 and a light chain with three CDRs including the amino acid sequences 1247, 1248, and 1249 respectively.

[00087] CCR4 (65)

[00088] Exemplary anti-CC-chemokine receptor 4 (CCR4) antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 1329 and a VL nucleotide sequence having SEQ ID NO: 1331; a VH nucleotide sequence having SEQ ID NO: 1333 and a VL nucleotide sequence having SEQ ID NO:1335; a VH nucleotide sequence having SEQ ID NO: 1337 and a VL nucleotide sequence having SEQ ID NO: 1192; a VH nucleotide sequence having SEQ ID NO: 1341 and a VL nucleotide sequence having SEQ ID NO: 1343; or a VH nucleotide sequence having SEQ ID NO: 1357 and a VL nucleotide sequence having SEQ ID NO:1359.

[00089] Exemplary anti-CC-chemokine receptor 4 (CCR4) antibody include antibodies having a VH amino acid sequence having SEQ ID NO: 1330 and a VL amino acid sequence having SEQ ID NO: 1332; a VH amino acid sequence having SEQ ID NO: 1334 and a VL amino acid sequence having SEQ ID NO: 1336; a V_H amino acid sequence having SEQ ID NO: 1338 and a V_L amino acid sequence having SEQ ID NO: 1340; a V_H amino acid sequence having SEQ ID NO: 1342 and a V_L amino acid sequence having SEQ ID NO: 1344; or a V_H amino acid sequence having SEQ ID NO: 1358 and a V_L amino acid sequence having SEQ ID NO: 1360.

[00090] In other embodiments the anti-CC-chemokine receptor 4 (CCR4) antibody has a heavy chain with three CDRs including the amino acid sequences 1203, 1208, and 1211 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1216 respectively; or a heavy chain with three CDRs including the amino acid sequences 1204, 1208, and 1212 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1217 respectively; or a heavy chain with three CDRs including the amino acid sequences 1204, 1208, and 1213 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1217 respectively; or a heavy chain with three CDRs including the amino acid sequences 1205, 1208, and 1214 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1218 respectively; or a heavy chain with three CDRs including the amino acid sequences 1206, 1208, and 1210 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1220 respectively; or a heavy chain with three CDRs including the amino acid sequences 1202, 1208, and 1210 and a light chain with three CDRs including the amino acid sequences 1207, 1209, and 1219 respectively.

[00091] HUMAN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION GERMLINE GENE VH1-69 (57)

[00092] Exemplary anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 1153 and a VL nucleotide sequence having SEQ ID NO: 1155; or a VH nucleotide sequence having SEQ ID NO: 1163 and a VL nucleotide sequence having SEQ ID NO:1155.

[00093] Exemplary anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibody include antibodies having a V_H amino acid sequence having SEQ ID NO: 1154 and a V_L amino acid sequence having SEQ ID NO: 1156; or a V_H amino acid sequence having SEQ ID NO: 1164 and a V_L amino acid sequence having SEQ ID NO: 1156.

[00094] In other embodiments the anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibody has a heavy chain with three CDRs including the amino acid sequences 1157, 1158, and 1159 and a light chain with three CDRs including the amino acid sequences 1160, 1161, and 1162 respectively.

[00095] **INFLUENZA (49)**

[00096] Exemplary anti-influenza antibody include antibodies having a VH nucleotide sequence having SEQ ID NO: 981 and a VL nucleotide sequence having SEQ ID NO: 983; a VH nucleotide sequence having SEQ ID NO: 985 and a VL nucleotide sequence having SEQ ID NO: 989; a VH nucleotide sequence having SEQ ID NO: 987 and a VL nucleotide sequence having SEQ ID NO: 991; a VH nucleotide sequence having SEQ ID NO: 993 and a VL nucleotide sequence having SEQ ID NO: 997; a VH nucleotide sequence having SEQ ID NO: 995 and a VK nucleotide sequence having SEQ ID NO: 999; a VH nucleotide sequence having SEQ ID NO: 1001 and a VL nucleotide sequence having SEQ ID NO: 1005; a VH nucleotide sequence having SEQ ID NO: 1003 and a VL nucleotide sequence having SEQ ID NO: 1007; a VH nucleotide sequence having SEQ ID NO: 1009 and a VL nucleotide sequence having SEQ ID NO: 1011; a VH nucleotide sequence having SEQ ID NO: 1013 and a VL nucleotide sequence having SEQ ID NO: 1015; and a VH nucleotide sequence having SEQ ID NO: 1017 and a VK nucleotide sequence having SEQ ID NO: 1019; a VH nucleotide sequence having SEQ ID NO: 1020 and a VL nucleotide sequence having SEQ ID NO: 1022.

[00097] Exemplary anti-influenza antibody include antibodies having a VH amino acid sequence having SEQ ID NO: 982 and a VL amino acid sequence having SEQ ID NO: 984; a VH amino acid sequence having SEQ ID NO: 986 and a VL amino acid sequence having SEQ ID NO: 988; a VH amino acid sequence having SEQ ID NO: 986 and a VL amino acid sequence having SEQ ID NO: 990; a VH amino acid sequence having SEQ ID NO: 992 and a VL amino acid sequence having SEQ ID NO: 994; a VH amino acid sequence having SEQ ID NO: 992 and a VK amino acid sequence having SEQ ID NO: 996; a VH amino acid sequence having SEQ ID NO: 998 and a VL amino acid sequence having SEQ ID NO: 1000; a VH amino acid sequence having SEQ ID NO: 998 and a VL amino acid sequence having SEQ ID NO: 1002; a VH amino acid sequence having SEQ ID NO: 1004 and a VL amino acid sequence having SEQ ID NO: 1006; a VH amino acid sequence having SEQ ID NO: 1008 and a VL amino acid sequence having SEQ ID NO: 1010; a VH amino acid sequence having SEQ ID NO: 1012 and a VK amino acid sequence having SEQ ID NO: 1014; and a VH amino acid sequence having SEQ ID NO: 1016 and a VL amino acid sequence having SEQ ID NO: 1018.

[00098] In other embodiments the anti-influenza antibody has a heavy chain with three CDRs including the amino acid sequences of 1023, 1031, and 1039 and a light chain with three CDRs including the amino acid sequences 1047, 1059, and 1071; a heavy chain with three CDRs including the amino acid sequences of 1023, 1032, and 1040 and a light chain with three CDRs including the amino acid sequences 1048, 1060, and 1072; a heavy chain with three CDRs including the amino acid sequences of 1025, 1032, and 1040 and a light chain with three CDRs including the amino acid sequences 1057, 1069, and 1081; a heavy chain with three CDRs including the amino acid sequences of 1026, 1033, and 1041 and a light chain with three CDRs including the amino acid sequences 1049, 1061, and 1073; a heavy chain with three CDRs including the amino acid sequences of 1026, 1033, and 1041 and a light chain with three CDRs including the amino acid sequences 1054, 1066, and 1078; a heavy chain with three CDRs including the amino acid sequences of 1027, 1034, and 1042 and a light chain with three CDRs including the amino acid sequences 1050, 1062, and 1074; a heavy chain with three CDRs including the amino acid sequences of 1027, 1034, and 1042 and a light chain with three CDRs including the amino acid sequences 1056, 1068, and 1080; a heavy chain with three CDRs including the amino acid sequences of 1028, 1035, and 1043 and a light chain with three CDRs including the amino acid sequences 1051, 1063, and 1065; a heavy chain with three CDRs including the amino acid sequences of 1028, 1036, and 1044 and a light chain with three CDRs including the amino acid sequences 1052, 1064, and 1076; a heavy chain with three CDRs including the amino acid sequences of 1029, 1037, and 1045 and a light chain with three CDRs including the amino acid sequences 1053, 1065, and 1077; or a heavy chain with three CDRs including the amino acid sequences of 1030, 1038, and 1046 and a light chain with three CDRs including the amino acid sequences 1058, 1070, and 1082.

[00099] **Influenza (78)**

[000100] Exemplary anti-influenza antibodies include antibodies having a VH nucleotide sequence having SEQ ID NO: 397 and a VL nucleotide sequence having SEQ ID NO: 398; a VH nucleotide sequence having SEQ ID NO: 399 and a VL nucleotide sequence having SEQ ID NO:400; a VH nucleotide sequence having SEQ ID NO: 401 and a VL nucleotide sequence having SEQ ID NO: 402; a VH nucleotide sequence having SEQ ID NO: 403 and a VL nucleotide sequence having SEQ ID NO: 404; or a VH nucleotide sequence having SEQ ID NO: 405 and a VL nucleotide sequence having SEQ ID NO:406; or a VH nucleotide sequence having SEQ ID NO: 407 and a VL nucleotide sequence having SEQ ID NO:408; or a VH nucleotide sequence having SEQ ID NO: 409 and a VL nucleotide sequence having SEQ ID NO:410; or a VH nucleotide sequence having SEQ ID NO: 411 and a VL nucleotide sequence having SEQ ID NO:412; or a VH nucleotide sequence having SEQ ID NO: 413 and a VL nucleotide sequence having SEQ ID NO:414; or a VH nucleotide sequence having SEQ ID NO: 415 and a VL nucleotide sequence having SEQ ID NO:416; or a VH nucleotide sequence having SEQ ID NO: 417 and a VL nucleotide sequence having SEQ ID NO:418; or a VH nucleotide sequence having SEQ ID NO: 419 and a VL nucleotide sequence having SEQ ID NO:420;or a VH nucleotide sequence having SEQ ID NO: 421 and a VL nucleotide sequence having SEQ ID NO:422; or a VH nucleotide sequence having SEQ ID NO: 423 and a VL nucleotide sequence having SEQ ID NO:424; or a VH nucleotide sequence having SEQ ID NO: 425 and a VL nucleotide sequence having SEQ ID NO:426; or a VH nucleotide sequence having SEQ ID NO: 427 and a VL nucleotide sequence having SEQ ID NO:428; or a VH nucleotide sequence having SEQ ID NO: 429 and a VL nucleotide sequence having SEQ ID NO:430; or a VH nucleotide sequence having SEQ ID NO: 431 and a VL nucleotide sequence having SEQ ID NO:432; or a VH nucleotide sequence having SEQ ID NO: 433 and a VL nucleotide sequence having SEQ ID NO:434; or a VH nucleotide sequence having SEQ ID NO: 435 and a VL nucleotide sequence having SEQ ID NO:436; or a VH nucleotide sequence having SEQ ID NO: 437 and a VL nucleotide sequence having SEQ ID NO:438; or a VH nucleotide sequence having SEQ ID NO: 439 and a VL nucleotide sequence having SEQ ID NO:440; or a VH nucleotide sequence having SEQ ID NO: 441 and a VL nucleotide sequence having SEQ ID NO:442; ; or a VH nucleotide sequence having SEQ ID NO: 541 and a VL nucleotide sequence having SEQ ID NO: 542 ; or a VH nucleotide sequence having SEQ ID NO: 543 and a VL nucleotide sequence having SEQ ID NO: 544 ; or a VH nucleotide sequence having SEQ ID NO: 545 and a VL nucleotide sequence having SEQ ID NO: 546 ; or a VH nucleotide sequence having SEQ ID NO: 547 and a VL nucleotide sequence having SEQ ID NO: 548 ; or a VH nucleotide sequence having SEQ ID NO: 549 and a VL nucleotide sequence having SEQ ID NO: 550 ; or a VH nucleotide sequence having SEQ ID NO: 551 and a VL nucleotide sequence having SEQ ID NO: 552 ; or a VH nucleotide sequence having SEQ ID NO: 553 and a VL nucleotide sequence having SEQ ID NO: 554 ; or a VH nucleotide sequence having SEQ ID NO: 555 and a VL nucleotide sequence having SEQ ID NO: 556 ; or a VH nucleotide sequence having SEQ ID NO: 557 and a VL nucleotide sequence having SEQ ID NO: 558 ; or a VH nucleotide sequence having SEQ ID NO: 559 and a VL nucleotide sequence having SEQ ID NO: 560 ; or a VH nucleotide sequence having SEQ ID NO: 561 and a VL nucleotide sequence having SEQ ID NO: 562 ; or a VH nucleotide sequence having SEQ ID NO: 563 and a VL nucleotide sequence having SEQ ID NO: 564 ; or a VH nucleotide sequence having SEQ ID NO: 565 and a VL nucleotide sequence having SEQ ID NO: 566 ; or a VH nucleotide sequence having SEQ ID NO: 567 and a VL nucleotide sequence having SEQ ID NO: 568 ; or a VH nucleotide sequence having SEQ ID NO: 569 and a VL nucleotide sequence having SEQ ID NO: 570 ; or a VH nucleotide sequence having SEQ ID NO: 571 and a VL nucleotide sequence having SEQ ID NO: 572 ; or a VH nucleotide sequence having SEQ ID NO: 573 and a VL nucleotide sequence having SEQ ID NO: 574 ; or a VH nucleotide sequence having SEQ ID NO: 575 and a VL nucleotide sequence having SEQ ID NO: 576 ; or a VH nucleotide sequence having SEQ ID NO: 577 and a VL nucleotide sequence having SEQ ID NO: 578 ; or a VH nucleotide sequence having SEQ ID NO: 579 and a VL nucleotide sequence having SEQ ID NO: 580 ; or a VH nucleotide sequence having SEQ ID NO: 581 and a VL nucleotide sequence having SEQ ID NO: 582 ; or a VH nucleotide sequence having SEQ ID NO: 583 and a VL nucleotide sequence having SEQ ID NO: 584 ; or a VH nucleotide sequence having SEQ ID NO: 585 and a VL nucleotide sequence having SEQ ID NO: 586 ; or a VH nucleotide sequence having SEQ ID NO: 587 and a VL nucleotide sequence having SEQ ID NO: 588 ; or a VH nucleotide sequence having SEQ ID NO: 589 and a VL nucleotide sequence having SEQ ID NO: 590 ; or a VH nucleotide sequence having SEQ ID NO: 591 and a VL nucleotide sequence having SEQ ID NO: 592 ; or a VH nucleotide sequence having SEQ ID NO: 593 and a VL nucleotide sequence having SEQ ID NO: 594 ; or a VH nucleotide sequence having SEQ ID NO: 595 and a VL nucleotide sequence having SEQ ID NO: 596 ; or a VH nucleotide sequence having SEQ ID NO: 597 and a VL nucleotide sequence having SEQ ID NO: 598 ; or a VH nucleotide sequence having SEQ ID NO: 599 and a VL nucleotide sequence having SEQ ID NO: 600.

[000101] Exemplary anti-influenza antibodies antibody include antibodies having a VH amino acid sequence having SEQ ID NO: 469 and a VL amino acid sequence having SEQ ID

NO: 470; a VH amino acid having SEQ ID NO: 471 and a VL polypeptide sequence having SEQ ID NO:472; a VH amino acid sequence having SEQ ID NO: 473 and a VL amino acid sequence having SEQ ID NO: 474; a VH amino acid sequence having SEQ ID NO: 475 and a VL amino acid sequence having SEQ ID NO: 476; or a VH nucleotide sequence having SEQ ID NO: 477 and a VL nucleotide sequence having SEQ ID NO:478; a VH amino acid sequence having SEQ ID NO: 479 and a VL amino acid sequence having SEQ ID NO: 480; a VH amino acid sequence having SEQ ID NO: 481 and a VL amino acid sequence having SEQ ID NO: 482; a VH amino acid sequence having SEQ ID NO: 483 and a VL amino acid sequence having SEQ ID NO: 484; a VH amino acid sequence having SEQ ID NO: 485 and a VL amino acid sequence having SEQ ID NO: 486; a VH amino acid sequence having SEQ ID NO: 487 and a VL amino acid sequence having SEQ ID NO: 488; a VH amino acid sequence having SEQ ID NO: 489 and a VL amino acid sequence having SEQ ID NO: 490; a VH amino acid sequence having SEQ ID NO: 491 and a VL amino acid sequence having SEQ ID NO: 492; a VH amino acid sequence having SEQ ID NO: 493 and a VL amino acid sequence having SEQ ID NO: 494; a VH amino acid sequence having SEQ ID NO: 495 and a VL amino acid sequence having SEQ ID NO: 496; a VH amino acid sequence having SEQ ID NO: 497 and a VL amino acid sequence having SEQ ID NO: 498; a VH amino acid sequence having SEQ ID NO: 499 and a VL amino acid sequence having SEQ ID NO: 500; a VH amino acid sequence having SEQ ID NO: 501 and a VL amino acid sequence having SEQ ID NO: 502; a VH amino acid sequence having SEQ ID NO: 503 and a VL amino acid sequence having SEQ ID NO: 504; a VH amino acid sequence having SEQ ID NO: 505 and a VL amino acid sequence having SEQ ID NO: 506; a VH amino acid sequence having SEQ ID NO: 507 and a VL amino acid sequence having SEQ ID NO: 508; a VH amino acid sequence having SEQ ID NO: 509 and a VL amino acid sequence having SEQ ID NO: 510; a VH amino acid sequence having SEQ ID NO: 511 and a VL amino acid sequence having SEQ ID NO: 512; a VH amino acid sequence having SEQ ID NO: 513 and a VL amino acid sequence having SEQ ID NO: 514; a VH amino acid sequence having SEQ ID NO: 515 and a VL amino acid sequence having SEQ ID NO: 516; a VH amino acid sequence having SEQ ID NO: 517 and a VL amino acid sequence having SEQ ID NO: 518; a VH amino acid sequence having SEQ ID NO: 519 and a VL amino acid sequence having SEQ ID NO: 520; a VH amino acid sequence having SEQ ID NO: 521 and a VL amino acid sequence having SEQ ID NO: 522; a VH amino acid sequence having SEQ ID NO: 523 and a VL amino acid sequence having SEQ ID NO: 524; a VH amino acid sequence having SEQ ID NO: 525 and a VL amino acid sequence having SEQ ID NO: 526; a VH amino acid sequence having SEQ ID NO: 527 and a VL amino acid sequence having SEQ ID NO: 528; a VH amino acid sequence having SEQ ID NO: 529 and a VL amino acid sequence having SEQ ID NO: 530; a VH amino acid sequence having SEQ ID NO: 531 and a VL amino acid sequence having SEQ ID NO: 532; a VH amino acid sequence having SEQ ID NO: 533 and a VL amino acid sequence having SEQ ID NO: 534; a VH amino acid sequence having SEQ ID NO: 535 and a VL amino acid sequence having SEQ ID NO: 536; a VH amino acid sequence having SEQ ID NO: 537 and a VL amino acid sequence having SEQ ID NO: 538; a VH amino acid sequence having SEQ ID NO: 539 and a VL amino acid sequence having SEQ ID NO: 540 a VH amino acid sequence having SEQ ID NO: 601 and a VL amino acid sequence having SEQ ID NO: 602 a VH amino acid sequence having SEQ ID NO: 603 and a VL amino acid sequence having SEQ ID NO: 604 a VH amino acid sequence having SEQ ID NO: 605 and a VL amino acid sequence having SEQ ID NO: 606 a VH amino acid sequence having SEQ ID NO: 607 and a VL amino acid sequence having SEQ ID NO: 608 a VH amino acid sequence having SEQ ID NO: 609 and a VL amino acid sequence having SEQ ID NO: 610 a VH amino acid sequence having SEQ ID NO: 611 and a VL amino acid sequence having SEQ ID NO: 612 a VH amino acid sequence having SEQ ID NO: 613 and a VL amino acid sequence having SEQ ID NO: 614 a VH amino acid sequence having SEQ ID NO: 615 and a VL amino acid sequence having SEQ ID NO: 616 a VH amino acid sequence having SEQ ID NO: 617 and a VL amino acid sequence having SEQ ID NO: 618 a VH amino acid sequence having SEQ ID NO: 619 and a VL amino acid sequence having SEQ ID NO: 620 a VH amino acid sequence having SEQ ID NO: 621 and a VL amino acid sequence having SEQ ID NO: 622 a VH amino acid sequence having SEQ ID NO: 623 and a VL amino acid sequence having SEQ ID NO: 624 a VH amino acid sequence having SEQ ID NO: 625 and a VL amino acid sequence having SEQ ID NO: 626 a VH amino acid sequence having SEQ ID NO: 627 and a VL amino acid sequence having SEQ ID NO: 628 a VH amino acid sequence having SEQ ID NO: 629 and a VL amino acid sequence having SEQ ID NO: 630 a VH amino acid sequence having SEQ ID NO: 631 and a VL amino acid sequence having SEQ ID NO: 632 a VH amino acid sequence having SEQ ID NO: 633 and a VL amino acid sequence having SEQ ID NO: 634 a VH amino acid sequence having SEQ ID NO: 635 and a VL amino acid sequence having SEQ ID NO: 636 a VH amino acid sequence having SEQ ID NO: 637 and a VL amino acid sequence having SEQ ID NO: 638 a VH amino acid sequence having SEQ ID NO: 639 and a VL amino acid sequence having SEQ ID NO: 640 a VH amino acid sequence having SEQ ID NO: 641 and a VL amino acid sequence having SEQ ID NO: 642 a VH amino acid sequence having SEQ ID NO: 643 and a VL amino acid sequence having SEQ ID NO: 644 a VH amino acid sequence having SEQ ID NO: 645 and a VL amino acid sequence having SEQ ID NO: 646 a VH amino acid sequence having SEQ ID NO: 647 and a VL amino acid sequence having SEQ ID NO: 648 a VH amino acid sequence having SEQ ID NO: 649 and a VL amino acid sequence having SEQ ID NO: 650 a VH amino acid sequence having SEQ ID NO: 651 and a VL amino acid sequence having SEQ ID NO: 652 a VH amino acid sequence having SEQ ID NO: 653 and a VL amino acid sequence having SEQ ID NO: 654 a VH amino acid sequence having SEQ ID NO: 655 and a VL amino acid sequence having SEQ ID NO: 656 a VH amino acid sequence having SEQ ID NO: 657 and a VL amino acid sequence having SEQ ID NO: 658 a VH amino acid sequence having SEQ ID NO: 659 and a VL amino acid sequence having SEQ ID NO: 660.

[000102] In other embodiments the anti-influenza antibodies antibody has a heavy chain with three CDRs including the amino acid sequences SEQ ID NO: 1, 37, 73 respectively and a light chain with three CDRs including the amino acid sequences 109, 145, 181 respectively; or a heavy chain with three CDRs comprising the amino acid sequences 2, 38, 74 respectively and a light chain with three CDRs comprising the amino acid sequences 110, 146, 182, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 3, 39, 75 respectively and a light chain with three CDRs comprising the amino acid sequences 111, 147, 183, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 4, 40, 76 respectively and a light chain with three CDRs comprising the amino acid sequences 112, 148, 184, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 5, 41, 77 respectively and a light chain with three CDRs comprising the amino acid sequences 113, 149, 185, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 6, 42, 78 respectively and a light chain with three CDRs comprising the amino acid sequences 114, 150, 186, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 7, 43, 79 respectively and a light chain with three CDRs comprising the amino acid sequences

115, 151, 187, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 8, 44, 80 respectively and a light chain with three CDRs comprising the amino acid sequences 116, 152, 188, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 9, 45, 81 respectively and a light chain with three CDRs comprising the amino acid sequences 117, 153, 189, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 10, 46, 82 respectively and a light chain with three CDRs comprising the amino acid sequences 118, 154, 190, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 11, 47, 83 respectively and a light chain with three CDRs comprising the amino acid sequences 119, 155, 191, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 12, 48, 84 respectively and a light chain with three CDRs comprising the amino acid sequences 120, 156, 192, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 13, 49, 85 respectively and a light chain with three CDRs comprising the amino acid sequences 121, 157, 193, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 14, 50, 86 respectively and a light chain with three CDRs comprising the amino acid sequences 122, 158, 194, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 15, 51, 87 respectively and a light chain with three CDRs comprising the amino acid sequences 123, 159, 195, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 16, 52, 88 respectively and a light chain with three CDRs comprising the amino acid sequences 124, 160, 196, respectively; ; or a heavy chain with three CDRs comprising the amino acid sequences 17, 53, 89 respectively and a light chain with three CDRs comprising the amino acid sequences 125, 161, 197, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 18, 54, 90 respectively and a light chain with three CDRs comprising the amino acid sequences 126, 162, 198, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 19, 55, 91 respectively and a light chain with three CDRs comprising the amino acid sequences 127, 163, 199, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 20, 56, 92 respectively and a light chain with three CDRs comprising the amino acid sequences 128, 164, 200, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 21, 57, 93 respectively and a light chain with three CDRs comprising the amino acid sequences 129, 165, 201, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 22, 58, 94 respectively and a light chain with three CDRs comprising the amino acid sequences 130, 166, 202, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 23, 59, 95 respectively and a light chain with three CDRs comprising the amino acid sequences 131, 167, 203, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 24, 60, 96 respectively and a light chain with three CDRs comprising the amino acid sequences 132, 168, 204, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 25, 61, 95 respectively and a light chain with three CDRs comprising the amino acid sequences 133, 169, 205, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 26, 62, 96 respectively and a light chain with three CDRs comprising the amino acid sequences 134, 170, 206, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 27, 63, 97 respectively and a light chain with three CDRs comprising the amino acid sequences 135, 171, 207, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 28, 64, 98 respectively and a light chain with three CDRs comprising the amino acid sequences 136, 172, 208, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 29, 65, 99 respectively and a light chain with three CDRs comprising the amino acid sequences 137, 173, 209, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 30, 66, 100 respectively and a light chain with three CDRs comprising the amino acid sequences 138, 174, 210, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 31, 67, 101 respectively and a light chain with three CDRs comprising the amino acid sequences 139, 175, 211, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 32, 68, 102 respectively and a light chain with three CDRs comprising the amino acid sequences 140, 176, 212, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 33, 69, 103 respectively and a light chain with three CDRs comprising the amino acid sequences 141, 177, 213, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 34, 70, 104 respectively and a light chain with three CDRs comprising the amino acid sequences 142, 178, 214, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 35, 71, 105 respectively and a light chain with three CDRs comprising the amino acid sequences 143, 179, 215, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 36, 72, 106 respectively and a light chain with three CDRs comprising the amino acid sequences 144, 180, 216, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 217, 247, 277 respectively and a light chain with three CDRs comprising the amino acid sequences 307, 337, 367, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 218, 248, 278 respectively and a light chain with three CDRs comprising the amino acid sequences 308, 338, 368, respectively; ; or a heavy chain with three CDRs comprising the amino acid sequences 219, 249, 279 respectively and a light chain with three CDRs comprising the amino acid sequences 309, 339, 369, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 220, 250, 280 respectively and a light chain with three CDRs comprising the amino acid sequences 310, 340, 370, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 221, 251, 281 respectively and a light chain with three CDRs comprising the amino acid sequences 311, 341, 371, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 222, 252, 282 respectively and a light chain with three CDRs comprising the amino acid sequences 312, 342, 372, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 223, 253, 283 respectively and a light chain with three CDRs comprising the amino acid sequences 313, 343, 373, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 224, 254, 284 respectively and a light chain with three CDRs comprising the amino acid sequences 314, 344, 374, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 225, 255, 285 respectively and a light chain with three CDRs comprising the amino acid sequences 315, 345, 375, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 226, 256, 286 respectively and a light chain with three CDRs comprising the amino acid sequences 316, 346, 376, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 227, 257, 287 respectively and a light chain with three CDRs comprising the amino acid sequences 317, 347, 377, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 228, 258, 288 respectively and a light chain with three CDRs comprising the amino acid sequences 318, 348, 378, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 229, 259, 289 respectively and a light chain with three CDRs comprising the amino acid sequences 319, 349, 379, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 230, 260, 290 respectively and a light chain with three CDRs comprising the amino acid sequences 320, 350, 380, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 231, 261, 291 respectively and a light chain with three CDRs comprising the amino acid sequences 321, 351, 381, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 232, 262, 292 respectively and a light chain with three CDRs comprising the amino acid sequences 322, 352, 382, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 233, 263, 293 respectively and a light chain with three CDRs comprising the amino acid sequences 323, 353, 383, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 234, 273, 294 respectively and a light chain with three CDRs comprising the amino acid sequences 324, 354, 384, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 235, 274, 295 respectively and a light chain with three CDRs comprising the amino acid sequences 325, 355, 385, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 236, 275, 296 respectively and a light chain with three CDRs comprising the amino acid sequences 326, 356, 386, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 237, 276, 297 respectively and a light chain with three CDRs comprising the amino acid sequences 327, 357, 387, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 237, 277, 298 respectively and a light chain with three CDRs comprising the amino acid sequences 328, 358, 388, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 238, 278, 299 respectively and a light chain with three CDRs comprising the amino acid sequences 329, 359, 389, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 239, 279, 300 respectively and a light chain with three CDRs comprising the amino acid sequences 330, 360, 390, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 240, 280, 301 respectively and a light chain with three CDRs comprising the amino acid sequences 331, 361, 391, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 241, 281, 302 respectively and a light chain with three CDRs comprising the amino acid sequences 332, 362, 392, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 242, 282, 303 respectively and a light chain with three CDRs comprising the amino acid sequences 333, 363, 393, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 243, 283, 304 respectively and a light chain with three CDRs comprising the amino acid sequences 334, 364, 394, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 244, 284, 305 respectively and a light chain with three CDRs comprising the amino acid sequences 335, 365, 395, respectively; or a heavy chain with three CDRs comprising the amino acid sequences 245, 285, 306 respectively and a light chain with three CDRs comprising the amino acid sequences 336, 366, 396, respectively.

[000103] Other anti-influenza antibodies include those having the amino acid or nucleic acid sequences shown in the below Table 1.

Table 1A. Antibody 3I14Variable Region nucleic acid sequences
V_H chain of 3I14 (SEQ ID NO:1665)
CAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATCATTTGATGGAAGTAAAAAATATTATGCAAACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTCTCTGCAAATGAACAGCCTGGGACCTGAGGACACGGCTCTATATTACTGTGCGAAACTGCCCTCCCCGTATTACTTTGATAGTCGGTTCGTGTGGGTCGCCGCCAGCGCATTTCACTTCTGGGGCCAGGGAATCCTGGTCACCGTCTCTTCA
V_L chain of 3I14 (SEQ ID NO:1667)
AATTTTATGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGCTCTGGAAGCAGCTCCAACATCGGAGGTAATACTGTACACTGGTTCCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAGTCTGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTAAATGGTCAGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA

Table 1B. Antibody3I14Variable Region amino acid sequences
V_H chain of 3I14 (SEQ ID NO: 1666)
QVQLLESGGGVVQPGRSLRLSCAAS**GFTFSNYG**MHWVRQAPGKGLEWVAI**ISFDGSKK**YYANSVKGRSTISRDNSKNTLSLQMNSLGPEDTALYY**CAKLPSPYYFDSRFVWVAASAFHFW**GQGILVTVSS
V_L chain of 3I14 (SEQ ID NO:1668)
NFMLTQPPSASGTPGQRVTISCSGS**SSNIGGNT**VHWFQQLPGTAPKLLIY**TNS**LRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYY**CAAWDDSLNGQVF**GGGTKLTVL

Table 1C. Antibody 3I14V_LD94N Variable Region nucleic acid sequence
V_L chain of 3I14V_LD94N (SEQ ID NO:1669)
AATTTTATGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGCTCTGGAAGCAGCTCCAACATCGGAGGTAATACTGTACACTGGTTCCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAGTCTGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTAC

TGTGCAGCATGGGATAACAGCCTAAATGGTCAGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA

Table 1C. Antibody 3I14V$_L$D94N Variable Region amino acid sequence
V$_L$ chain of 3I14V$_L$D94N (SEQ ID NO:1670)
NFMLTQPPSASGTPGQRVTISCSGS**SSNIGGNT**VHWFQQLPGTAPKLLIY**TNS**LRPSGVPD RFSGSKSGTSASLAISGLQSEDEADYY**CAAWDNSLNGQVF**GGGTKLTVL

[000104] The amino acid sequences of the heavy and light chain complementary determining regions of the 3I14 and3I14V$_L$D94N neutralizing influenza antibodies are shown in the below Table 2

[000105] **Table 2**

HCDR1	GFTFSNYG	(SEQ ID NO:1671)
HCDR2	ISFDGSKK	(SEQ ID NO:1672)
HCDR3	CAKLPSPYYFDSRFVWVA ASAFHFW	(SEQ ID NO:1673)
LCDR1	SSNIGGNT	(SEQ ID NO:1674)
LCDR2	TNS	(SEQ ID NO:1675)
LCDR3	CAAWDDSLNGQVF	(SEQ ID NO:1676)
3I14V$_L$D94N LCDR3	CAAWDNSLNGQVF	(SEQ ID NO:1677)

[000106] **CC-Chemokine Receptor 4 CCR4 (94)**

[000107] Exemplary anti-CCR4 antibodies include antibodies having a VH nucleotide sequence having SEQ ID NO: 1678 and a VL nucleotide sequence having SEQ ID NO: 1679; or a VH nucleotide sequence having SEQ ID NO: 1680 and a VL nucleotide sequence having SEQ ID NO: 1681; or a VH nucleotide sequence having SEQ ID NO: 1682 and a VL nucleotide sequence having SEQ ID NO: 1683; or a VH nucleotide sequence having SEQ ID NO: 1684 and a VL nucleotide sequence having SEQ ID NO: 1685; or a VH nucleotide sequence having SEQ ID NO: 1686 and a VL nucleotide sequence having SEQ ID NO: 1687; or a VH nucleotide sequence having SEQ ID NO: 1688 and a VL nucleotide sequence having SEQ ID NO: 1689.

[000108] Exemplary anti-CCR4 antibodies include antibodies having a VH amino acid sequence having SEQ ID NO: 1690 and a VL amino acid sequence having SEQ ID NO: 1691; or a VH amino acid sequence having SEQ ID NO: 1692 and a VL amino acid sequence having SEQ ID NO: 1693; or a VH amino acid sequence having SEQ ID NO: 1694 and a VL amino acid sequence having SEQ ID NO: 1695; or a VH amino acid sequence having SEQ ID NO: 1696 and a VL amino acid sequence having SEQ ID NO: 1697; or a VH amino acid sequence having SEQ ID NO: 1698 and a VL amino acid sequence having SEQ ID NO: 1699; or a VH amino acid sequence having SEQ ID NO: 1700 and a VL amino acid sequence having SEQ ID NO: 1701.

[000109] In other embodiments the anti-influenza antibodies have a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1702, 1703, 1704, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1705, 1706, 1707, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1708, 1709, 1710, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1711, 1712, 1713, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1714, 1715, 1716, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1717, 1718, 1719, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1720, 1721, 1722, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1723, 1724, 1725, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1726, 1727, 1728, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1729, 1730, 1731, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1732, 1733, 1734, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1735, 1736, 1737, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1738, 1739, 1740, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1741, 1742, 1743, respectively.

[000110] HUMAN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION GERMLINE GENE (VH1-69) (133)

[000111] Exemplary anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibodies include a VH nucleotide sequence having SEQ ID NO: 1744 and a VL nucleotide sequence having SEQ ID NO: 1745; or a VH nucleotide sequence having SEQ ID NO: 1748 and a VL nucleotide sequence having SEQ ID NO: 1749; or a VH nucleotide sequence having SEQ ID NO: 1752 and a VL nucleotide sequence having SEQ ID NO: 1753.

[000112] Exemplary anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibodies include a VH amino acid sequence having SEQ ID NO: 1746 and a VL amino acid sequence having SEQ ID NO: 1747; or a VH amino acid sequence having SEQ ID NO: 1750 and a VL amino acid sequence having SEQ ID NO: 1751; or a VH amino acid sequence having SEQ ID NO: 1754 and a VL amino acid sequence having SEQ ID NO: 1755.

[000113] In other embodiments the anti-human immunoglobulin heavy chain variable region germline gene VH1-69 antibodies have a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1756, 1757, 1758, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1759, 1760, 1761, respectively.

[000114] <u>ZIKA VIRUS ANTIBODIES (140)</u>

[000115] Exemplary antibodies that target and neutralize zika virus include antibodies having a VH nucleotide sequence having SEQ ID NO: 1762 and a VL nucleotide sequence having SEQ ID NO: 1763.

[000116] Exemplary antibodies that target and neutralize zika virus include antibodies having a VH amino acid sequence having SEQ ID NO: 1764 and a VL amino acid sequence having SEQ ID NO: 1765.

[000117] In other embodiments, the antibodies that target and neutralize zika virus have a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1766, 1767, 1768, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1769, 1770, 1771, respectively.

[000118] <u>GLUCOCORTICOID-INDUCED TUMOR NECROSIS FACTOR RECEPTOR (GITR) (141)</u>

[000119] Exemplary anti-glucocorticoid-induced tumor necrosis factor receptor (GITR) antibodies include a VH nucleotide sequence having SEQ ID NO: 1772 and a VL nucleotide sequence having SEQ ID NO: 1773; or a VH nucleotide sequence having SEQ ID NO: 1774 and a VL nucleotide sequence having SEQ ID NO: 1775; or a VH nucleotide sequence having SEQ ID NO: 1776 and a VL nucleotide sequence having SEQ ID NO: 1777; or a VH nucleotide sequence having SEQ ID NO: 1778 and a VL nucleotide sequence having SEQ ID NO: 1779; or a VH nucleotide sequence having SEQ ID NO: 1780 and a VL nucleotide sequence having SEQ ID NO: 1781; or a VH nucleotide sequence having SEQ ID NO: 1782 and a VL nucleotide sequence having SEQ ID NO: 1783; or a VH nucleotide sequence having SEQ ID NO: 1784 and a VL nucleotide sequence having SEQ ID NO: 1785; or a VH nucleotide sequence having SEQ ID NO: 1786 and a VL nucleotide sequence having SEQ ID NO: 1787; or a VH nucleotide sequence having SEQ ID NO: 1788 and a VL nucleotide sequence having SEQ ID NO: 1789; or a VH nucleotide sequence having SEQ ID NO: 1790 and a VL nucleotide sequence having SEQ ID NO: 1791; or a VH nucleotide sequence having SEQ ID NO: 1792 and a VL nucleotide sequence having SEQ ID NO: 1793; or a VH nucleotide sequence having SEQ ID NO: 1794 and a VL nucleotide sequence having SEQ ID NO: 1795; or a VH nucleotide sequence having SEQ ID NO: 1796 and a VL nucleotide sequence having SEQ ID NO: 1797.

[000120] Exemplary anti-glucocorticoid-induced tumor necrosis factor receptor (GITR) antibodies include a VH amino acid sequence having SEQ ID NO: 1798 and a VL amino acid sequence having SEQ ID NO: 1799; or a VH amino acid sequence having SEQ ID NO: 1800 and a VL amino acid sequence having SEQ ID NO: 1801; or a VH amino acid sequence having SEQ ID NO: 1802 and a VL amino acid sequence having SEQ ID NO: 1803; or a VH amino acid sequence having SEQ ID NO: 1804 and a VL amino acid sequence having SEQ ID NO: 1805; or a VH amino acid sequence having SEQ ID NO: 1806 and a VL amino acid sequence having SEQ ID NO: 1807; or a VH amino acid sequence having SEQ ID NO: 1808 and a VL amino acid sequence having SEQ ID NO: 1809; or a VH amino acid sequence having SEQ ID NO: 1810 and a VL amino acid sequence having SEQ ID NO: 1811; or a VH amino acid sequence having SEQ ID NO: 1812 and a VL amino acid sequence having SEQ ID NO: 1813; or a VH amino acid sequence having SEQ ID NO: 1814 and a VL amino acid sequence having SEQ ID NO: 1815; or a VH amino acid sequence having SEQ ID NO: 1816 and a VL amino acid sequence having SEQ ID NO: 1817; or a VH amino acid sequence having SEQ ID NO: 1818 and a VL amino acid sequence having SEQ ID NO: 1819; or a VH amino acid sequence having SEQ ID NO: 1820 and a VL amino acid sequence having SEQ ID NO: 1821; or a VH amino acid sequence having SEQ ID NO: 1822 and a VL amino acid sequence having SEQ ID NO: 1823.

[000121] In other embodiments, anti-glucocorticoid-induced tumor necrosis factor receptor (GITR) antibodies have a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1824, 1825, 1826, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1827, 1828, 1829, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1830, 1831, 1832, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1833, 1834, 1835, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1836, 1837, 1838, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1839, 1840, 1841, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1842, 1843, 1844, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1845, 1846, 1847, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1848, 1849, 1850, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1851, 1852, 1853, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1854, 1855, 1856, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1857, 1858, 1859, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1860, 1861, 1862, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1863, 1864, 1865, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1866, 1867, 1868, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1869, 1870, 1871, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1872, 1873, 1874, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1875, 1876, 1877, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1878, 1879, 1880, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1881, 1882, 1883, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1884, 1885, 1886, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1887, 1888, 1889, respectively; or a heavy chain with three CDRs having the amino acid sequences of SEQ ID NO: 1890, 1891, 1892, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1893, 1894, 1895, respectively; or a heavy chain with three CDRs having the amino acid sequences of

SEQ ID NO: 1896, 1897, 1898, respectively, and a light chain with three CDRs having the amino acid sequences of SEQ ID NO: 1899, 1900, 1901.

[000122] The tetravalent antibody is a dimer of a bispecific scFv fragment having a first binding site for a first antigen, a second binding site for a second antigen. The scFv is preferably a tandem scFv. The variable domains of the two binding sites are joined together via a linker domain. In preferred embodiments the linker domain includes an immunoglobulin hinge region amino acid sequence. The hinge region is an IgG1, an IgG2, an IgG3, or an IgG4 hinge region. Exemplary hinge region amino acids sequences include EPKSCDKTHTCPPCP (SEQ ID NO:1902); ERKCCVECPPCP (SEQ ID NO:1903); and ESKYGPPCPSCP (SEQ ID NO:1904).

[000123] In some embodiments the linker domain further includes at least a portion of an immunoglobulin Fc domain. The at least a portion of an immunoglobulin Fc domain is an IgG1, an IgG2, an IgG3, or an IgG4 Fc domain. The at least a portion of an immunoglobulin Fc domain is linked to the C-terminus of the hinge region. By at least a portion of an immunoglobulin Fc domain is meant for example, an immunoglobulin CH2 domain amino acid sequence, CH3 domain amino acid sequence, CH4 domain amino acid sequence or any combination thereof.

[000124] Inclusion of at least a portion of an immunoglobulin Fc domain (e.g. CH2 domain) provides a third functional binding site (i.e. Fc effector function) resulting in a trifunctional bispecific antibody. Accordingly, it can be desirable to modify the at least a portion of with respect to effector function, so as to enhance, e.g., the effectiveness of the tBsAb. For example, amino acids substitution, insertion or deletion can be introduced into the at least a portion of the immunoglobulin Fc domain to generate tBsAbs having improved internalization capability and/or increased complement mediated cell killing and antibody dependent cellular cytotoxicity (ADCC). Alternatively, the at least a portion of the immunoglobulin Fc domain is glycosylated as to improve the stability and solubility of the tBsAbs. For example, the at least a portion of the immunoglobulin Fc domain is glycosylated at the amino acid corresponding to asparagine at amino acid position 297. While glycosylation is important for stability defucosylation of the CH2 carbohydrate can also increase the binding affinity to FcγRs and lead to further enhancement of ADCC.

[000125] In certain embodiments, the tBsAbs of the invention may comprise an Fc variant comprising an amino acid substitution which alters the antigen-independent effector functions of the antibody, in particular the circulating half-life of the antibody. Such antibodies exhibit either increased or decreased binding to FcRn when compared to antibodies lacking these substitutions, therefore, have an increased or decreased half-life in serum, respectively. Fc variants with improved affinity for FcRn are anticipated to have longer serum half-lives, and such molecules have useful applications in methods of treating mammals where long half-life of the administered antibody is desired, e.g., to treat a chronic disease or disorder. In contrast, Fc variants with decreased FcRn binding affinity are expected to have shorter half-lives, and such molecules are also useful, for example, for administration to a mammal where a shortened circulation time may be advantageous, e.g. for in vivo diagnostic imaging or in situations where the starting antibody has toxic side effects when present in the circulation for prolonged periods. In one embodiment, an Fc domain having one or more amino acid substitutions within the "FcRn binding loop" of an Fc domain. The FcRn binding loop is comprised of amino acid residues 280-299 (according to EU numbering). Exemplary amino acid substitutions which altered FcRn binding activity are disclosed in International PCT Publication No. WO05/047327 which is incorporated by reference herein. In certain exemplary embodiments, the antibodies, or fragments thereof, of the invention comprise an Fc domain having one or more of the following substitutions: V284E, H285E, N286D, K290E and S304D (EU numbering).

[000126] Preferably the at least a portion of the Fc domain is a CH2 domain amino acid sequence. An exemplary CH2 domain amino acid sequence includes APELLGGPDVFLF (SEQ ID NO: 1905).

[000127] In other aspects the immunoglobulin hinge region amino acid sequence or the immunoglobulin hinge region/Fc domain amino acid sequence is flanked by a flexible linker amino acid sequence. Flexible linker amino acid sequences include for example is $(GGGS)_{X=1-6}$, $(GGGGS)_{X=1-6}$, or GSAGSAAGSGEF.

[000128] Increasing the linker by adding multiple repeats (e.g., four or more) will predominantly result in a monomeric scFv, thus it can increase the accessibility to an epitope. Length and composition of the linkers can be chosen to optimize the stability and functional activity and takes into account the topography of the epitope on the target protein.

[000129] Also included in the invention is a nucleic acid construct including nucleic acids molecules encoding: a light chain and a heavy chain variable region of an antibody specifically binding to a first antigen; a light chain and heavy chain variable region of an antibody specifically binding to a second antigen; and a linker domain.

[000130] In yet a further aspect the invention provides a genetically engineered cell which expresses and bears on the cell surface membrane tBsAbs of the invention. The cell is a T-cell, a B-cell, a follicular T-Cell or an NK cell. The T cell is CD4+ or CD8+. The cell is a mixed population of CD4+ and CD8 cells+. The cell is further engineered to express and secrete the tBsAb.

[000131] Vectors including the nucleic acid constructs according to the invention and host cell, e.g., a mammalian cell, expressing the vectors of the invention.

[000132] ***Chimeric Antigen Receptors***

[000133] The tBsAb of the invention can be used to produce a chimeric antigen receptor (CAR). The CAR generally comprises at least one transmembrane polypeptide comprising at least one extracellular ligand-binding domain comprising the tBsAb of the invention and; one transmembrane polypeptide comprising at least one intracellular signaling domain.

[000134] In a preferred embodiment said transmembrane domain further comprises a stalk region between said extracellular ligand-binding domain and said transmembrane domain. The term “stalk region” used herein generally means any oligo- or polypeptide that functions to link the transmembrane domain to the extracellular ligand-binding domain. In particular, stalk region are used to provide more flexibility and accessibility for the extracellular ligand-binding domain. A stalk region may comprise up to 300 amino acids, preferably 10 to 100 amino acids and most preferably 25 to 50 amino acids. Stalk region may be derived from all or part of naturally occurring molecules, such as from all or part of the extracellular region of CD8, CD4 or CD28, or from all or part of an antibody constant region. Alternatively the stalk region may be a synthetic sequence that corresponds to a naturally occurring stalk sequence, or may be an entirely synthetic stalk sequence. In a preferred embodiment said stalk region is a part of human CD8 alpha chain

[000135] The signal transducing domain or intracellular signaling domain of the CAR of the invention is responsible for intracellular signaling following the binding of extracellular ligand binding domain to the target resulting in the activation of the immune cell and immune response. In other words, the signal transducing domain is responsible for the activation of at least one of the normal effector functions of the immune cell in which the CAR is expressed. For example, the effector function of a T cell can be a cytolytic activity or helper activity including the secretion of cytokines. Thus, the term “signal transducing domain” refers to the portion of a protein which transduces the effector signal function signal and directs the cell to perform a specialized function.

[000136] Signal transduction domain comprises two distinct classes of cytoplasmic signaling sequence, those that initiate antigen-dependent primary activation, and those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal. Primary cytoplasmic signaling sequence can comprise signaling motifs which are known as immunoreceptor tyrosine-based activation motifs of ITAMs. ITAMs are well defined signaling motifs found in the intracytoplasmic tail of a variety of receptors that serve as binding sites for syk/zap70 class tyrosine kinases. Examples of ITAM used in the invention can include as non limiting examples those derived from TCR zeta, FcR gamma, FcR beta, FcR epsilon, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b and CD66d. In a preferred embodiment, the signaling transducing domain of the CAR can comprise the CD3 zeta signaling domain, or the intracytoplasmic domain of the Fc epsilon RI beta or gamma chains. In another preferred embodiment, the signaling is provided by CD3 zeta together with co-stimulation provided by CD28 and/or a tumor necrosis factor receptor (TNFr), such as 4-1BB or OX40), for example.

[000137] In particular embodiment the intracellular signaling domain of the CAR of the present invention comprises a co-stimulatory signal molecule. In some embodiments the intracellular signaling domain contains 2, 3, 4 or more co-stimulatory molecules in tandem. A co-stimulatory molecule is a cell surface molecule other than an antigen receptor or their ligands that is required for an efficient immune response.

[000138] “Co-stimulatory ligand” refers to a molecule on an antigen presenting cell that specifically binds a cognate co-stimulatory molecule on a T-cell, thereby providing a signal which, in addition to the primary signal provided by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, mediates a T cell response, including, but not limited to, proliferation activation, differentiation and the like. A co-stimulatory ligand can include but is not limited to CD7, B7-1 (CD80), B7-2 (CD86), PD-L1, PD-L2, 4-1BBL, OX40L, inducible costimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM, CD30L, CD40, CD70, CD83, HLA-G, MICA, M1CB, HVEM, lymphotoxin beta receptor, 3/TR6, ILT3, ILT4, an agonist or antibody that binds Toll ligand receptor and a ligand that specifically binds with B7-H3. A co-stimulatory ligand also encompasses, inter alia, an antibody that specifically binds with a co-stimulatory molecule present on a T cell, such as but not limited to, CD27, CD28, 4-IBB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LTGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83.

[000139] A "co-stimulatory molecule" refers to the cognate binding partner on a T-cell that specifically binds with a co-stimulatory ligand, thereby mediating a co-stimulatory response by the cell, such as, but not limited to proliferation. Co-stimulatory molecules include, but are not limited to an MHC class 1 molecule, BTLA and Toll ligand receptor. Examples of costimulatory molecules include CD27, CD28, CD8, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3 and a ligand that specifically binds with CD83 and the like. The In another particular embodiment, said signal transducing domain is a TNFR-associated Factor 2 (TRAF2) binding motifs, intracytoplasmic tail of costimulatory TNFR member family. Cytoplasmic tail of costimulatory TNFR family member contains TRAF2 binding motifs consisting of the major conserved motif (P/S/A)X(Q/E)E) or the minor motif (PXQXXD), wherein X is any amino acid. TRAF proteins are recruited to the intracellular tails of many TNFRs in response to receptor trimerization.

[000140] The distinguishing features of appropriate transmembrane polypeptides comprise the ability to be expressed at the surface of an immune cell, in particular lymphocyte cells or Natural killer (NK) cells, and to interact together for directing cellular response of immune cell against a predefined target cell. The different transmembrane polypeptides of the CAR of the present invention comprising an extracellular ligand-biding domain and/or a signal transducing domain interact together to take part in signal transduction following the binding with a target ligand and induce an immune response. The transmembrane domain can be derived either from a natural or from a synthetic source. The transmembrane domain can be derived from any membrane-bound or transmembrane protein although certain transmembrane domains that that best accommodate the chimeras are preferred, e.g., those that promote self-aggregation or promote an increase in CART cell basal activation in the absence of target binding, which could lead to premature exhaustion.

[000141] The term "a part of" used herein refers to any subset of the molecule, that is a shorter peptide. Alternatively, amino acid sequence functional variants of the polypeptide can be prepared by mutations in the DNA which encodes the polypeptide. Such variants or functional variants include, for example, deletions from, or insertions or substitutions of, residues within the amino acid sequence. Any combination of deletion, insertion, and substitution may also be made to arrive at the final construct, provided that the final construct possesses the desired activity, especially to exhibit a specific anti-target cellular immune activity. The functionality of the CAR of the invention within a host cell is detectable in an assay suitable for demonstrating the signaling potential of said CAR upon binding of a particular target. Such assays are available to the skilled person in the art. For example, this assay allows the detection of a signaling pathway, triggered upon binding of the target, such as an assay involving measurement of the increase of calcium ion release, intracellular tyrosine phosphorylation, inositol phosphate turnover, or interleukin (IL) 2, interferon .gamma., GM-CSF, IL-3, IL-4 production thus effected.

[000142] ***Methods of Use***

[000143] The tBsAbs, the cells expressing the tBsAbs or the CARs according to the invention can be used for treating cancer, viral infections or autoimmune disorders in a patient in need thereof. In another embodiment, tBsAbs, the cells expressing the tBsAbs or the CARs according to the invention can be used in the manufacture of a medicament for treatment of a cancer, viral infections of autoimmune disorders, in a patient in need thereof.

[000144] Said treatment can be ameliorating, curative or prophylactic. It may be either part of an autologous immunotherapy or part of an allogenic immunotherapy treatment. By autologous, it is meant that cells, cell line or population of cells used for producing the tBsAbs or the cells expressing the tBsAbs are originating from the patient or from a Human Leucocyte Antigen (HLA) compatible donor. By allogeneic is meant that the cells or population of cells used for producing the tBsAbs or the cells expressing the tBsAbs are not originating from the patient but from a donor.

[000145] Treatment can be used to treat patients diagnosed with cancer, viral infection, autoimmune disorders or Graft versus Host Disease (GvHD). Cancers that may be treated include tumors that are not vascularized, or not yet substantially vascularized, as well as vascularized tumors. The cancers may comprise nonsolid tumors (such as hematological tumors, for example, leukemias and lymphomas) or may comprise solid tumors. Types of cancers to be treated with the CARs of the invention include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies e.g., sarcomas, carcinomas, and melanomas. Adult tumors/cancers and pediatric tumors/cancers are also included.

[000146] It can be a treatment in combination with one or more therapies against cancer selected from the group of antibodies therapy, chemotherapy, cytokines therapy, dendritic cell therapy, gene therapy, hormone therapy, laser light therapy and radiation therapy.

[000147] In a further embodiment, the compositions of the present invention are administered to a patient in conjunction with (e.g., before, simultaneously or following) bone marrow transplantation, T cell ablative therapy using either chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, or antibodies such as OKT3 or CAM PATH.

[000148] ***Definitions***

[000149] It is to be noted that the term “a” or “an” entity refers to one or more of that entity: for example, “a bispecific antibody,” is understood to represent one or more bispecific antibodies. As such, the terms “a” (or “an”), “one or more,” and “at least one” can be used interchangeably herein.

[000150] As used herein, the term “polypeptide” is intended to encompass a singular “polypeptide” as well as plural “polypeptides,” and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term “polypeptide” refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, “protein,” “amino acid chain,” or any other term used to refer to a chain or chains of two or more amino acids, are included within the definition of “polypeptide,” and the term “polypeptide” may be used instead of, or interchangeably with any of these terms. The tern “polypeptide” is also intended to refer to the products of post-expression modifications of the polypeptide, including without limitation glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids. A polypeptide may be derived from a natural biological source or produced by recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. It may be generated in any manner, including by chemical synthesis.

[000151] The term “isolated” as used herein with respect to cells, nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs or RNAs, respectively, that are present in the natural source of the macromolecule. The term "isolated" as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to cells or polypeptides which are isolated from other cellular proteins or tissues. Isolated polypeptide is meant to encompass both purified and recombinant polypeptides.

[000152] As used herein, the term "recombinant" as it pertains to polypeptides or polynucleotides intends a form of the polypeptide or polynucleotide that does not exist naturally, a non-limiting example of which can be created by combining polynucleotides or polypeptides that would not normally occur together.

[000153] "Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present disclosure.

[000154] A polynucleotide or polynucleotide region (or a polypeptide or polypeptide region) has a certain percentage (for example, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99%) of "sequence identity" to another sequence means that, when aligned, that percentage of bases (or amino acids) are the same in comparing the two sequences. This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those described in Ausubel et al. eds. (2007) Current Protocols in Molecular Biology. Preferably, default parameters are used for alignment. One alignment program is BLAST, using default parameters. In particular, programs are BLASTN and BLASTP, using the following default parameters: Genetic code=standard; filter=none; strand=both; cutoff=60; expect=10; Matrix=BLOSUM62; Descriptions=50 sequences; sort by=HIGH SCORE; Databases=non-redundant, GenBank+EMBL+DDBJ+PDB+GenBank CDS translations+SwissProtein+SPupdate+PIR. Details of these programs can be found at the World Wide Web (www) ncbi.nlm.nih.gov/blast/Blast.cgi, last accessed on May 21, 2008. Biologically equivalent polynucleotides are those having the above-noted specified percent homology and encoding a polypeptide having the same or similar biological activity.

[000155] The term "an equivalent nucleic acid or polynucleotide" refers to a nucleic acid having a nucleotide sequence having a certain degree of homology, or sequence identity, with the nucleotide sequence of the nucleic acid or complement thereof. A homolog of a double stranded nucleic acid is intended to include nucleic acids having a nucleotide sequence which has a certain degree of homology with or with the complement thereof. In one aspect, homologs of nucleic acids are capable of hybridizing to the nucleic acid or complement thereof. Likewise, "an equivalent polypeptide" refers to a polypeptide having a certain degree of homology, or sequence identity, with the amino acid sequence of a reference polypeptide. In some aspects, the sequence identity is at least about 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%. In some aspects, the equivalent sequence retains the activity (e.g., epitope-binding) or structure (e.g., salt-bridge) of the reference sequence.

[000156] Hybridization reactions can be performed under conditions of different "stringency". In general, a low stringency hybridization reaction is carried out at about 40^0C. in about 10x SSC or a solution of equivalent ionic strength/temperature. A moderate stringency hybridization is typically performed at about 50^0C. in about 6xSSC, and a high stringency hybridization reaction is generally performed at about 60^0C. in about 1x SSC. Hybridization reactions can also be performed under "physiological conditions" which is well known to one of skill in the art. A non-limiting example of a physiological condition is the temperature, ionic strength, pH and concentration of Mg^2+ normally found in a cell.

[000157] A polynucleotide is composed of a specific sequence of four nucleotide bases: adenine (A); cytosine (C); guanine (G); thymine (T); and uracil (U) for thymine when the polynucleotide is RNA. Thus, the term "polynucleotide sequence" is the alphabetical representation of a polynucleotide molecule. This alphabetical representation can be input into databases in a computer having a central processing unit and used for bioinformatics applications such as functional genomics and homology searching. The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a “polymorphic region of a gene”. A polymorphic region can be a single nucleotide, the identity of which differs in different alleles.

[000158] The terms “polynucleotide” and “oligonucleotide” are used interchangeably and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides or analogs thereof. Polynucleotides can have any three-dimensional structure and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment (for example, a probe, primer, EST or SAGE tag), exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, dsRNA, siRNA, miRNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes and primers. A polynucleotide can comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure can be imparted before or after assembly of the polynucleotide. The sequence of nucleotides can be interrupted by non-nucleotide components. A polynucleotide can be further modified after polymerization, such as by conjugation with a labeling component. The term also refers to both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of this disclosure that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

[000159] The term “encode” as it is applied to polynucleotides refers to a polynucleotide which is said to “encode” a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the mRNA for the polypeptide and/or a fragment thereof. The antisense strand is the complement of such a nucleic acid, and the encoding sequence can be deduced therefrom.

[000160] As used herein, the term “detectable label” intends a directly or indirectly detectable compound or composition that is conjugated directly or indirectly to the composition to be detected, e.g., polynucleotide or protein such as an antibody so as to generate a “labeled” composition. The term also includes sequences conjugated to the polynucleotide that will provide a signal upon expression of the inserted sequences, such as green fluorescent protein (GFP) and the like. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable. The labels can be suitable for small scale detection or more suitable for high-throughput screening. As such, suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and proteins, including enzymes. The label may be simply detected or it may be quantified. A response that is simply detected generally comprises a response whose existence merely is confirmed, whereas a response that is quantified generally comprises a response having a quantifiable (e.g., numerically reportable) value such as an intensity, polarization, and/or other property. In luminescence or fluorescence assays, the detectable response may be generated directly using a luminophore or fluorophore associated with an assay component actually involved in binding, or indirectly using a luminophore or fluorophore associated with another (e.g., reporter or indicator) component.

[000161] As used herein, an “antibody” or “antigen-binding polypeptide” refers to a polypeptide or a polypeptide complex that specifically recognizes and binds to an antigen. An antibody can be a whole antibody and any antigen binding fragment or a single chain thereof. Thus the term “antibody” includes any protein or peptide containing molecule that comprises at least a portion of an immunoglobulin molecule having biological activity of binding to the antigen. Examples of such include, but are not limited to a complementarity determining region (CDR) of a heavy or light chain or a ligand binding portion thereof, a heavy chain or light chain variable region, a heavy chain or light chain constant region, a framework (FR) region, or any portion thereof, or at least one portion of a binding protein.

[000162] The terms “antibody fragment” or “antigen-binding fragment”, as used herein, is a portion of an antibody such as $F(ab')_2$, $F(ab)_2$, 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” includes aptamers, spiegelmers, and diabodies. The term “antibody fragment” also includes any synthetic or genetically engineered protein that acts like an antibody by binding to a specific antigen to form a complex.

[000163] A “single-chain variable fragment” or “scFv” refers to a fusion protein of the variable regions of the heavy (V_H) and light chains (V_L) of immunoglobulins. In some aspects, the regions are connected with a short linker peptide of ten to about 25 amino acids. The linker can be rich in glycine for flexibility, as well as serine or threonine for solubility, and can either connect the N-terminus of the V_H with the C-terminus of the V_L, or vice versa. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and the introduction of the linker. ScFv molecules are known in the art and are described, e.g., in U.S. Pat. No. 5,892,019.

[000164] A "tandem scFv" is composed of two scFvs connected through a short linker, which allows the free rotation of the two separate antigen binding units, thus resulting in a flexible structure.

[000165] The term antibody encompasses various broad classes of polypeptides that can be distinguished biochemically. Those skilled in the art will appreciate that heavy chains are classified as gamma, mu, alpha, delta, or epsilon with some subclasses among them (e.g., .gamma.1-.gamma.4). It is the nature of this chain that determines the "class" of the antibody as IgG, IgM, IgA IgG, or IgE, respectively. The immunoglobulin subclasses (isotypes) e.g., IgG_1, IgG_2, IgG_3, IgG_4, IgG_5, etc. are well characterized and are known to confer functional specialization. Modified versions of each of these classes and isotypes are readily discernable to the skilled artisan in view of the instant disclosure and, accordingly, are within the scope of the instant disclosure. All immunoglobulin classes are clearly within the scope of the present disclosure, the following discussion will generally be directed to the IgG class of immunoglobulin molecules. With regard to IgG, a standard immunoglobulin molecule comprises two identical light chain polypeptides of molecular weight approximately 23,000 Daltons, and two identical heavy chain polypeptides of molecular weight 53,000-70,000. The four chains are typically joined by disulfide bonds in a "Y" configuration wherein the light chains bracket the heavy chains starting at the mouth of the "Y" and continuing through the variable region.

[000166] Antibodies, antigen-binding polypeptides, variants, or derivatives thereof of the disclosure include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized, primatized, or chimeric antibodies, single chain antibodies, epitope-binding fragments, e.g., Fab, Fab' and $F(ab)_2$, Fd, Fvs, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv), fragments comprising either a V_K or V_H domain, fragments produced by a Fab expression library, and anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to LIGHT antibodies disclosed herein). Immunoglobulin or antibody molecules of the disclosure can be of any type e.g., IgG, IgE, IgM, IgD, IgA, and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

[000167] Light chains are classified as either kappa or lambda. Each heavy chain class may be bound with either a kappa or lambda light chain. In general, the light and heavy chains are covalently bonded to each other, and the "tail" portions of the two heavy chains are bonded to each other by covalent disulfide linkages or non-covalent linkages when the immunoglobulins are generated either by hybridomas, B cells or genetically engineered host cells. In the heavy chain, the amino acid sequences run from an N-terminus at the forked ends of the Y configuration to the C-terminus at the bottom of each chain.

[000168] 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 (V_K) and heavy (V_H) chain portions determine antigen recognition and specificity. Conversely, the constant domains of the light chain (CK) and the heavy chain (CH1, CH2 or 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 increases as they become more distal from the antigen-binding site or amino-terminus of the antibody. The N-terminal portion is a variable region and at the C-terminal portion is a constant region: the CH3 and CK domains actually comprise the carboxy-terminus of the heavy and light chain, respectively.

[000169] As indicated above, the variable region allows the antibody to selectively recognize and specifically bind epitopes on antigens. That is, the V_K domain and V_H domain, or subset of the complementarity determining regions (CDRs), of an antibody combine to form the variable region that defines a three dimensional antigen-binding site. This quaternary antibody structure forms the antigen-binding site present at the end of each arm of the Y. More specifically, the antigen-binding site is defined by three CDRs on each of the V_H and V_K chains i.e. CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3). In some instances, e.g., certain immunoglobulin molecules derived from camelid species or engineered based on camelid immunoglobulins, a complete immunoglobulin molecule may consist of heavy chains only, with no light chains. See, e.g., Hamers-Casterman et al., Nature 363:446-448 (1993).

[000170] In naturally occurring antibodies, the six "complementarity determining regions" or "CDRs" present in each antigen-binding domain are short, non-contiguous sequences of amino acids that are specifically positioned to form the antigen-binding domain as the antibody assumes its three dimensional configuration in an aqueous environment. The remainder of the amino acids in the antigen-binding domains, referred to as "framework" regions, show less inter-molecular variability. The framework regions largely adopt a b-sheet conformation and the CDRs form loops which connect, and in some cases form part of, the .beta.-sheet structure. Thus, framework regions act to form a scaffold that provides for positioning the CDRs in correct orientation by inter-chain, non-covalent interactions. The antigen-binding domain formed by the positioned CDRs defines a surface complementary to the epitope on the immunoreactive antigen. This complementary surface promotes the non-covalent binding of the antibody to its cognate epitope. The amino acids comprising the CDRs and the framework regions, respectively, can be readily identified for any given heavy or light chain variable region by one of ordinary skill in the art, since they have been precisely defined (see "Sequences of Proteins of Immunological Interest," Kabat, E., et al., U.S. Department of Health and Human Services, (1983); and Chothia and Lesk, J. Mol. Biol., 196:901-917 (1987), which are incorporated herein by reference in their entireties).

[000171] In the case where there are two or more definitions of a term which is used and/or accepted within the art, the definition of the term as used herein is intended to include all such meanings unless explicitly stated to the contrary. A specific example is the use of the term "complementarity determining region" ("CDR") to describe the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. This particular region has been described by Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of Proteins of Immunological Interest" (1983) and by Chothia et al., J. Mol. Biol. 196:901-917 (1987), which are incorporated herein by reference in their entireties. The CDR definitions according to Kabat and Chothia include overlapping or subsets of amino acid residues when compared against each other. Nevertheless, application of either definition to refer to a CDR of an antibody or variants thereof is intended to be within the scope of the term as defined and used herein. The appropriate amino acid residues which encompass the CDRs as defined by each of the above cited references are set forth in the table below as a comparison. The exact residue numbers which encompass a particular CDR will vary depending on the sequence and size of the CDR. Those skilled in the art can routinely determine which residues comprise a particular CDR given the variable region amino acid sequence of the antibody.

[000172] Kabat et al. also defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. As used herein, "Kabat numbering" refers to the numbering system set forth by Kabat et al., U.S. Dept. of Health and Human Services, "Sequence of Proteins of Immunological Interest" (1983).

[000173] In addition to table above, the Kabat number system describes the CDR regions as follows: CDR-H 1 begins at approximately amino acid 31 (i.e., approximately 9 residues after the first cysteine residue), includes approximately 5-7 amino acids, and ends at the next tryptophan residue. CDR-H2 begins at the fifteenth residue after the end of CDR-H1, includes approximately 16-19 amino acids, and ends at the next arginine or lysine residue. CDR-H3 begins at approximately the thirty third amino acid residue after the end of CDR-H2; includes 3-25 amino acids; and ends at the sequence W-G-X-G, where X is any amino acid. CDR-L1 begins at approximately residue 24 (i.e., following a cysteine residue); includes approximately 10-17 residues; and ends at the next tryptophan residue. CDR-L2 begins at approximately the sixteenth residue after the end of CDR-LI and includes approximately 7 residues. CDR-L3 begins at approximately the thirty third residue after the end of CDR-L2 (i.e., following a cysteine residue); includes approximately 7-11 residues and ends at the sequence For W-G-X-G, where X is any amino acid.

[000174] Antibodies disclosed herein may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine, donkey, rabbit, goat, guinea pig, camel, llama, horse, or chicken antibodies. In another embodiment, the variable region may be condricthoid in origin (e.g., from sharks).

[000175] 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 another embodiment, 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). As set forth above, it will be understood by one of ordinary skill in the art that the heavy chain constant region may be modified such that they vary in amino acid sequence from the naturally occurring immunoglobulin molecule.

[000176] 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 IgG, molecule and a hinge region derived from an IgG_3 molecule. In another example, a heavy chain constant region can comprise a hinge region derived, in part, from an IgG, molecule and, in part, from an IgG_3 molecule. In another example, a heavy chain portion can comprise a chimeric hinge derived, in part, from an IgG, molecule and, in part, from an IgG_4 molecule.

[000177] 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.

[000178] 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.

[000179] As previously indicated, the subunit structures and three dimensional configuration of the constant regions of the various immunoglobulin classes are well known. As used herein, the term “V_H 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 V_H domain and is amino terminal to the hinge region of an immunoglobulin heavy chain molecule.

[000180] 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; see Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of Proteins of Immunological Interest" (1983). 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. It is also well documented that the CH3 domain extends from the CH2 domain to the C-terminal of the IgG molecule and comprises approximately 108 residues.

[000181] 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 (Roux et al., J. Immunol 161:4083 (1998)).

[000182] As used herein the term "disulfide bond" includes the covalent bond formed between two sulfur atoms. The amino acid cysteine comprises a thiol group that can form a disulfide bond or bridge with a second thiol group. In most naturally occurring IgG molecules, the CH1 and CK regions are linked by a disulfide bond and the two heavy chains are linked by two disulfide bonds at positions corresponding to 239 and 242 using the Kabat numbering system (position 226 or 229, EU numbering system).

[000183] As used herein, the term "chimeric antibody" will be held to mean any antibody wherein the immunoreactive region or site is obtained or derived from a first species and the constant region (which may be intact, partial or modified in accordance with the instant disclosure) is obtained from a second species. In certain embodiments the target binding region or site will be from a non-human source (e.g. mouse or primate) and the constant region is human.

[000184] As used herein, "percent humanization" is calculated by determining the number of framework amino acid differences (i.e., non-CDR difference) between the humanized domain and the germline domain, subtracting that number from the total number of amino acids, and then dividing that by the total number of amino acids and multiplying by 100.

[000185] By "specifically binds" or "has specificity to," it is generally meant that an antibody binds to an epitope via its antigen-binding domain, and that the binding entails some complementarity between the antigen-binding domain and the epitope. According to this definition, an antibody is said to “specifically bind” to an epitope when it binds to that epitope, via its antigen-binding domain more readily than it would bind to a random, unrelated epitope. The term “specificity” is used herein to qualify the relative affinity by which a certain antibody hinds to a certain epitope. For example, antibody “A” may be deemed to have a higher specificity for a given epitope than antibody “B,” or antibody “A” may be said to bind to epitope “C” with a higher specificity than it has for related epitope “D.”

[000186] As used herein, the terms “treat” or “treatment” refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) an undesired physiological change or disorder, such as the progression of cancer. Beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilized (i.e., not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. “Treatment” can also mean prolonging survival as compared to expected survival if not receiving treatment. Those in need of treatment include those already with the condition or disorder as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

[000187] By “subject” or “individual” or “animal” or “patient” or “mammal,” is meant any subject, particularly a mammalian subject, for whom diagnosis, prognosis, or therapy is desired. Mammalian subjects include humans, domestic animals, farm animals, and zoo, sport, or pet animals such as dogs, cats, guinea pigs, rabbits, rats, mice, horses, cattle, cows, and so on.

[000188] As used herein, phrases such as “to a patient in need of treatment” or “a subject in need of treatment” includes subjects, such as mammalian subjects, that would benefit from administration of an antibody or composition of the present disclosure used, e.g., for detection, for a diagnostic procedure and/or for treatment.

[000189] This disclosure describes the development of bispecific antibodies, which can be applied to cancer therapy. To accomplish this goal, two tetrameric bispecific antibodies (tBsAbs) with dual specificity for the GITR protein and the PD-L1 protein were created. An advantage of these constructs is that they will enhance anti-tumor response by activating T cells and abrogating regulatory T cell suppression. Also described are the anti-CCR4-anti-PDL1 tBsAb (Figures 3 and 4) and anti-CAIX-anti-PDL1 (Figures 5 and 6).

[000190] Here is described two different formats of tandem scFv fragment dimerization units in a pcDNA3.4 mammalian expression vector. In the first construct, the tandem scFvs comprise two scFvs derived from distinct parental antibodies. The αGITR scFv and αPD-L1 scFv are connected in tandem by an IgG1 hinge region between two flexible linkers. The first construct has a structure of VH GITR10-linker-VL GITR10-linker-hinge-linker-VH PD-L1-linker-VL PD-L1 and its sequence was confirmed by DNA sequencing. The second format was constructed equivalently to the first one. Yet, it includes an additional domain, e.g., a CH2 domain, introduced between the hinge and one linker region. The second construct has a structure of VH GITR-linker-VL GITR-linker-hinge-CH2-linker-VH PD-L1-linker-VL PD-L1. In contrast to the first construct, the second construct includes an Fc domain, potentially resulting in a trifunctional tBsAb.

[000191] Both tBsAbs were successfully expressed by transient transfection in HEK cells and purified by affinity chromatography using Ni-NTA agarose.

[000192] The purified proteins were evaluated by SDS-PAGE and results showed that under reducing conditions all protein profiles of the tBsAbs exhibit one single band and are congruent with the theoretical value of a tandem scFv (taFv): 65kDa for αGITR-αPD-L1 taFv and 75 kDA for αGITR-αPD-L1 with CH2 taFv. Under non-reducing conditions the predicted molecular weight of αGITR-αPD-L1 (130kDa) and αGITR-αPD-L1 with CH2 (150kDa) tBsAbs match the apparent molecular weight (See, Figure 18).

[000193] ELISA and flow cytometry demonstrated the biological activities of the newly designed tBsAbs. In ELISA the retained binding activity of the αPD-L1 arm of the produced BsAb was preserved *in vitro* and showed similar binding activity as the αPD-L1 mAb. Unspecific binding of the tBsAbs was to be ruled out since CCR4, to which the αGITR-αPD-L1 antibodies do not bind, did not show any signal. Furthermore, similar binding activity of the αGITR arm for both produced BsAb (αGITR-αPD-L1 and αGITR-αPD-L1 with CH2) to the GITR protein was observed. Unspecific binding was likewise excluded from this arm since the αGITR-αPD-L1 antibodies did not show any binding specificity for GITR-CF2 cells. When comparing the αGITR IgG to each BsAb, the αGITR IgG showed higher binding in the ELISA experiment, suggesting a lower affinity of the tBsAbs. Nevertheless depending on the spatial arrangement of the antigen binding sites as well as the antigen surface distribution bivalency of the tBsAbs can increase avidity, which can compensate for weak binding.

[000194] The flow cytometry analyses of αGITR-αPD-L1 tested with GITR+CF2 cells suggests that the novel tBsAb recognize the GITR protein in its native conformation when expressed on cells. A similar binding affinity of the αGITR-αPD-L1 tBsAbcompared to the GITR mAb was observed. The ELISA and Flow cytometry analyses therefore demonstrated the capability of the αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 to specifically recognize the corresponding antigen when expressed on cells, as would be the case *in vivo*. These characterization studies exhibited similar binding behavior of the αGITR-αPD-L1 and αGITR-αPD-L1 with CH2.

[000195] An important aspect of the αGITR10-αPD-L1 with CH2 lays in its function in inducing complement-dependent cytotoxicity (CDC) and antibody-dependent cellular cytotoxicity (ADCC). These functions further the beneficial effects of the tBsAb when targeting tumor cells for destruction.

[000196] In the ADCC analysis the αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 displayed surprising results using GITR+CF2 as target cells and WIL2-S as effector cells (E/T=5:1). For αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 antibodies the raw signal of the luciferase activity decreased with higher antibody concentrations and was substantially lower than the signal for sole target and effector cells (See Figure 30).

[000197] The herein-described methods allow generation of tBsAb involving only one cloning step. The tBsAb preserves the dual affinity towards the GITR protein and PD-L1 antigen in a small-sized molecule of only about 150 kDa. Such tBsAbs will be critical for effective cancer therapeutics.

EXAMPLES

[000198] **EXAMPLE 1:** Cloning of αGITR-αPD-L1 tetrameric bispecific antibody (tBsAb).

[000199] *Cloning strategy*

[000200] The goal was to clone a plasmid that contained two recombinant single chain variable fragments (scFvs), originating from different parental antibodies and joined by a flexible linker. While one of the scFvs is directed against the GITR protein, the other is directed against PD-L1. Such a plasmid will produce two scFvs that are covalently joined by a linker-hinge-linker domain and result in a tetrameric bispecific antibody (αGITR-αPD-L1 tBsAb).

[000201] The mammalian expression vector pcDNA3.4 plasmid was the basis for constructs (V_HGITR-linker-V_LGITR-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1). The fundamental structure of pcDNA 3.4 expression vector contained beforehand the V_H^X-linker-V_L^X-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1 gene fused to an N-terminal 6x-His tag (Figure 12).

[000202] *Restriction enzyme digestion and ligation*

[000203] Six αGITR scFv gene sequences were individually cloned into the pcDNA3.4 expression vector. The six V_HGITR-linker-V_LGITR gene sequences were labeled as V_HGITRL1-V_LGITRL1, V_HGITRL10-V_LGITRL10, V_HGITRL11-V_LGITRL11, V_HGITRL14-V_LGITRL14, V_HGITRL15-V_LGITRL15 and V_HGITRL17-V_LGITRL17. All six αGITR gene sequences are flanked by SfiI and NotI restriction sites and were isolated from the respective donor plasmids by digestion (Table 1). Similarly, the pcDNA3.4 expression vector was also digested with the SfiI and NotI restriction enzymes. The digested vectors and fragments were analyzed on a 1% agarose gel and were purified using a QIAquick Gel Extraction Kit. Cohesive inserts from the SfiI and NotI digestion were ligated into the corresponding vector pcDNA 3.4 at a fivefold molar ratio using the T4 Ligation Kit. Fifty nanograms of the recipient vector were used per ligation reaction. The ligation product resulted in the final configuration of V_HGITR-linker-V_LGITR-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1 (Figure 12).

[000204] Three additional clones were constructed each to generate the control antibodies. The F10 gene was chosen as the 'control arm'; since V_HF10-V_LF10 binding domain does not have binding affinity to GITR nor to PD-L1 protein. Thus, this domain was defined as negative control. F10 is a validated antibody directed against influenza HA protein. To keep the same antibody format, its gene sequences only replace either V_HGITR1-linker-V_LGITR1 or V_HPD-L1-linker-V_LPD-L1, respectively. The three control plasmids exhibit the following sequencing order:

(1) V_HF10-linker-V_LF10-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1 (F10-αPD-L1)
(2) V_HGITR1-linker-V_LGITR1-linker-hinge-linker-V_HF10-linker-V_LF10 (αGITR1-F10)
(3) V_HGITR10-linker-V_LGITR10-linker-hinge-linker-V_HF10-linker-V_LF10 (αGITR10-F10)

[000205] *Construction of plasmid (1):*

[000206] The V_HF10-linker-V_LF10 gene was isolated from a pcDNA 3.1 vector through the digestion with SfiI and NotI RE. As for the expression vector, the same pcDNA3.4 vector was used (Figure 13). It contains the SfiI and NotI restriction sites at the desired site of insertion and was therefore digested with the corresponding restriction enzymes. The final plasmid was obtained by ligating both digested products to each other. The ligation was performed using T4 Ligation Kit at 16°C overnight.

[000207] *Procedure for the construction of plasmids (2) and (3):*

[000208] In order to replace the αPD-L1 scFv in the previous construct, a forward and a reverse primer were designed and synthesized to introduce the BsiWI and BamHI restriction site and the 5′ and 3′ of the V_HF10-linker-V_LF10 fragment, respectively. After PCR amplification, the PCR products containing V_HF10-linker-V_LF10 and the pcDNA3.4 expression vector were digested with BsiWI and BamHI and used to replace the DNA fragments encoding V_HPD-L1-linker-V_LPD-L1 within the previously constructed expression plasmids, V_HGITR^1-linker-V_LGITR^1-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1 and V_HGITR^{10}-linker-V_LGITR^{10}-linker-hinge-linker-V_HPD-L1-linker-V_LPD-L1. The digested expression vector and inserts were gel-purified (1% agarose) using QIAquick gel extraction Kit and subsequently ligated to each other by Quick ligation (5 minutes, at RT). This procedure yielded the plasmids (2) and (3) (Figure 14).

[000209] *Primer design for the construction of the control plasmid constructs*

As described above, two primers were designed for control plasmids (2) and (3) to isolate V_HF10-linker-V_LF10. The forward primer (5′-3′) was designed to bind on the 3′ prime end of the complementary strand of the DNA; the reverse primers (3′-5′) were designed to bind on the 3′ prime end of the main DNA strand and were reverse complementary. The primers were about 20 bp long with an optimal melting temperature between 62 and 65°C and not deviating more than ± 1°C. The forward primer (containing the BsiWI restriction site (No.1) and the reverse primer (containing the BamHI restriction site (No.2)) were synthesized by Genewiz. For the PCR reaction 100ng DNA template (pcDNA 3.1) was used in the thermal cycling. The PCR product was purified with a QIAquick PCR Purification Kit according to the manufactures protocol and analyzed on a 1% agarose gel.

[000210] Example 2: Cloning of αGITR10-αPD-L1 tetrameric bispecific antibody(tBsAb) containing a CH2 domain

[000211] *Cloning strategy*

[000212] The aim of this example was to introduce a CH2 domain from an IgG1 into the previously-constructed plasmid, leading to the basic structure of V_HGITR-linker-V_LGITR-linker-hinge-CH2-linker-V_HPD-L1-linker-V_LPD-L1. The addition of CH2 adds an effector function, resulting in a trifunctional tBsAb.

[000213] The pcDNA3.4 expression vector containing αGITR10-αPDL1 served as the template used for the construction of the new plasmid. A new restriction site HindIII was introduced by site-directed mutagenesis between the IgG1 hinge region and the linker $(GGGGS)_6$. This newly constructed restriction site served as the cloning site for the IgG1 constant CH2 domain (see Figure 15). The HindIII restriction site was chosen for several reasons. The HindIII restriction site is unique in the plasmid and its genomic sequence is not similar to its adjacent coding region. Nevertheless, HindIII features some drawbacks such as the relative long length (6 nucleotides) possibly diminishing the mutagenesis efficacy.

[000214] The IgG1 plasmid was used as a template to isolate the CH2 domain. The CH2 sequence was amplified by PCR using primers containing the restriction site HindIII. The pcDNA 3.4 expression vector (V_HGITR^{10}-linker-V_LGITR^{10}-linker-hinge-HindIII*-V_HPD-L1-linker-V_LPD-L1) and the amplified CH2 fragments were digested with the corresponding restriction enzymes. The digested vectors and fragments were gel-purified (1% agarose) using QIAquick gel extraction Kit. Cohesive inserts from the HindIII digest were ligated into the vector (pcDNA 3.4) with twentyfold insert using the Quick Ligation Kit resulting in the construction of a new plasmid V_HGITR^{10}-linker-V_LGITR^{10}-linker-hinge-CH2-linker-V_HPD-L1-linker-V_LPD-L1.

[000215] *Site-directed mutagenesis*

[000216] Mutagenesis of the GITR10-PDL1 vector was accomplished with the use of QuikChange Lightning Site-Directed Mutagenesis Kit (Aligent technologies®) following the manufacturer's protocol. Two oligonucleotide primers were synthesized, each complementary to the opposite strand of the vector. Both primers contained HindIII as the desired mutation.

[000217] The primers were designed to exhibit the HindIII mutation in the middle of the primer flanked by 7 to 10 bases. The oligonucleotide primers were used for extension by PfuUltra HF DNA Polymerase during temperature cycling. This approach enabled the generation of a mutated plasmid containing staggered nicks. During the next temperature cycle, the product was treated with DpnI to digest the parental DNA template containing methylated and hemimethylated DNA. As a control, the 4.5-kp pWhitescript plasmid was used to test the mutant plasmid. The pWhitescript plasmid codes a stop codon (TAA) at the position where a glutamine codon would appear in the β-galactosidase gene of the pBluescript II, usually obliterating the blue color of the colonies on LB-ampicillin agar plate containing IPTG and Xgal. However, the oligonucleotide control primers create a point mutation on the pWhitescript 4.5-kb control plasmid that reverts the T residue of the stop codon to C, thereby producing the phenotype of blue color on media containing IPTG and X-gal. After the cycling, 2 µL of the DpnI restriction enzyme was added (37°C, 5 min) to digest the parental dsDNA. The mutagenesis plasmid was then transformed into XL10Gold® Ultracompetent cells and spread on LB-ampicillin agar plates containing 80µg/ml X-gal and 20mM IPTG (37°C; > 16 hours). On the following day, 16 clones were picked from the LB-ampicillin plates, purified using QIAprep spin Miniprep Kit and digested with HindIII and NotI restriction enzymes to identify successfully-mutated clones. Positive clone No. 10 (GITR10-PDL1 with HindIII) was subjected to another digestion to compare it with the original plasmid GITR10-PDL1 (no HindIII). Each sample was individually digested with HindIII or BamHI and simultaneously with HindIII and BamHI–HF together, resulting in a total of six digestions (see Table 1 below).

Table 1 | Parameters and volumes for the total six restriction enzyme digestions

Digestion Parameters	**GITR10-PDL1 with HindIII restriction site**			**GITR10-PDL1**		
	1	2	3	1	2	3
Plasmid (2.0 µg) [µL]	3.1	3.1	3.1	3.1	3.1	3.1
10x Cutsmart (NEB®) [µL]	3.0	3.0	3.0	3.0	3.0	3.0
HindIII-HF (20,000U/mL, NEB®) [µL]	0.5	-	0.5	0.5	-	0.5
BamHI-HF 20,000U/ mL [µL]	-	0.5	0.5	-	0.5	0.5
ddH2O (Mili-Q®) [µL]	ad. 30	ad. 30	ad. 30	ad. 30	ad. 30	ad. 30

The six samples were incubated for 2 hours at 37°C and analyzed in a 1% agarose gel.

[000218] The bacteria containing the positively-mutated clone No.10 were amplified overnight at 37°C in 120mL YT medium followed by plasmid DNA purification, using the QIAGEN Plasmid Maxi Kit. The correct construct, containing HindIII restriction site, was confirmed by sequencing (Genewiz®, using pre-designed primers. A glycerol stock was prepared and stored at -80°C. The recipient plasmid containing HindIII domain and the CH2 fragment were digested with HindIII and subsequently ligated to each other. Ligation products were transformed by heat-pulse into XL10-Gold® Ultracompetent cells according to the protocol described herein. The correct plasmid was verified by sequencing (Genewiz®).

[000219] *Transformation*

[000220] Ligation products were transformed by heat-pulse into XL10-Gold® Ultracompetent cells. These cells were gently thawed on ice. For each transformation, 45µL of the cells were mixed with 2µL of B-Mercaptoethanol and 1.5 µL of the interested DNA. The transformation reaction was incubated for 30 minutes followed by heat-pulse in a 42°C water bath for 40 seconds. 0.5 mL of S.O.C Medium (Life Technologies®) was added to each tube and incubated for one hour at 37°C. The transformation reaction was grown overnight on LB-ampicillin plates at 37°C.

[000221] Several colonies per ligation sample were picked individually and grown in 1.5 mL 2-YT medium for 8 hours. Plasmids of the picked clones were purified using the QIAprep Spin Miniprep Kit as specified by the manufacturer. Correct plasmids were verified by sequencing (Genewiz®). Bacteria of positive clones were grown overnight in 120mL YT medium (37°C, 240rpm) and plasmid DNA was purified using the QIAGEN Plasmid Maxi Kit (as per manufacturer's protocol). Glycerol stocks were prepared by adding 400 µL glycerol and 600 µL of the culture into cryotube vials and then stored at -80°C.

[000222] *Cell culture & Transfection*

[000223] For protein expression 293F human cell lines 293F were obtained from Life Technologies® and 293 T adherent cell line from the ATCC cell bank.
For cell-based ELISA assays, CF2-GITR cell lines were generated in the Marasco Laboratory to express GITR on cell surface.

[000224] *293F cells in suspension for protein expression*

[000225] Suspension cultures of 293F cells (derived from human embryonic kidney cells; HEK cells) were maintained in Erlenmeyer flasks (Corning®) and in 293 freestyle medium (Life Technologies®) at 37°C and with 5% CO_2. Cells were passaged during log growth phase and were diluted into an optimal density (200,000 cells/mL) with fresh medium for continued growth.

[000226] *293T and the CF2-GITR adherent cells*

[000227] Adherent 293T or CF2-GITR cells were maintained in 75 cm2 flasks (Cellstar) and DMEM medium (Life Technologies®) supplemented with 10% FBS (fetal bovine serum) (Life Technologies®) and 1% SP (Sodium Pyruvate) (Life Technologies®) at 37°C in 5% CO_2. Cells were passaged at 80-100% confluency and were diluted to an optimal seeding density ($2x10^6$ cells) with fresh medium for continued growth.

[000228] *Transfection*

[000229] For the production of the tetrameric bispecific antibody (tBsAb) (αGITR1-αPD-L1, αGITR10-αPD-L1, αGITR11-αPD-L1, αGITR14-αPD-L1, αGITR15-αPD-L1, αGITR17-αPDL1 and αGITR10-αPD-L1 (with CH2)) and the control antibodies (αGITR1-F10, αGITR10-F10, F10-αPD-L1, αGITR IgG), 293 F or 293T cells were transfected with the respective plasmids.

[000230] *Polyethlenimine (PEI)-mediated transient transfection in 293F HEK cells*

[000231] One day before transfection, cells were passed into a final concentration of $6x10^5$ cells/mL in a total volume of 300 mL. On the day of transfection, the cell density was between 1.0 $x10^6$ and 1.4 $x10^6$ cells/mL. The respective plasmids were prepared for transfection. The overall charge of the transfection complexes is determined by the ratio of transfection reagent to the DNA. The negative charge contributed by the phosphates in the DNA backbone is offset by the positive charge of the transfection reagent. This allowed good complex formation and for neutralization of the electrostatic repulsion imparted on the DNA by the negatively-charged cell membrane. A 1:1 ratio of Plasmid:PEI allowed full binding of polymer to DNA and full condensation occurred to protect the cargo; however, the excess of PEI is critical for overcoming the inhibitory effects of the anionic cell surface. For every million cells, 1 μg plasmid and 3 μg PEI were used for transfection and each was diluted into 15mL Opti-MEM (Reduced Serum Medium) (Life Technologies®) separately. Diluted PEI was added to the plasmid and incubated at RT for 20 minutes. The efficiency of neutralization increases with time of exposure to the PEI-DNA complex; however excessively long exposure to lipid reagents can be toxic. The PEI/Plasmid complex was poured into the 293F suspension cells ($1x10^6$ cells/mL; 300 mL per flask) and was incubated at 37°C at 140 rpm for 6 days.

[000232] *Polyethlenimine (PEI) mediated transient transfection in 293T HEK cells*

[000233] Transfection of 293T HEK with use of PEI cells follows the same protocol as described above for the 293F suspension HEK cells with a couple of small changes.

Transfection was done on 293T cells growing at 80% confluency in tissue culture dishes (200mm) diluted DMEM medium supplemented with 10% FBS. For 40µg of DNA, 200µg of PEI was used (a 1:5 ratio) and each was diluted separately in 1mL Opti-MEM (Reduced Serum Medium) (Life Technologies®) separately. The diluted PEI was added to the plasmid and stored at RT for 20 minutes. The DNA/PEI complex was added gently, drop wise, into the dish to prevent cell detachment and death. The cells were then incubated at 37°C for 2 days.

[000234] **Example 3: Protein Purification**

[000235] *Ni-NTA Purification of bispecific antibody antibodies*

Suspension of 293 HEK cells were harvested and centrifuged at 5000 rpm, 4°C for 35 minutes. To purify the bi-specific antibodies via their N-terminal 6xHis-tags, the filtered supernatant (0.22 µm PEV, Costar®) was incubated for 2 hours (240 rpm, RT) with 1mL of Ni-NTA agarose (Qiagen). The supernatant was passed twice over a 15 ml Ni-NTA Sepharose gravity flow column. After washing, the column containing the beads were washed with four column volumes of Ni-NTA washing buffer (0.02M Imidazole, 0.3M NaCl, 1M Tris HCl (pH=7.0)) the protein was slowly eluted with 13 mL of Ni-NTA elution buffer (0.5M Imidazole, 0.3 NaCl, 0.02 Tris HCl (pH= 7.0)). The buffer of the eluted protein was exchanged by PBS buffer using centrifugal filter units 100,000 MW (Amicon®). The yield of the tBsAbs and was measured with the NanoDrop ND-1000.

[000236] *Protein A Purification of αGITR IgG antibody*

[000237] The αGITR IgG antibodies were harvested from the suspension of 293 HEK cells and centrifuged at 5000 rpm, 4°C for 35 minutes. To purify the αGITR IgG antibodies via the Fc domain, the filtered supernatant was incubated (RT, shaking) with 1mL of Protein A (GE Lifesciences) for 2 hours then passed twice over a 15 ml gravity flow column (Biorad) followed by 10mL PBS for washing. The αGITR IgG was eluted with 2ml TEA (100nM) and 200 µL of Tris-HCl (1M, (pH=7)) was added to the elution in order to neutralize TEA. An additional 2mL PBS was added onto column, and was collected into the tube with the eluted protein.

[000238] **Example 4: Protein characterization**

[000239] *SDS-PAGE analysis*

[000240] SDS-PAGE analysis was used to verify the purity of proteins, according to the NuPAGE NuPAGE® technical guide (Invitrogen). NuPAGE Bis-Tris Gels (4-12%)

(Novex) were used in MES SDS running buffer, with a total protein amount between 3µg and 5µg. The protein samples were mixed with 4x LDS sample buffer (Novex), containing dodecylsulfate, to denature the protein. Under reducing conditions the protein samples were additionally boiled at 100°C for 10 minutes. The samples were then loaded onto Novex Bis-Tris Gels in MES SDS running buffer. The gel was run in a Xcell SureLock Mini-Cell at 200V for 35 minutes and then processed with Coomassie G-250 staining with simplyBlue™ Safe Stain (Novex).

[000241] *Direct ELISA of αGITR-αPD-L1 on passively adsorbed soluble PD-L1 antigen* A Maxisorb 96 well plate (Costar®) was coated with 100µL of 5 µg/mL PD-L1 rabbit Fc antigen and CCR4 protein (negative control) in PBS overnight at RT. On the following day, the plate was washed 3 times with PBS and blocked for 2 hours at RT with 200µL blocking solution (2% BSA in PBS). The plate was washed 3 times with PBS. The primary antibodies αGITR1-αPD-L1, αGITR10-αPD-L1, αGITR11-αPD-L1, αGITR14-αPD-L1, αGITR15-αPD-L1, αGITR17-αPD-L1, F10-αPD-L1 BsAB and commercial anti-mouse PD-L1 mAb (Biolegend) prepared in 1X PBS with variable concentrations and added to the wells (100µL) for 2 hours incubation at room temperature. The highest concentration of antibody tested was at 1µg/mL and then serially diluted in a ten-fold manner until the $1x10^{-5}$ µg/mL dilution. Each sample was run in triplicate at every concentration. Several controls were set-up and are listed in the table below (Table 2). The 96 well plate (Costar) was washed three times with 1X PBS buffer. A solution of the secondary antibody (6xHis-HRP (Thermoscientific) and Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific) were diluted (1:2000 and 1:5000) in 1X PBS. The secondary antibodies (100µL) were added to each well and incubated for 2 hours at room temperature. Finally, each well was washed four times with PBS. The 96 well plate was developed with 100 µL TBM substrate solution (Thermoscientific); after development 100 µL phosphoric acid stop solution (Thermoscientific) was added. The endpoint OD data was recorded at 450nm with Bio-Rad Benchmark Plus and analyzed with the Microplate Manager 5.2.1 software.

Table 2 | Experimental Overview on tested samples and controls for direct ELISA of αGITR-αPD-L1 on passively adsorbed PD-1 antigen

Antigen	Test-Type	Primary AB	Secondary AB	Purpose	Expected signal

PD-L1 rabbit Fc fusion protein	Sample	αGITR-αPD-L1 tetrameric bispecific antibodies	Anti 6xHis-HRP (Thermoscientific)	Sample testing	Positive
		Commercial mouse anti human PD-L1 mAb (Biolegend)	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Standard and verification that PD-1 rabbit Fc can be labeled	Positive
	Control	No	Anti 6xHis-HRP (Thermoscientific)	Measure unspecific binding	Negative
		No	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Measure unspecific binding	Negative
CCR4-human Fc	Control	Commercial anti mouse PD-L1 mAb (Biolegend)	Anti 6xHis-HRP (Thermoscientific)	Verification of specific binding of samples	Negative
		No	Anti 6xHis-HRP (Thermoscientific)	Measure unspecific binding	Negative
		No	Goat anti-mouse IgG Fc, HRP conjugate	Measure unspecific binding	Negative

[000242] *Cell-based ELISA of αGITR-αPD-L1 BsAbs on GITR$^+$ CF2*

For the cell-based ELISA, the αGITR1-αPD-L1, αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 antibodies were tested for retained binding capability on GITR+CF2 cells. In total, four ELISA experiments were set up.

[000243] The first cell-based ELISA the αGITR1-F10 and the αGITR10-F10 tetrameric bispecific antibodies (tBsAbs) were analyzed. For GITR+ CF2 and GITR– CF2 cell (negative control) seeding, 1,000 cells per well were added in 200 μL of 1% DNEM medium and were incubated overnight to allow attachment. On the following day, the cells were fixed with 100 μL of Acetone-Methanol solution (1:1 ratio) and incubated for 20 minutes at RT. The Acetone-Methanol solution was aspirated from the plate and the cells were washed three times with 1X PBS. The general assay procedure and development was performed according to the protocol for ELISA mentioned in chapter 2.6.2. The primary antibodies αGITR1-αPD-L1 and αGITR10-αPD-L1 were tested in variable concentrations. The tBsAbs were serially diluted by one third in 1X incubation buffer; 3.33mg/ mL being the highest concentration and 0.0411 mg/mL the lowest. Several controls were set-up and are listed on the table below (Table 3).

Table 3 | Experimental Overview on tested samples and controls for cell based ELISA of αGITR1-αPD-L1 and αGITR10-αPD-L1 on GITR+CF2 cells

Antigen	Test-Type	Primary AB	Secondary AB	Purpose	Expected signal
GITR^{+}CF2	Sample	αGITR1-αPD-L1	Anti 6xHis-HRP (Thermoscientific)	Sample test	Positive
		αGITR10-αPD-L1	Anti 6xHis-HRP (Thermoscientific)	Sample test	Positive
		F10-αPDL1	Anti 6xHis-HRP (Thermoscientific)	Negative control	Negative
	Control	No	Anti 6xHis-HRP (Thermoscientific)	Unspecific binding	Negative
GITR^{-}CF2	Sample	αGITR1-αPD-L1	Anti 6xHis-HRP (Thermoscientific)	Sample test	Negative
		αGITR10-αPD-L1	Anti 6xHis-HRP (Thermoscientific)	Sample test	Negative
		F10-αPDL1	Anti 6xHis-HRP (Thermoscientific)	Sample	Negative
	Control	No	Anti 6xHis-HRP (Thermoscientific)	Unspecific binding	Negative

[000244] After evaluating the results of the cell-based ELISA (Figure 20), the experiment for a second cell-based ELISA was repeated using the same procedure to that described above, except that cells were fixed with 8% paraformaldehyde.

[000245] A third cell based ELISA was performed to compare αGITR10-αPD-L1 tBsAb to the commercial human αGITR mAb. For GITR^{+} CF2 and GITR^{-}CF2 cell (negative control) seeding, 10,000 cells per well were added in 200 μL of 1% DMEM medium and were incubated overnight to allow attachment. On the following day, the cells were fixed with 100 μL of 8% paraformaldehyde and incubated for 20 minutes at RT. The paraformaldehyde solution was aspirated from the plate and the cells were washed three times with 1X PBS. The general assay procedure and development was performed according to the protocol for ELISA mentioned herein. The primary antibodies αGITR10-αPD-L1 and αGITR mAb were tested in variable concentrations. The antibodies were serially diluted (1:2) in 1X incubation buffer; 5mg/ mL being the highest concentration and 0.078 mg/mL the lowest. Several controls were set-up and are listed on the table below (Table 4).

Table 4 | Experimental Overview on tested samples and controls for cell based ELISA of αGITR10-αPD-L1 and αGITR mAb on GITR+CF2 cells

Antigen	Test-Type	Primary AB	Secondary AB	Purpose	Expected signal
$GITR^+CF2$	Sample	αGITR10-αPD-L1	His-HRP	Sample test	Positive
		Commercial GITR mAb (Purified anti-hu CD357)(Biolegend)	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Standard	Positive
	Control	F10-αPDL1	His-HRP	Control	Negative
		No	His-HRP	Measure unspecific binding	Negative
		No	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Measure unspecific binding	Negative
$GITR^-CF2$	Sample	αGITR10-αPD-L1	His-HRP	Sample test	Negative
		Commercial GITR mAb (Purified anti-hu CD357)(Biolegend)	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Standard	Negative
		F10-αPDL1	His-HRP	Control	Negative

Control	No	His-HRP	Measure unspecific binding	Negative
	No	Goat anti-mouse IgG Fc, HRP conjugate (Thermoscientific)	Measure unspecific binding	Negative

[000246] The fourth ELISA was performed to compare αGITR10-αPD-L1 with CH2 tBsAb to the commercial αGITR mAb. The assay procedure was identical to the third ELISA (mentioned above).

[000247] *Flow cytometry analysis for αGITR1-αPD-L1 & αGITR10-αPD-L1*

[000248] The biological activity of αGITR on GITR+CF2 cells was analyzed by means of fluorescence-activated cell sorting FACS analysis. The cells GITR+CF2 cells and GITR-CF2 were grown in a 75 cm^2 flask (Cellstar) until they reached roughly 80% confluence. They were detached by adding 1:10 diluted Trypsin with 0.25% Trypsin-EDTA (Life Technologies) in PBS and resuspended and then added to 96-well round bottom plate in FACS buffer (PBS, 1% FBS, 2mM EDTA). In the following step the αGITR1-αPD-L1 and αGITR10-αPD-L1 were added at variable concentrations for 1 hour at 4°C. The highest concentration of antibody tested was at 100μg/mL and then serially diluted in a two-fold manner until the 0.05 μg/mL dilution. The primary antibodies were detected with His Tag Alexa Fluor 488-conjugated (Biotechne). The secondary antibody was diluted in PBS (Life Technologies) and added to each well for 30 minutes. The cells were then washed three times with PBS buffer and resuspended in FACS buffer. In total 10,000 events were analyzed with FACSCalibur. Results were analyzed by FlowJo 10.1 software. Several controls were performed and are listed in the table below. (Table 5)

Table 5 | Experimental Overview on control samples for FACS analysis of αGITR1-αPD-L1α and GITR10-αPD-L1 on GITR+CF2 cells and GITR-CF2 cells.

Antigen	Test-Type	Primary AB	Secondary AB	Purpose	Expected signal
GITR$^+$CF2	Control	none	Alexa 488; anti-His (APC)	Unspecific binding of secondary AB	negative

		F10-αPD-L1	Alexa 488; anti-His (APC)	Exclude the PD-L1 binding to GITR+ CF2	negative
		αGITR1 mAb	Anti-human IgG Fc (FITC)	Verify that αGITR arm can recognize the GITR binding site	positive
		none	Anti-human IgG Fc (FITC)	Unspecific binding of secondary	negative
		Commercial mouse αGITR IgG	Anti-mouse IgG Fc (FITC)	Verify that CF2 cells are expressing GITR	positive
		none	Anti-mouse IgG Fc (FITC)	Unspecific binding of secondary	negative
		none	Alexa 488; anti-His (APC)	Unspecific binding of secondary	negative
GITR$^-$CF2	Control	F10-αPD-L1	Alexa 488; anti-His (APC)	Exclude the PD-L1 binding to GITR+ CF2	negative
		αGITR1 IgG	Anti-human IgG Fc (FITC)	Verify that αGITR arm binds specifically to GITR+ CF2 cells	negative

[000249] **Example 5: Functional studies**

[000250] *ADCC assay of αGITR-αPDL1 with CH2 on GITR+CF2 cells*

[000251] The antibody-dependent cell-mediated cytotoxicity of αGITR-αPD-L1 with CH2 on GITR+CF2 cells was analyzed using ADCC Reporter Bioassay Complete Kit (WIL2-S) (Promega) and implemented according to the manufacturers protocol. The aim was to test the αGITR10-αPD-L1 with CH2 for ADCC. The assay was performed using ADCC reporter cells (WIL2-S) that have Fcγ receptors and the response element-driven luciferase gene.

[000252] The cells GITR$^+$CF2 cells and GITR$^-$CF2 were grown in a 75 cm^2 flask (Cellstar) until they reached roughly 80% confluence. They were detached by adding 1:10 diluted 0.25% Trypsin-EDTA (Life Technologies) in PBS and tested for viability. The GITR$^+$CF2 cells were used as target cells and plated in 96-well cell flat bottom microplate (PerkinElmer) at a density of 2x10^4 cells per well diluted in RPMI 1640 medium (Life Technologies®; serum free). The αGITR10-αPD-L1 (with CH2) and the controls (αGITR10-IgG (positive control) and GITR10-PD-L1 and F10-PDL1 (negative control) were serially diluted in ADCC assay medium. The four antibodies were added in a concentration-dependent manner, starting at 20 mg/mL (highest concentration), followed by 2 mg/mL, 0.2 mg/mL and 0.02 mg/mL, respectively (1:10 serial dilution) and incubated for 5 minutes at RT. Following incubation, the effector cells WIL2-S were suspended in ADCC assay medium and added to the target cell/antibody mixture at 10x10^6 cells per well. The ratio of effector cells to target cells was set up as 5:1 (E/T). After approximately a 6 hour incubation at 37°C (5% CO_2), an equal volume of the Bio-Gio Luciferase assay reagent (Promega) was added to the wells and incubated (RT, 10 min). The luminescence of the cells was measured using Polarstar Omega. Assays were performed in triplicate. All data were plotted using Excel.

[000253] *CDC assay of αGITR-α-PDL1 with CH2 on GITR$^+$CF2 cells*

[000254] For the testing of complement-dependent cytotoxicity (CDC) of the αGITR10-α-PDL1 with CH2 tBsAb, baby rabbit complement (Cedarlane Laboratories) was used in the CellTox™ Green Cytotoxicity assay (Promega) using CellTox Green Dye (Promega) that binds DNA in comprised cells. The fluorescent signal produced by the dye binding to the dead-cell DNA is proportional to cytotoxicity. The assay was performed according the manufacturers protocol. The experimental procedure and set-up for the testing of complement-dependent cytotoxicity was similar to the CDC test mentioned above, with exception of the assay development and analysis which was performed with the CellTox™ Green Cytotoxicity assay (Promega). The antibodies tested for complement-dependent cytotoxicity were the αGITR10-αPDL1 and the αGITR10-α-PDL1 with CH2 tetrameric bispecific antibodies (tBsAbs). The αGITR mAb was used for positive control and the F10-αPD-L1 was used as negative control.

[000255] After approximately a 4 hour incubation at 37°C (5% CO_2) an equal volume of CellTox Green Dye assay reagent (Promega) was added to the wells and incubated (RT, 10 min). The fluorescence was measured using Polarstar Omega. Assays were performed in triplicate. All data were plotted using Excel.

[000256] Example 6: Isolation and characterization of the αGITR-αPD-L1 BsAbs

[000257] *Generation of expression vector*

[000258] In total six vectors (αGITR-αPD-L1) were constructed to produce the desired tBsAbs and additional three vectors for the production of control Abs (αGITR1-F10, αGITR10-F10 and F10-αPD-L1). The expression vector was generated according to the cloning strategy described above.

[000259] The recipient expression vector pcDNA 3.4 and all donor vectors (six V_HGITR-linker-V_LGITR and inserts and one V_HF10-V_LF10 insert) were digested with SfiI and NotI restriction enzymes and the fragments were separated on a 1% agarose gel, stained with ethidium-bromide. The SfiI and NotI digestion patterns of the seven digestions were in agreement with the theoretically calculated values. The digested recipient vector pcDNA 3.4 vector comprises 7500 bp and can be detected at the correct level (lane1; 8000 bp) of the ladder. The smaller fragment in lane 1 displayed between 500 and a 1000 bp and corresponds to V_H^X-linker-V_L^X of a previously-used scFv. The GITR inserts (lanes 2-6) and the F10 insert (lane 7) were clustered between 500 and 1000bp. The larger bands seen at the level of 8000 bp (lanes 2-7) represent the corresponding descendent vectors.

[000260] Two additional control plasmids (2) and (3) were constructed. The recipient expression vectors pcDNA3.4 encoding the αGITR1-αPDL1 and αGITR10-αPDL1 scFvs were digested with BsiWI and BamHI Res to replace the V_HPD-L1-linker-V_LPD-L1 fragment with V_HF10-linker-V_LF10 fragment. To isolate the V_HF10-linker-V_LF10 fragment from the pcDNA3.1 donor vector, a forward and a reverse primer (No.1 and No.2) were designed, containing the BsiWI and BamHI restriction site. After isolating the cDNA using PCR, it was digested with BsiWI and BamHI RE. The gel analyses of all 3 digestions were consistent with the theoretical number. As anticipated the PCR of F10 fragment only shows one band at the correct position relative to the ladder. The two digested recipient vectors (containing V_HGITR1-V_LGITR1 or V_HGITR10-V_LGITR10, respectively) are approximately 8000 bp in size and match the theoretical size of the vector (7500bp).

[000261] All digested fragments were extracted and purified form the agarose gel and the respective ligation reactions were performed. The yielded plasmids were successfully constructed and confirmed by sequencing (Genewiz).

[000262] Expression of GITR-PDL1 bispecific Antibodies and αGITR-IgG

The αGITR-αPD-L1 proteins were expressed in 293F HEK cells and isolated via Ni-NTA purification. The αGITR IgG protein was expressed in HEK 293F cells and isolated via Protein A purification. The yields measured by NanoDrop spectrophotometer are listed in table 6.

Table 6 | Antibody yield of 293F HEK expression

Antibody	Yield per 300 mL cell culture [mg]	Antibody	per 300 mL cell culture [mg]
αGITR1-αPD-L1	3.3	αGITR17-αPD-L1	2.5
αGITR10-αPD-L1	5.5	F10-αPD-L1	1.1
αGITR11-αPD-L1	2.8	αGITR1-F10	1.4
αGITR14-αPD-L1	1.7	αGITR10-F10	1.5
αGITR15-αPD-L1	2.7	αGITR IgG	2.9

[000263] *SDS-PAGE analysis*

[000264] The purity of the tBsAbs αGITR1-αPDL1, αGITR10-αPDL1, αGITR11-αPDL1, αGITR14-αPDL1, αGITR15-αPDL1, αGITR17-αPDL1 and F10-αPD-L1 were analyzed by SDS-PAGE. Between 3μg-5μg of protein sample was loaded on the gel, separated electrophoretically and stained with Coomassie blue.

[000265] Notable, under non-reducing conditions, there are two bands that particularly draw attention. The upper band lies within the 115 kDa and 140 kDa range. The quantitative predominance of this band in each of the protein profiles and the proximity of its apparent molecular size to that of the αGITR-αPD-L1 tetrameric bispecific antibodies (tBsAbs) (130 kDa) indicate successful antibody production. The lower band lies between 70 and 80 kDa and thus, may account for a substantial amount of monomeric tandem scFv (65 kDa). Apart from this, some weaker bands above 140 kDa are observable, suggesting the formation of aggregates.

[000266] Under reducing conditions, only one band can be seen between 70 and 80 kDa, which suggests the disulfide bond reduction of tBsAbs into tandem scFv (65 kDa).

Deviating molecular weights between apparent and theoretical calculated values can stem from post-translational modifications (such as glycosylation and phosphorylation) as well as protein conformation as it is running through the SDS PAGE. Differences amounts loaded onto the gel can account for differences in the intensity of the bands between the αGITR-αPD-L1 tBsAbs.

[000267] Further, the purity of the αGITR-IgG was also analyzed by SDS-PAGE. Under non-reducing conditions, the analysis exhibited one band with an apparent molecular weight of 140 kDa and is approximate equal to the theoretical calculated molecular weight of an αGITR IgG (150 kDa). The reduced SDS analysis revealed two bands, which proposes the successful disulfide bond reduction of the αGITR IgG resulting in heavy chain (50 kDa) and light chain (25 kDa).

[000268] *Direct ELISA of αGITR-αPD-L1 BsAbs on passively adsorbed PD-L1 antigen*

[000269] Direct ELISA of the αGITR-αPD-L1 BsAbs was performed to characterize their reactivity to the PD-L1 antigen. As shown in Figure 19, reactivity to PD-L1 antigen could be observed in all αGITR-αPD-L1 tBsAbs, while no unspecific stickiness to CCR4 was seen (not shown). The readout signal was very similar for all αGITR-αPD-L1 tBsAbs at all concentrations. Highest ELISA signals were measured at highest concentrations. In addition the absorbance value of αGITR-αPD-L1 tBsAbs binding was comparable to that for the commercial αPD-L1 mAb and the intensity signal decreased with lower concentrations. The ELISA does not show saturation at the higher concentration and has very weak signal at concentrations below 0.01 mg/mL.

[000270] *Cell-based ELISA of αGITR-αPD-L1 tBsAbs on GITR+ CF2*

[000271] In previous studies of αGITR IgGs, αGITR1 IgG and αGITR10 IgG were proven to have the best characteristics, which is why the project here was narrowed down the following experiments to αGITR10-αPD-L1 and αGITR1-αPD-L1 tBsAbs. The cell based enzyme-linked immunosorbent assay (ELISA) was used to test the αGITR1-αPD-L1, αGITR10-αPD-L1 at different concentrations against GITR+ CF2 cells to analyze their reactivity. As shown in Figure 20, reactivity to GITR+ CF2 could be observed for αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies. The OD value of αGITR1-αPD-L1 and αGITR10-αPD-L1 depend on their respective concentrations. Consistent with the expectations, the stronger signal was measured at the higher concentration; then gradually diminished as the concentration decreased.

[000272] The signal intensity of αGITR10-αPD-L1 is superior to that by αGITR1-αPD-L1 at all concentrations. Surprisingly, the negative control F10-αPD-L1 antibody not only shows absorbance but also seems to behave in a concentration-dependent manner. For αGITR1-αPD-L1 and F10-αPD-L1, no readout signal was detected below the threshold of 0.1235 mg/mL. Overall, the standard deviations of the mean were exceptionally high.

[000273] Due to the surprising results of the previous ELISA (see Figure 20), the experiment was repeated. The set-up remained identical, with the exception that the GITR+ CF2 cells were fixed with 8% paraformaldehyde instead of acetone-methanol solution. Results of this second approach revealed similar signal readout observations of αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies, but with slightly higher absorption values (See, Figure 21). However, the F10-αPD-L1 antibody continues to display signal activity and its absorbance is still dependent on the concentration used. The tBsAbs showed no binding when incubated with GITR-CF2 cells. See, Figure 32.

[000274] A third cell-based ELISA was performed to compare αGITR10-αPD-L1 antibody to a commercial αGITR IgG. Reactivity of both antibodies was observed in GITR+CF2 cells (Figure 22) but not GITR-CF2 cells (See, Figure 33). Again, the results of the αGITR10- αPD-L1 matched previous recorded data. The signal intensity of the αGITR mAb is superior to that by αGITR10-αPD-L1 at all concentrations. Surprisingly, at higher concentrations, no saturation of the signal readout could be observed. The control antibody F10-αPD-L1 (neg. control) showed concentration-dependent signal activity for GITR+CF2 cells but not for CF2 cells (without GITR+ expression). See, Figure 33.

[000275] *Flow cytometry analysis of αGITR-αPD-L1 BsAbs on GITR+ cells*

[000276] Flow cytometry analysis assesses the binding of αGITR1-αPD-L1 and αGITR10-αPD-L1 antibodies to GITR+CF2 cells (Figures 23 and 24). The results show, that both antibodies (co-stained with an APC-labeled His-Tag Alexa Fluor 488) can bind specifically the GITR+CF2. Further, the tBsAbs had no reactivity against GITR-CF2 (Figure 34) Note that some non-specific binding is caused by the secondary antibodies as shown in the controls (Figure 34). The comparison of the two antibodies to each other shows that they display similar binding under the identical conditions. Therefore, only the αGITR10-αPD-L1 tBsAb was selected for further characterization. The standard measurement of the αGITR1 IgG and αGITR10 IgG revealed similar binding properties when compared to the tBsAbs.

[000277] Example 7: Isolation and characterization of αGITR-αPD-L1 with CH2 bsAb

[000278] *Generation of bacterial expression vector*

[000279] In previous studies, the αGITR10 mAb was proven to exhibit the best characteristics, which is why αGITR10-αPD-L1 was chosen as the expression vector for the engineering of the new construct containing a CH2 domain. The vector was generated according to the cloning strategy described above, resulting in the gene order V_HGITR-linker-V_LGITR-linker-hinge-CH2-linker-V_HPD-L1-linker-V_LPD-L1.

[000280] Site-directed mutagenesis enabled introduction of a HindIII restriction site into the recipient pcDNA 3.4 vector between the IgG1 Hinge region and the linker $(GGGGS)_6$. After transformation into E.coli strain XL10-Gold® Ultracompetent cells, 16 clones were picked then underwent DNA purification. A restriction enzyme digestion analysis using HindIII and BamHI restriction enzymes, displayed on a 1% agarose gel, tested for the correct introduction of HindIII restriction site (See Figure 25). Of the 16 clones, only clone No. 10 showed two bands. The size of the smaller band clustered between 500 and 1000 bp, corresponds to the theoretical size of HindIII and BamHI digestion (800 bp). Since HindIII and BamHI represent unique restriction sites in the plasmid, this result indicated a successful introduction of HindIII into the DNA of cells in clone No. 10.

[000281] An additional gel analysis of clone No. 10 was undertaken to compare it to the original GITR10-PDL1 (that does not contain the HindIII restriction site); see Figure 26. Clone No. 10 (GITR10-PDL1 with HindIII) and GITR10-PDL1 (without HindIII) each individually underwent three digestions. The first digestion was performed with only HindIII restriction enzyme, a second one with only NotI restriction enzyme and a third digestion with both HindIII and NotI restriction enzymes. The digestions of clone No.10 with a single enzyme resulted in open-circular conformation and were clustered around 8000 bp. In contrast, the double digestion of clone No. 10 with HindIII and NotI restriction enzymes resulted in two bands. The lower band is clustered below 500 bp and corresponds to the theoretical calculated value for the HindIII/NotI digestion fragment (117 bp). The αGITR10-αPD-L1 plasmid does not contain a HindIII restriction site, which is why the gel analysis of HindIII single digestion revealed, as anticipated, the supercoiled plasmid DNA. These results strongly suggest the correct introduction of the HindIII restriction site.

[000282] The sequencing results (Genewiz) of clone No. 10 confirmed the correct introduction of HindIII between the hinge and the linker domain. However, deletion of five linker-repeats of the total six (GGGGS) repeats occurred during site directed mutagenesis. The new construct consequently exhibited only one repeat of the linker sequence rather than six linker repeats. Nevertheless, it was decided to continue plasmid construction with this new created plasmid containing a hinge region followed by one single linker repeat (GGGGS).

[000283] Two primers (forward and reverse) were designed to isolate the CH2 domain from an IgG1 plasmid. Each primer included a HindIII restriction site. The recipient vector GITR10-PDL1 (containing the HindIII site) and the CH2 fragment were single digested with the HindIII restriction enzyme and analyzed in a 1% agarose gel (Figure 27). Both digestions resulted in a fragment size that matches the theoretical calculated values: 7.5bp for the recipient vector GITR10-PDL1 with HindIII and 350bp for the CH2 fragment.

[000284] Therefore, the pcDNA 3.4 expression vector αGITR10-αPD-L1 with CH2 was successfully constructed and confirmed by sequencing (Genewiz).

[000285] *SDS-PAGE analysis*

The αGITR10-αPD-L1 with CH2 protein was expressed in 293T HEK cells and isolated via Ni-NTA purification. A total of 100 mL culture media resulted in 200ng protein yield (NanoDrop analysis). The purity of the GITR10-PDL1 with CH2 tBsAb was analyzed by SDS-PAGE (Figure 28). In total 3µg of protein sample was loaded on the gel, separated electrophoretically and stained with Coomassie blue. Notable, under non-reducing conditions there are two bands that particularly draw attention. The upper band lies slightly above 140 kDa. The quantitative predominance of this band and the proximity of its apparent molecular size to that of the αGITR10-αPD-L1 with CH2 tBsAb (150 kDa) propose the successful antibody production. The lower band has an apparent molecular weight of 80 kDa and thus, may account for a substantial amount of tandem scFv containing the CH2 (75 kDa) that did not dimerize. Under reducing conditions only one band can be seen at 80 kDa, which suggests that the disulfide bond reduction of the tBsAb into tandem scFv (75 kDa).

[000286] *Cell-based ELISA of αGITR-αPD-L1 with CH2 tetrameric bispecific antibody (tBsAb) on GITR$^+$ CF2*

[000287] The cell-based enzyme-linked immunosorbent assay (ELISA) was performed to test the αGITR10-αPD-L1 with CH2 at different concentrations against GITR$^+$ CF2 to analyze their signal intensity.

[000288] As shown in Figure 29, reactivity to GITR$^+$ CF2 could be observed in αGITR10-αPD-L1 with CH2 antibodies, while no unspecific stickiness to GITR$^-$ CF2 was noted; see Figure 35. The OD value of αGITR10-αPD-L1 with CH2 depends on their respective concentrations. Consistent with the expectations, the strongest signal was measured at the highest concentration; then gradually diminished as the concentration decreased. The signal intensity of the αGITR IgG is superior to that of αGITR10-αPD-L1 with CH2 at most concentrations. Surprisingly, at higher concentrations, no saturation of the signal readout could be observed. The control antibody (F10-αPD-L1) was tested at highest concentration (5μg/mL) and had, as previously seen (Figures 22 and 21), some reactivity.

[000289] **Example 8: Functional studies of αGITR-αPD-L1 with CH2 BsAb**

[000290] In an initial attempt to establish functional data, complement-dependent cytotoxicity (CDC) and antibody dependent cellular cytotoxicity (ADCC) was tested for the αGITR-αPD-L1 with CH2 BsAbs. However, the results were inconclusive.

[000291] *ADCC Reporter Assay of αGITR-αPD-L1 with CH2 BsAb on GITR+ CF2*

[000292] The αGITR10-αPD-L1 with CH2 BsAb was tested for ADCC activity using GITR+CF2 cells (target cells) and the WIL2-S (effector cells) (E/T= 5:1). Antibody biological activity in ADCC was quantified through the luciferase produced as a result of NFAT pathway activation and its activity in the effector cell was quantified with luminescence readout. In the ADCC analysis, the αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 displayed surprising results (Figure 30). The negative control F10-αPD-L1 displayed similar signal intensity for ADCC compared to solely target and effector cells and is unbiased to variable concentrations. The positive control αGITR IgG on the other hand, exhibited, as expected, increasing values with higher concentrations. Surprisingly, for the αGITR10-αPD-L1 and αGITR10-αPD-L1 with CH2 the ADCC signal intensity decreased with higher concentrations and was substantially lower than the signal of solely target and effector cells at 20μg/mL tBsAbs.

[000293] The ADCC activity ofααGITR10-αPD-L1 with CH2 and was measures at variable concentrations. All antibodies were serially diluted (1:2), starting the highest concentration at 20 mg/mL until 0.02 mg/mL and tested against 20,000 GITR+CF2 cells per well. The ratio of effector cells (GITR+CF2) to target cells (Wils-2) was 5:1. The αGITR IgG represents the positive control and F10-αPD-L1 the negative control. The vertical axis represents the raw value of luciferase activity in the effector cell quantified with luminescence readout. Each sample was run in triplicates at every concentration; the mean standard deviation is indicated in brackets. The background of GITR+CF2 cells in RPMI medium was subtracted from the obtained values.

[000294] *CDC analysis of αGITR10-αPD-L1 BsAb with CH2 on GITR+CF2 cells*

[000295] The αGITR10-αPD-L1 with CH2 antibody was tested for complement-dependent cytotoxicity against CF2 cells expressing the GITR by measuring the amount of fluorescent CellTox Green bound to comprised DNA. The percentage of lysis is calculated as the ratio of the intensity of the signal obtained from the sample, to the intensity of the signal from fully lysed GITR+ CF2 cells (Figure 31).

[000296] The negative control F10-αPD-L1 BsAb displayed similar percentages of cytotoxicity as the positive control αGITR IgG. αGITR10-αPD-L1 with CH2 exhibited similar cytotoxicity levels at all concentrations ranging between 65% and 70% and did not appear to be concentration dependent. Neither of the measured antibodies had a substantial higher percentage of cellular cytotoxicity. These findings largely contradict the expected outcome; a possible reason for these incongruities is a potentially low viability of the used GITR+CF2 cells.

OTHER EMBODIMENTS

[000297] While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

[000298] It is an object of the present invention to overcome or ameliorate at least one of the disadvantages of the prior art, or to provide a useful alternative.

[000299] The term "comprise" and variants of the term such as "comprises" or "comprising" are used herein to denote the inclusion of a stated integer or stated integers but not to exclude any other integer or any other integers, unless in the context or usage an exclusive interpretation of the term is required.

[000300] Any reference to publications cited in this specification is not an admission that the disclosures constitute common general knowledge in Australia.

[000301] Definitions of the specific embodiments of the invention as claimed herein follow.

According to a first embodiment of the invention, there is provided a tetravalent antibody molecule, wherein the tetravalent antibody molecule is a dimer of a bispecific scFv fragment, wherein the bispecific scFV fragment comprises a first binding site specific for GITR, a second binding site specific for PD-L1, and a linker-hinge-linker domain, wherein the two binding sites are joined together via a linker-hinge-linker domain, wherein the linker-hinge-linker domain consists of an immunoglobulin hinge region amino acid sequence according to SEQ ID NO: 1902, SEQ ID NO: 1903, or SEQ ID NO: 1904, flanked by a flexible linker amino acid sequence at both termini, wherein the hinge region is an IgG1, an IgG2, an IgG3, or an IgG4 hinge region, wherein the flexible linker amino acid sequence independently comprises the amino acid sequence (GGGS)X1-6 (SEQ ID NO: 1906), (GGGGS)X1-6 (SEQ ID NO: 1907), or GSAGSAAGSGEF (SEQ ID NO: 1908), and wherein the tetravalent antibody molecule does not comprise an antibody constant region or portion thereof.

According to a second embodiment of the invention, there is provided a nucleic acid construct comprising nucleic acid molecules encoding:

a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to GITR;

a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to PD-L1; and

a linker-hinge-linker domain,

wherein the linker-hinge-linker domain consists of an immunoglobulin hinge region acid sequence according to SEQ ID NO: 1902, SEQ ID NO: 1903, or SEQ ID NO: 1904, flanked by a flexible linker amino acid sequence at both termini, wherein the hinge region is an IgG1, an IgG2, an IgG3, or an IgG4 hinge region, wherein the flexible linker amino acid sequence independently comprises the amino acid sequence (GGGS)$_{X1-6}$ (SEQ ID NO: 1906), (GGGGS)$_{X1-6}$ (SEQ ID NO: 1907), or GSAGSAAGSGEF (SEQ ID NO: 1908), and wherein the tetravalent antibody molecule does not comprise an antibody constant region or portion thereof.

According to a third embodiment of the invention, there is provided a vector comprising the nucleic acid construct of the second embodiment.

According to a fourth embodiment of the invention, there is provided a host cell comprising the vector of the third embodiment.

According to a fifth embodiment of the invention, there is provided a chimeric antigen receptor (CAR) comprising an intracellular signaling domain, a transmembrane domain and an extracellular domain comprising the tetravalent antibody molecule of the first embodiment.

According to a sixth embodiment of the invention, there is provided a genetically engineered cell which expresses and bears on the cell surface membrane the chimeric antigen receptor of the fifth embodiment.

According to a seventh embodiment of the invention, there is provided a genetically engineered cell which is engineered to express and secrete the tetravalent antibody molecule of the first embodiment.

We Claim:

1. A tetravalent antibody molecule, wherein the tetravalent antibody molecule is a dimer of a bispecific scFv fragment, wherein the bispecific scFv fragment comprises a first binding site specific for GITR, a second binding site specific for PD-L1, and a linker-hinge-linker domain, wherein the two binding sites are joined together via a linker-hinge-linker domain, wherein the linker-hinge-linker domain consists of an immunoglobulin hinge region amino acid sequence according to SEQ ID NO: 1902, SEQ ID NO: 1903, or SEQ ID NO: 1904, flanked by a flexible linker amino acid sequence at both termini, wherein the hinge region is an IgG1, an IgG2, an IgG3, or an IgG4 hinge region, wherein the flexible linker amino acid sequence independently comprises the amino acid sequence $(GGGS)_{X1-6}$ (SEQ ID NO: 1906), $(GGGGS)_{X1-6}$ (SEQ ID NO: 1907), or GSAGSAAGSGEF (SEQ ID NO: 1908), and wherein the tetravalent antibody molecule does not comprise an antibody constant region or portion thereof.

2. The tetravalent antibody molecule of claim 1, wherein the scFv fragment is a tandem scFv.

3. A nucleic acid construct comprising nucleic acid molecules encoding:

a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to GITR;

a light chain variable region and a heavy chain variable region of an antibody that can specifically bind to PD-L1; and

a linker-hinge-linker domain,

wherein the linker-hinge-linker domain consists of an immunoglobulin hinge region acid sequence according to SEQ ID NO: 1902, SEQ ID NO: 1903, or SEQ ID NO: 1904, flanked by a flexible linker amino acid sequence at both termini, wherein the hinge region is an IgG1, an IgG2, an IgG3, or an IgG4 hinge region, wherein the flexible linker amino acid sequence independently comprises the amino acid sequence $(GGGS)_{X1-6}$ (SEQ ID NO: 1906), $(GGGGS)_{X1-6}$ (SEQ ID NO: 1907), or GSAGSAAGSGEF (SEQ ID NO: 1908), and wherein the tetravalent antibody molecule does not comprise an antibody constant region or portion thereof.

4. A vector comprising the nucleic acid construct of claim 3.

5. A host cell comprising the vector of claim 4.

6. The host cell of claim 5, wherein the cell is a T-cell, a B-cell, a follicular T-cell, or an NK-cell.

7. A chimeric antigen receptor (CAR) comprising an intracellular signaling domain, a transmembrane domain and an extracellular domain comprising the tetravalent antibody molecule of claim 1.

8. The CAR of claim 7, wherein the transmembrane domain further comprises a stalk region positioned between the extracellular domain and the transmembrane domain.

9. The CAR of claim 7, wherein the transmembrane domain comprises CD28.

10. The CAR of claim 7, further comprising one or more additional costimulatory molecules positioned between the transmembrane domain and the intracellular signaling domain.

11. The CAR of claim 10, wherein the costimulatory molecules is CD28, 4-1BB, ICOS, or OX40.

12. The CAR of claim 7, wherein the intracellular signaling domain comprises a CD3 zeta chain.

13. A genetically engineered cell which expresses and bears on the cell surface membrane the chimeric antigen receptor of any one of claims 7-12.

14. The genetically engineered cell of claim 13, wherein the cell is a T-cell or an NK cell.

15. The genetically engineered cell of claim 14, wherein the T cell is CD4+ or CD8+.

16. The genetically engineered cell of claim 15, which comprises a mixed population of CD4+ and CD8 cells+.

17. A genetically engineered cell which is engineered to express and secrete the tetravalent antibody molecule of claim 1.

18. The genetically engineered cell of claim 17, wherein the cell is a T-cell or an NK cell.

19. The genetically engineered cell of claim 18, wherein the T cell is CD4+ or CD8+.

20. The genetically engineered cell of claim 19, which comprises a mixed population of CD4+ and CD8 cells+.

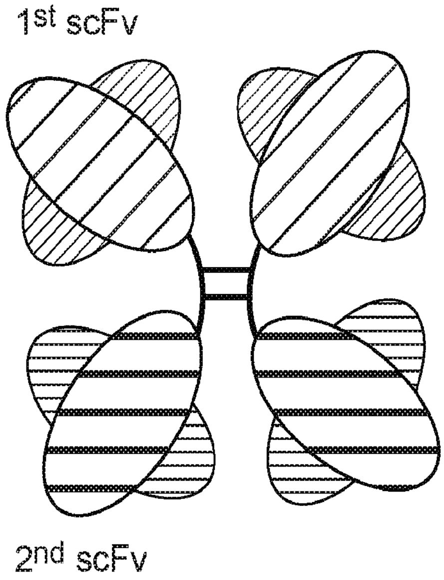


Figure 1

Figure 2

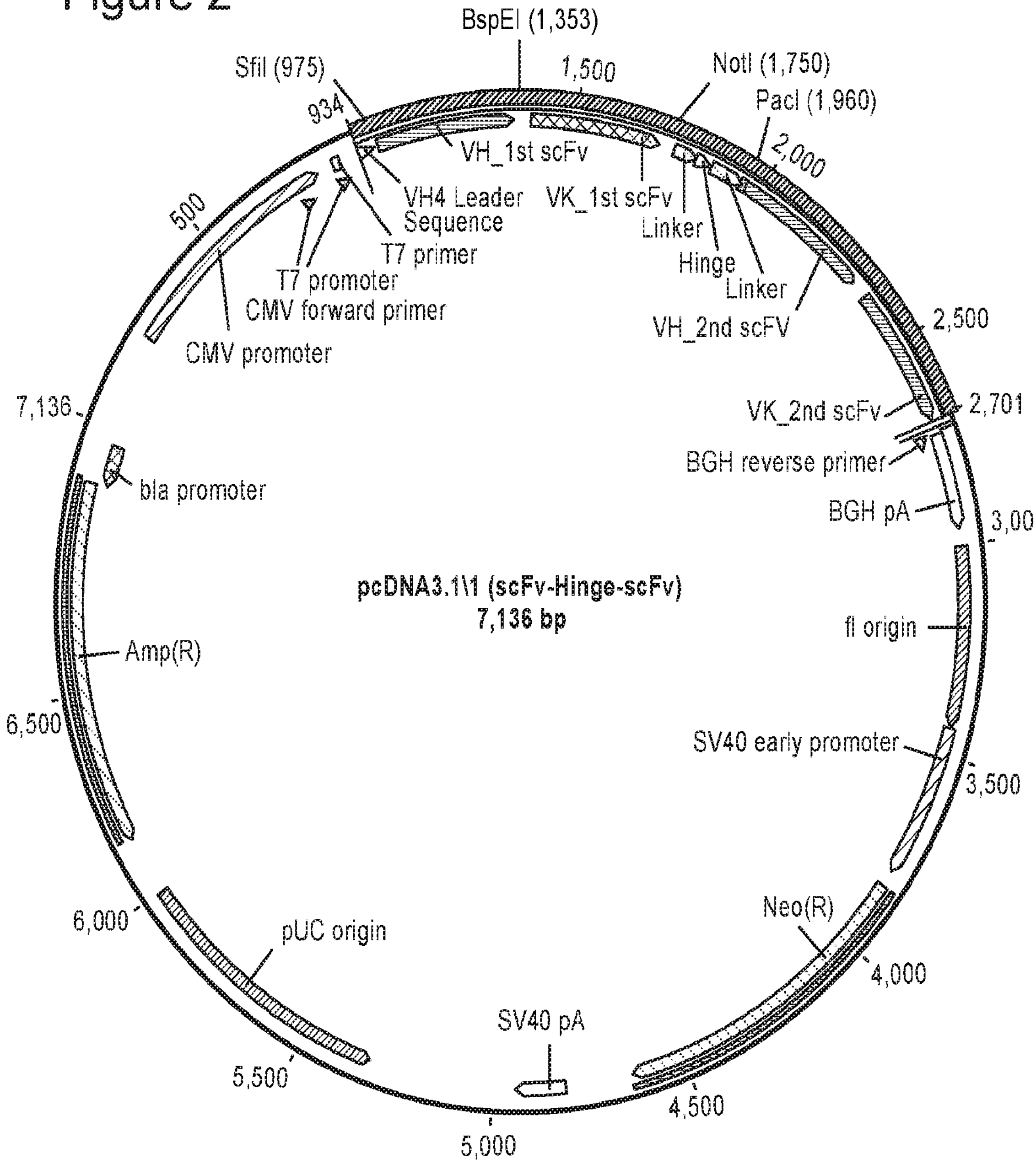

BspEI (1,353)
SfiI (975)
1,500
NotI (1,750)
PacI (1,960)
934
2,000
VH_1st scFv
VH4 Leader Sequence
VK_1st scFv
Linker
Hinge
Linker
T7 primer
T7 promoter
CMV forward primer
VH_2nd scFV
500
CMV promoter
2,500
7,136
VK_2nd scFv
2,701
BGH reverse primer
bla promoter
BGH pA
3,000
pcDNA3.1\1 (scFv-Hinge-scFv)
7,136 bp
Amp(R)
fl origin
6,500
SV40 early promoter
3,500
Neo(R)
6,000
pUC origin
4,000
SV40 pA
5,500
4,500
5,000

Figure 3A

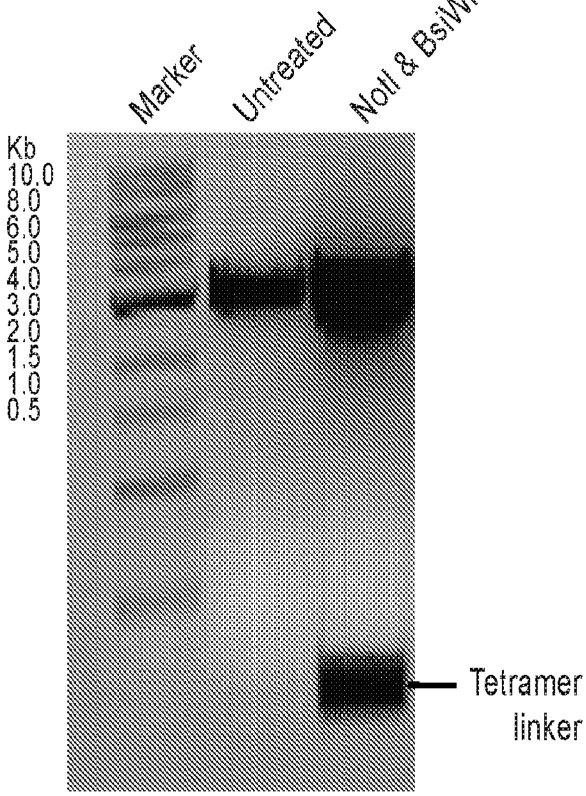


Figure 3B

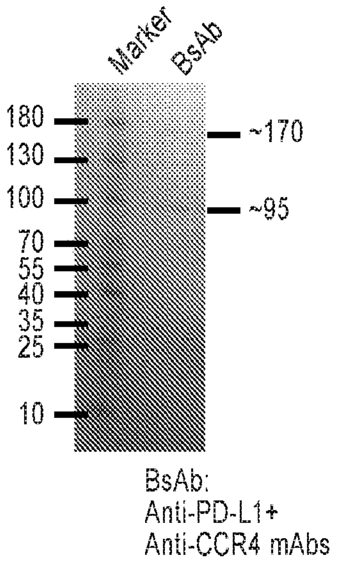


Figure 4A

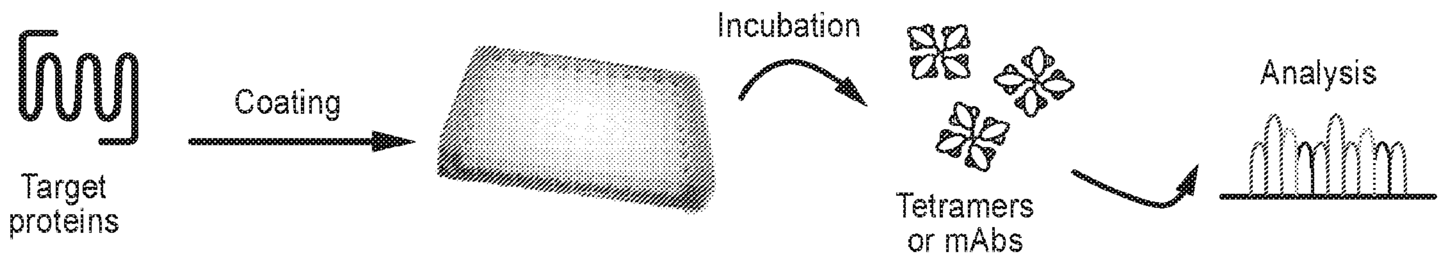


Figure 4B

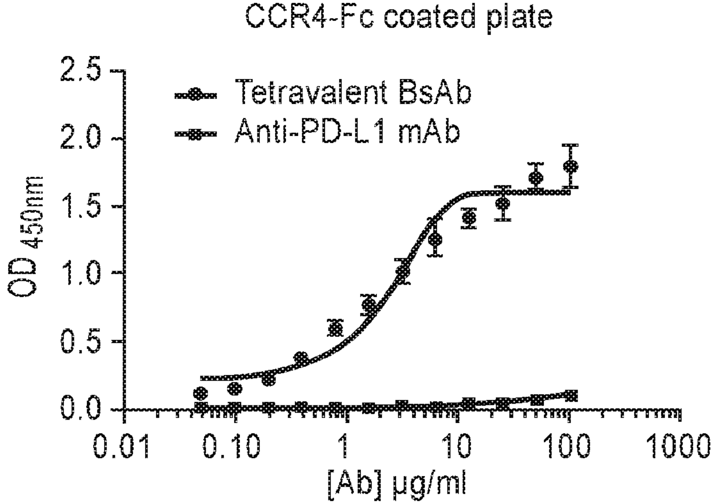

CCR4-Fc coated plate

Figure 4C

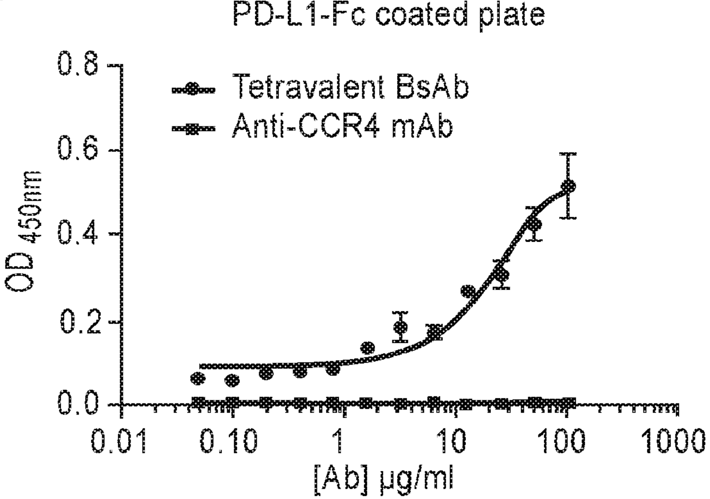
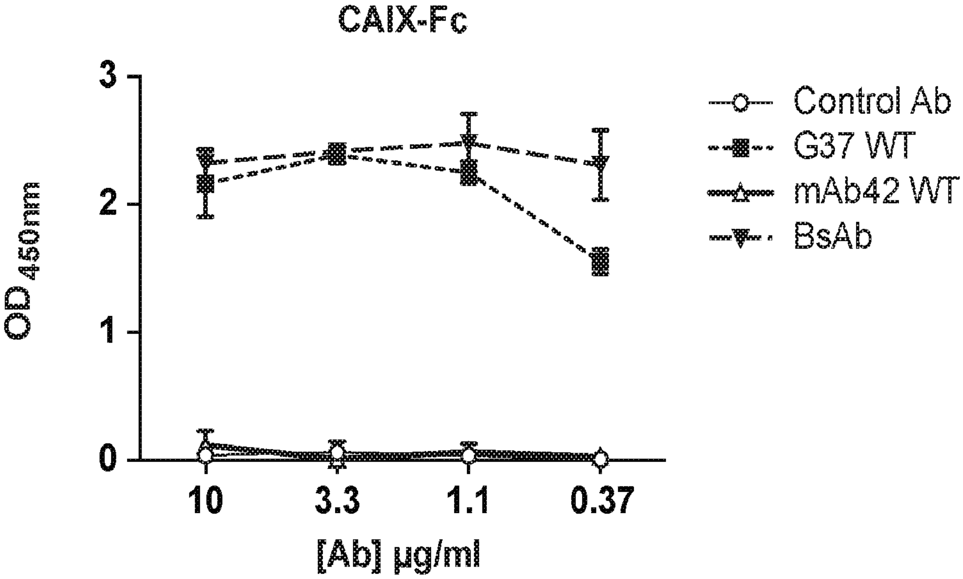

PD-L1-Fc coated plate

Figure 5


CAIX-Fc
3
2
1
0
OD 450nm
10
3.3
1.1
0.37
[Ab] µg/ml
Control Ab
G37 WT
mAb42 WT
BsAb

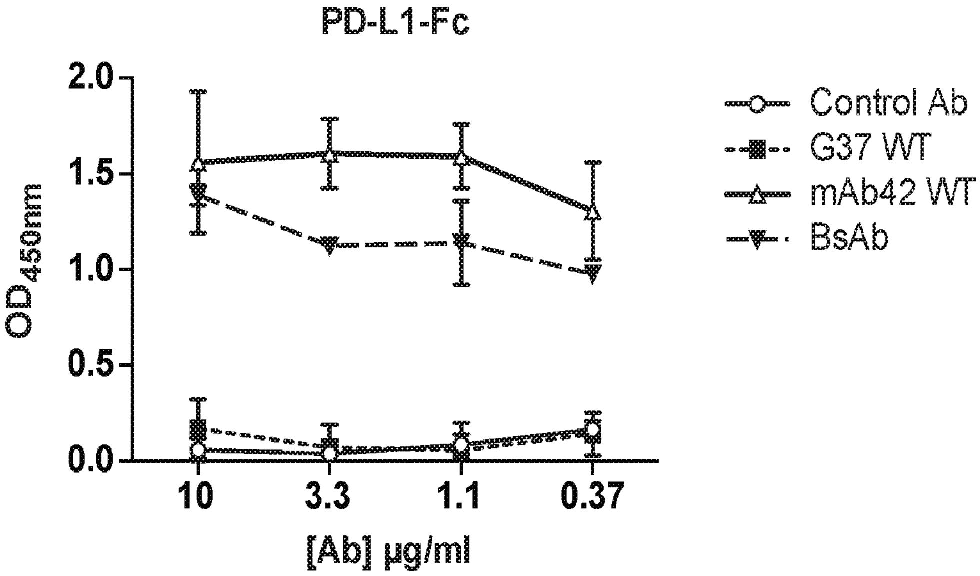

PD-L1-Fc
OD$_{450nm}$
2.0
1.5
1.0
0.5
0.0
10
3.3
1.1
0.37
[Ab] µg/ml
Control Ab
G37 WT
mAb42 WT
BsAb

Figure 6

Figure 7A

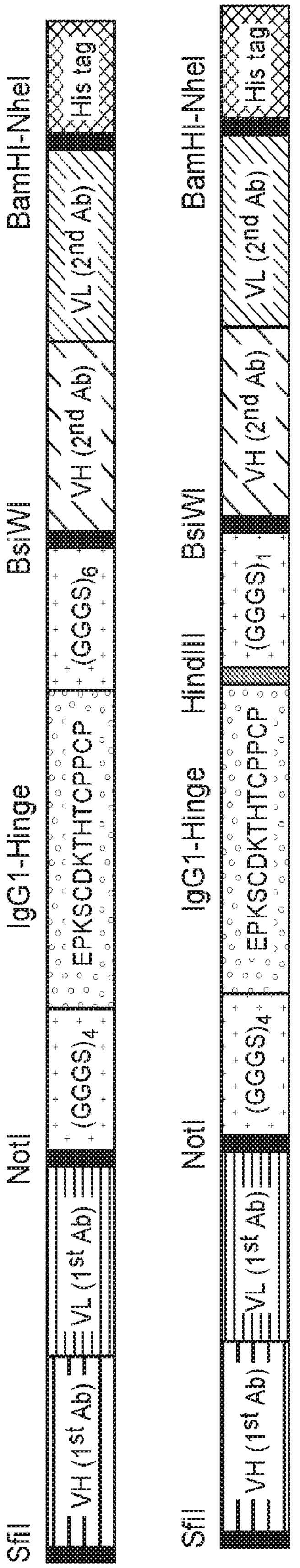


Figure 7B

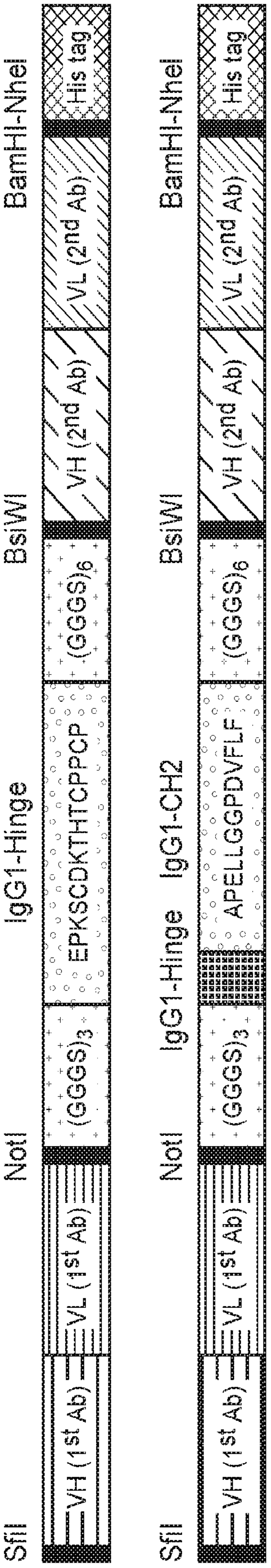


Figure 8A

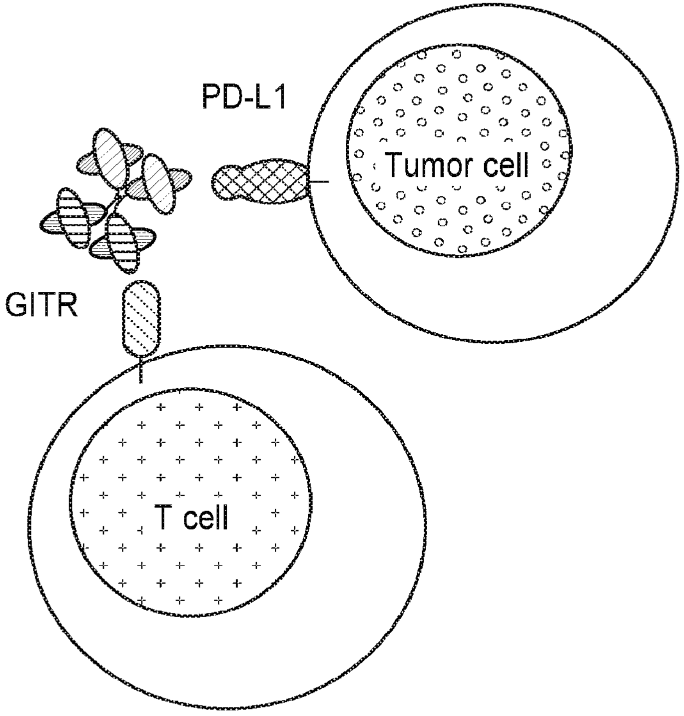


Figure 8B

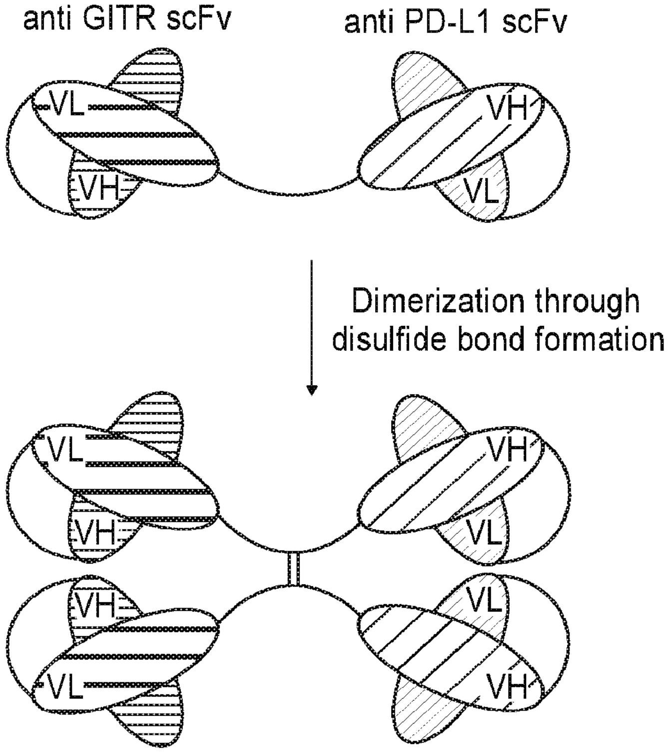


Figure 9

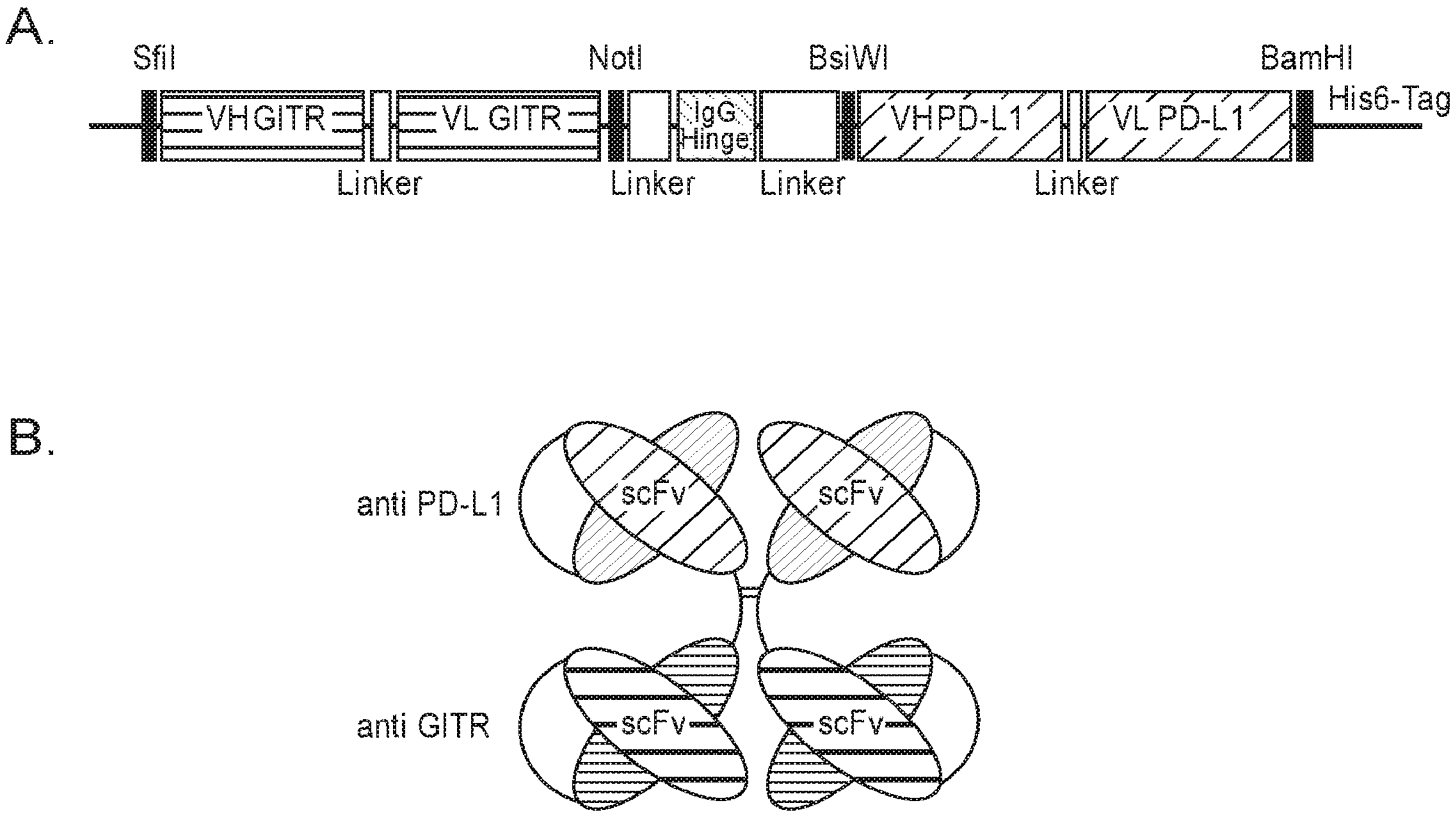

A.
SfiI
NotI
BsiWI
BamHI
VH GITR
VL GITR
IgG Hinge
VH PD-L1
VL PD-L1
His6-Tag
Linker
Linker
Linker
Linker
B.
anti PD-L1
anti GITR
scFv
scFv
scFv
scFv

Figure 10

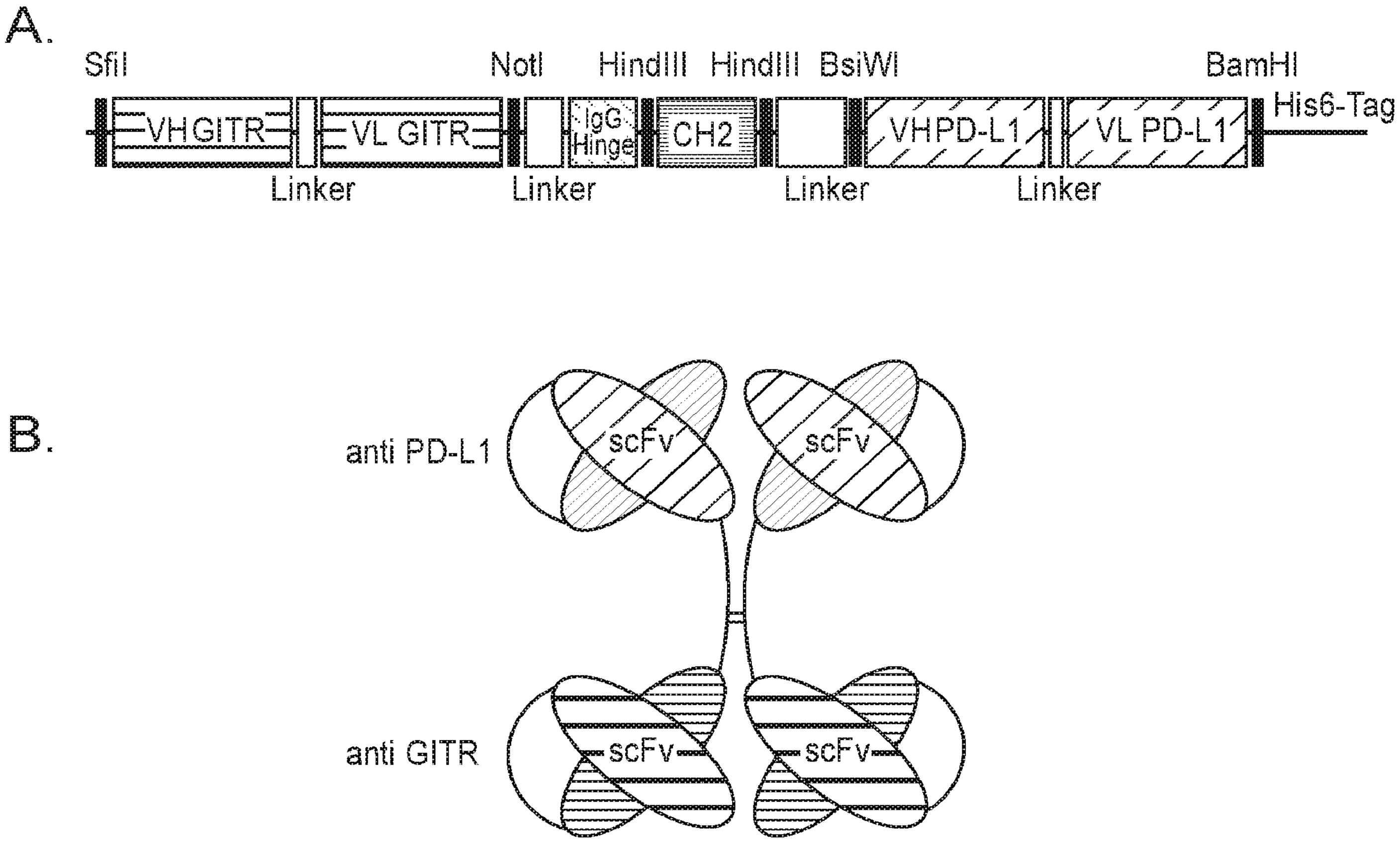

A.
SfiI
NotI
HindIII
HindIII
BsiWI
BamHI
His6-Tag
VHGITR
VL GITR
IgG Hinge
CH2
VHPD-L1
VL PD-L1
Linker
Linker
Linker
Linker
B.
anti PD-L1
anti GITR
scFv
scFv
scFv
scFv

Figure 11

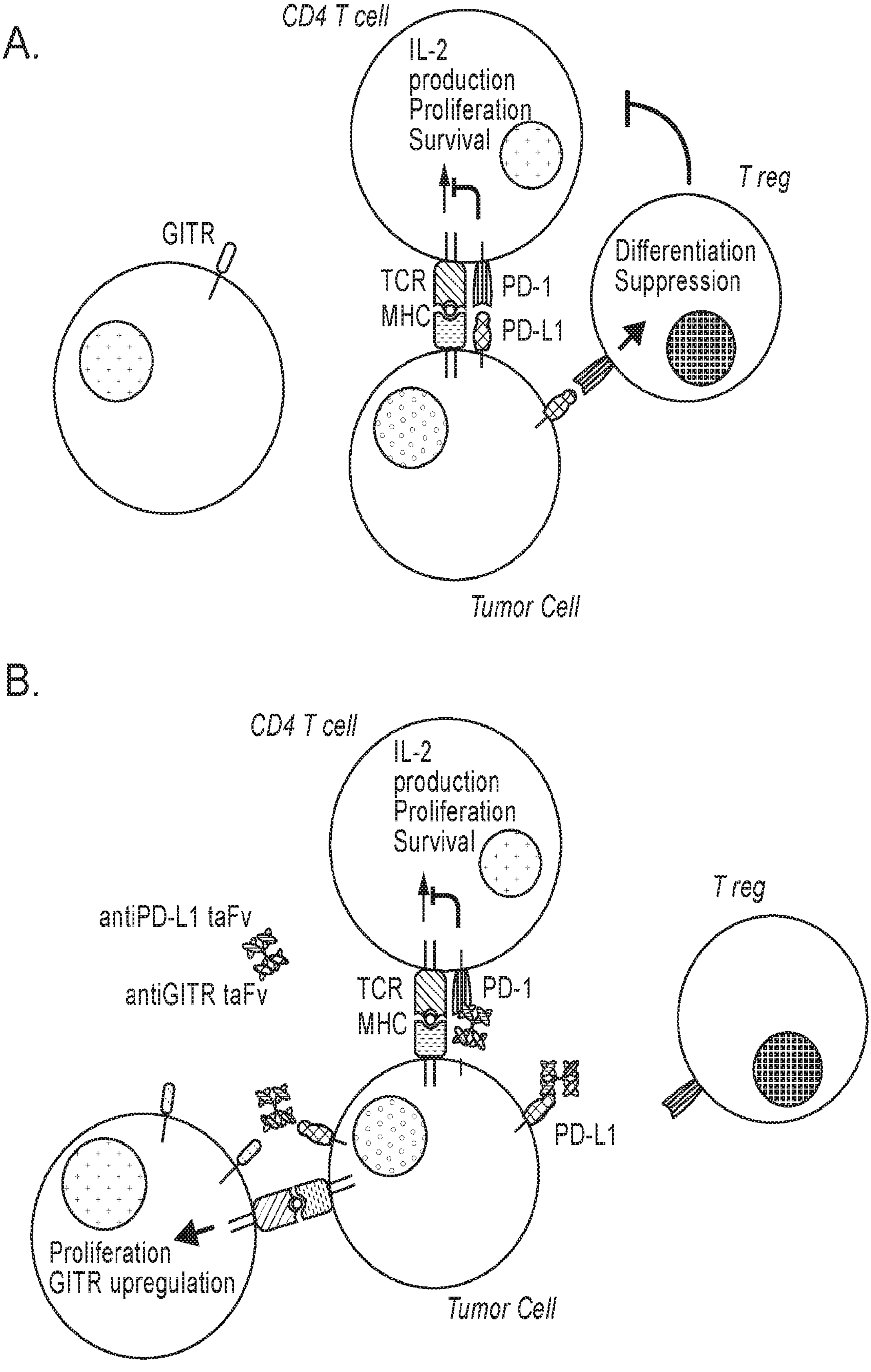

A.
CD4 T cell
IL-2
production
Proliferation
Survival
T reg
GITR
TCR
MHC
PD-1
PD-L1
Differentiation
Suppression
Tumor Cell
B.
CD4 T cell
IL-2
production
Proliferation
Survival
T reg
antiPD-L1 taFv
antiGITR taFv
TCR
MHC
PD-1
PD-L1
Proliferation
GITR upregulation
Tumor Cell

Figure 12

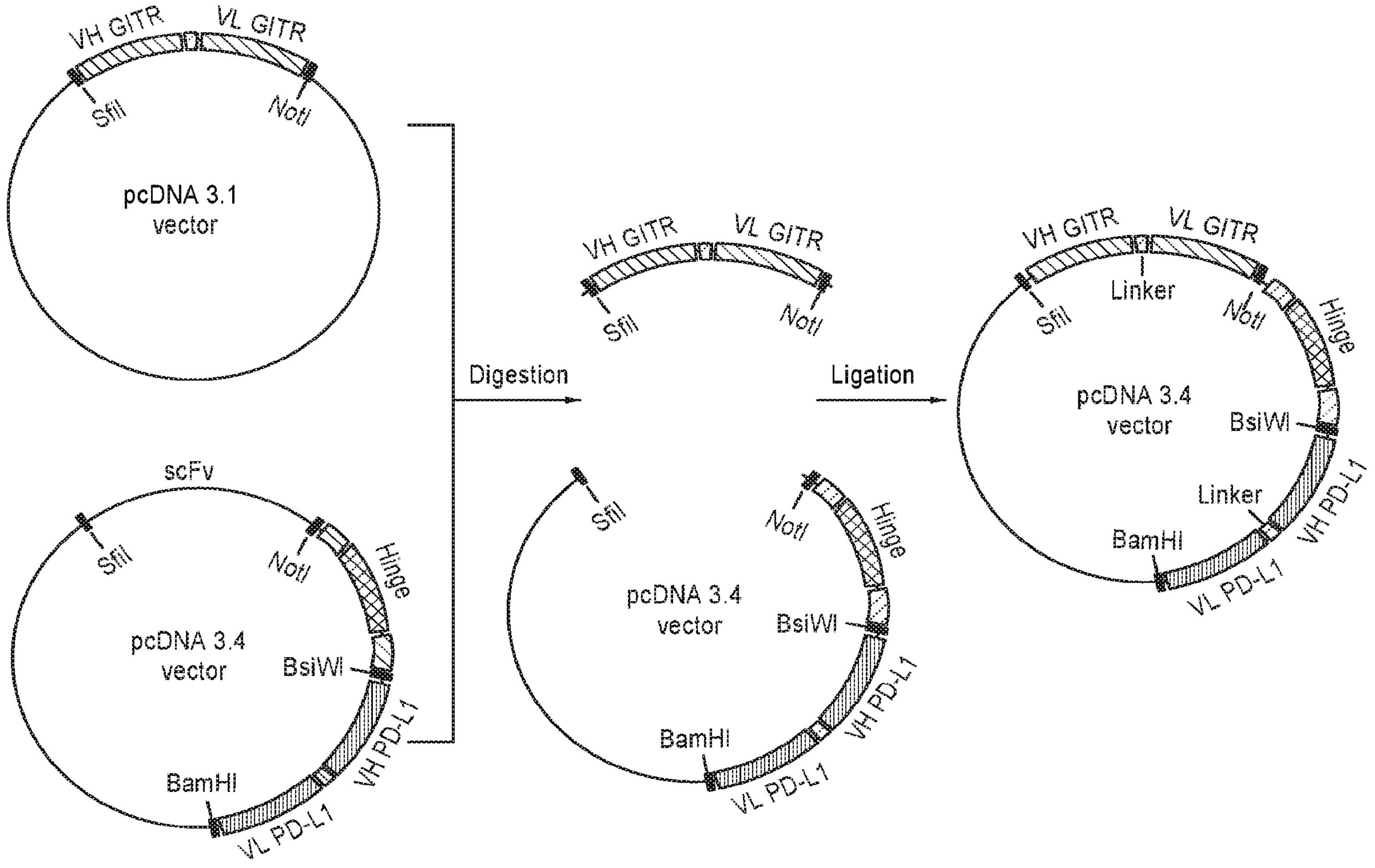

VH GITR
VL GITR
SfiI
NotI
pcDNA 3.1
vector
scFv
SfiI
NotI
Hinge
pcDNA 3.4
vector
BsiWI
VH PD-L1
BamHI
VL PD-L1
Digestion
VH GITR
VL GITR
SfiI
NotI
SfiI
NotI
Hinge
pcDNA 3.4
vector
BsiWI
VH PD-L1
BamHI
VL PD-L1
Ligation
VH GITR
VL GITR
SfiI
Linker
NotI
Hinge
pcDNA 3.4
vector
BsiWI
Linker
VH PD-L1
BamHI
VL PD-L1

Figure 13

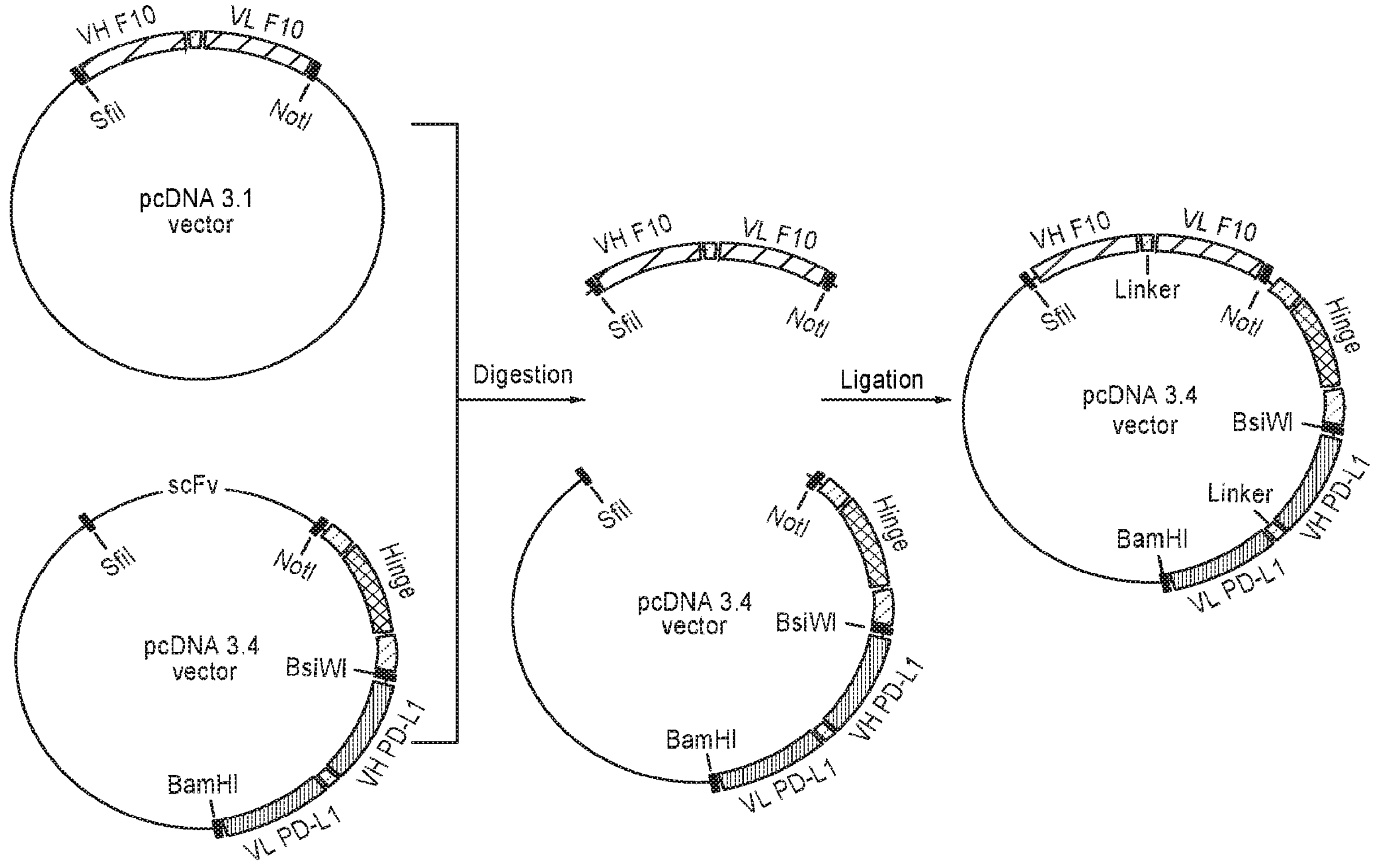

VH F10
VL F10
SfiI
NotI
pcDNA 3.1 vector
scFv
SfiI
NotI
Hinge
pcDNA 3.4 vector
BsiWI
VH PD-L1
BamHI
VL PD-L1
Digestion
VH F10
VL F10
SfiI
NotI
SfiI
NotI
Hinge
pcDNA 3.4 vector
BsiWI
VH PD-L1
BamHI
VL PD-L1
Ligation
VH F10
VL F10
SfiI
Linker
NotI
Hinge
pcDNA 3.4 vector
BsiWI
Linker
VH PD-L1
BamHI
VL PD-L1

Figure 14

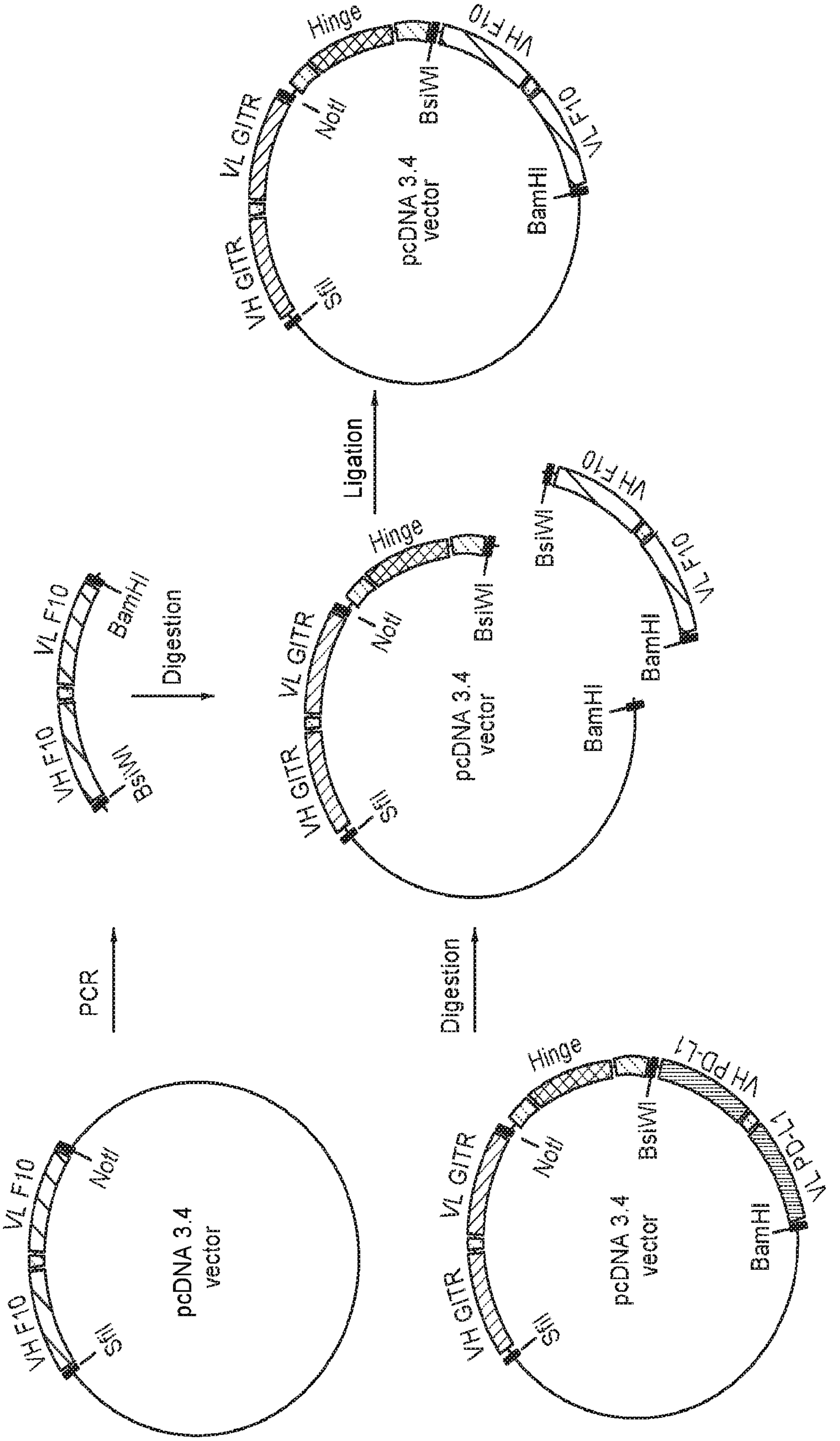

pcDNA 3.4
vector
VH F10
VL F10
SfiI
NotI
PCR
VH F10
VL F10
BsiWI
BamHI
Digestion
pcDNA 3.4
vector
VH GITR
VL GITR
Hinge
SfiI
NotI
BsiWI
BamHI
BsiWI
BamHI
VH F10
VL F10
Ligation
pcDNA 3.4
vector
VH GITR
VL GITR
Hinge
VH F10
VL F10
SfiI
NotI
BsiWI
BamHI
Digestion
pcDNA 3.4
vector
VH GITR
VL GITR
Hinge
VH PD-L1
VL PD-L1
SfiI
NotI
BsiWI
BamHI

Figure 15

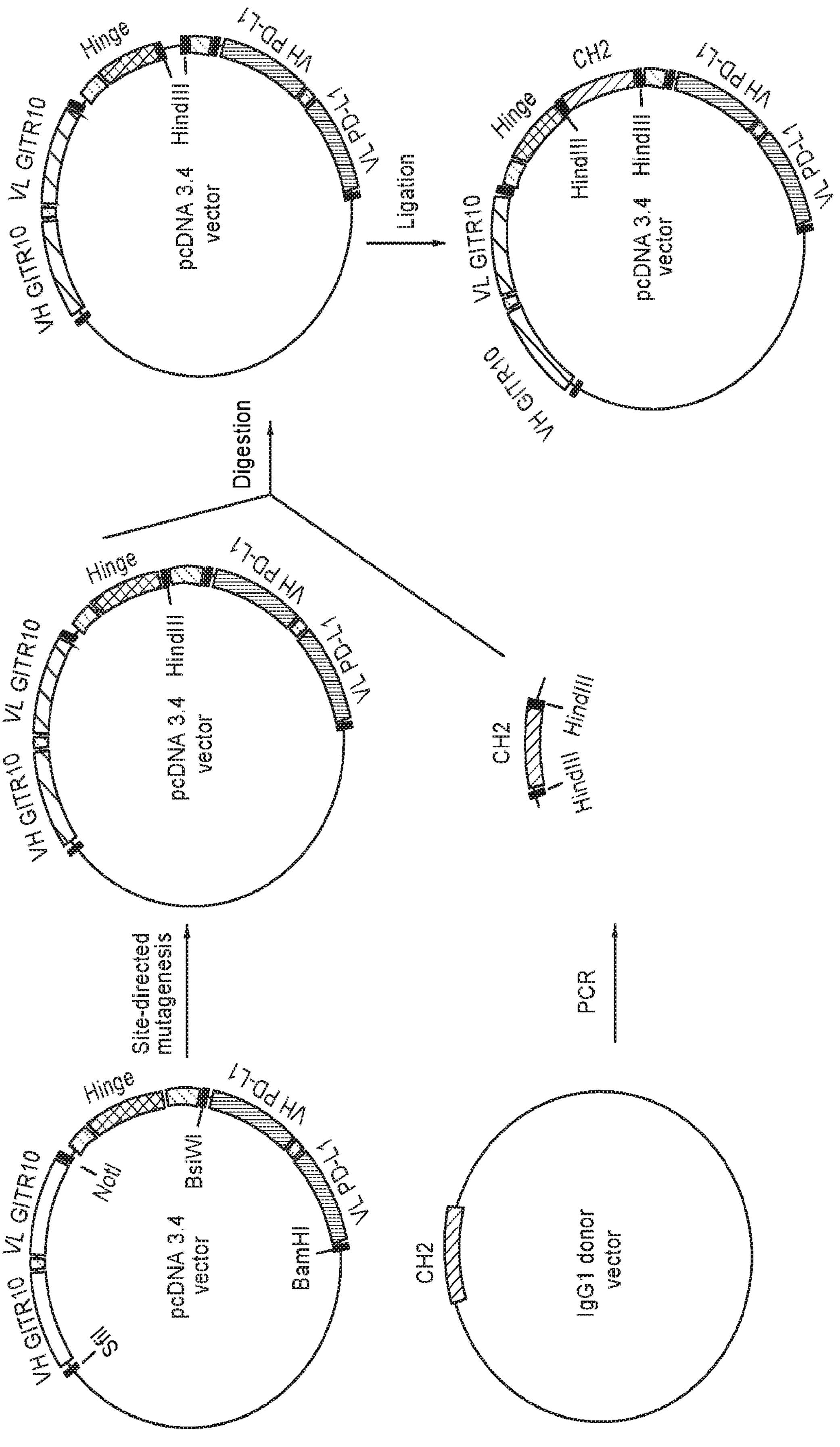
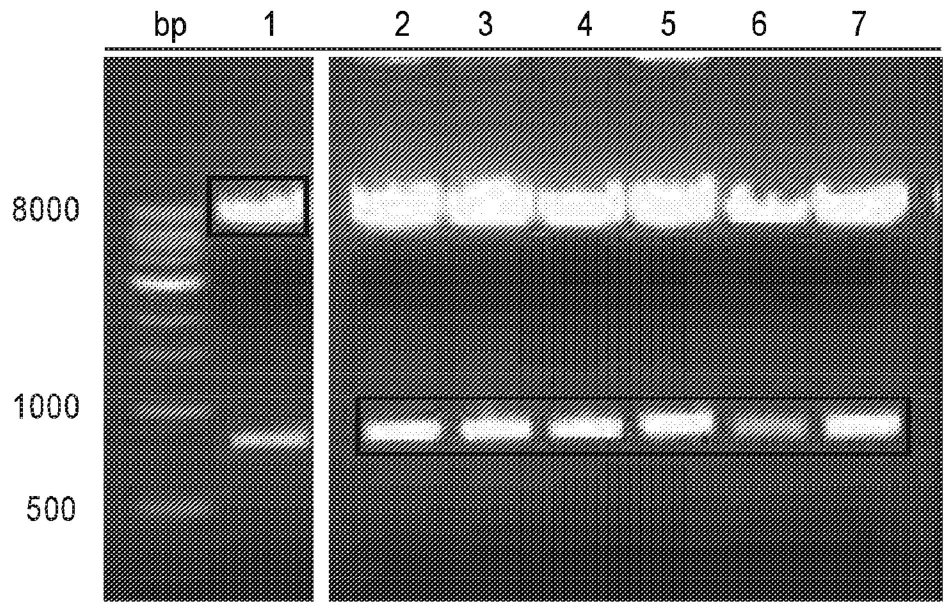

VH GITR10
VL GITR10
Hinge
VH PD-L1
VL PD-L1
SfiI
NotI
BsiWI
BamHI
pcDNA 3.4 vector
CH2
IgG1 donor vector
Site-directed mutagenesis
PCR
VH GITR10
VL GITR10
Hinge
HindIII
VH PD-L1
VL PD-L1
pcDNA 3.4 vector
CH2
HindIII
HindIII
Digestion
VH GITR10
VL GITR10
Hinge
HindIII
VH PD-L1
VL PD-L1
pcDNA 3.4 vector
Ligation
VH GITR10
VL GITR10
Hinge
HindIII
CH2
HindIII
VH PD-L1
VL PD-L1
pcDNA 3.4 vector

Figure 16



1 Recipient vector pcDNA 3.4
2 V_H GITR1-V_L GITR1
3 V_H GITR10-V_L GITR10
4 V_H GITR11-V_L GITR11
5 V_H GITR14-V_L GITR14
6 V_H GITR15-V_L GITR15
7 V_H GITR17-V_L GITR17

Figure 17

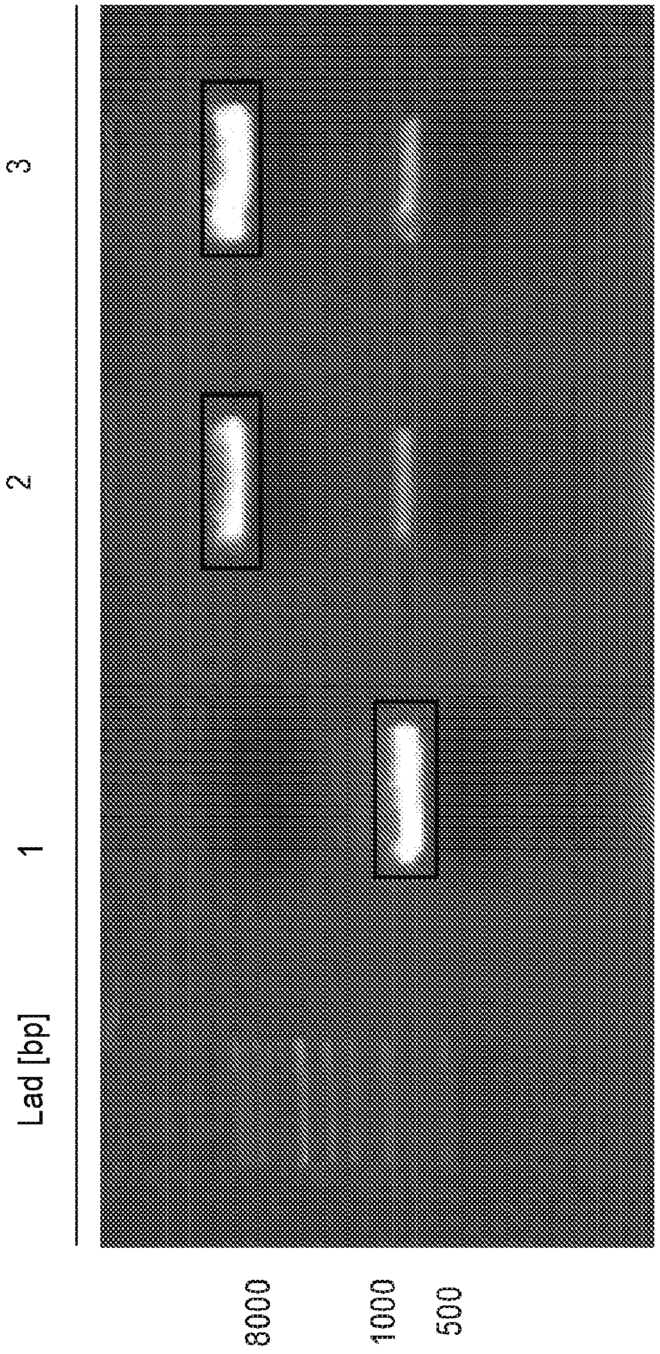


Figure 18

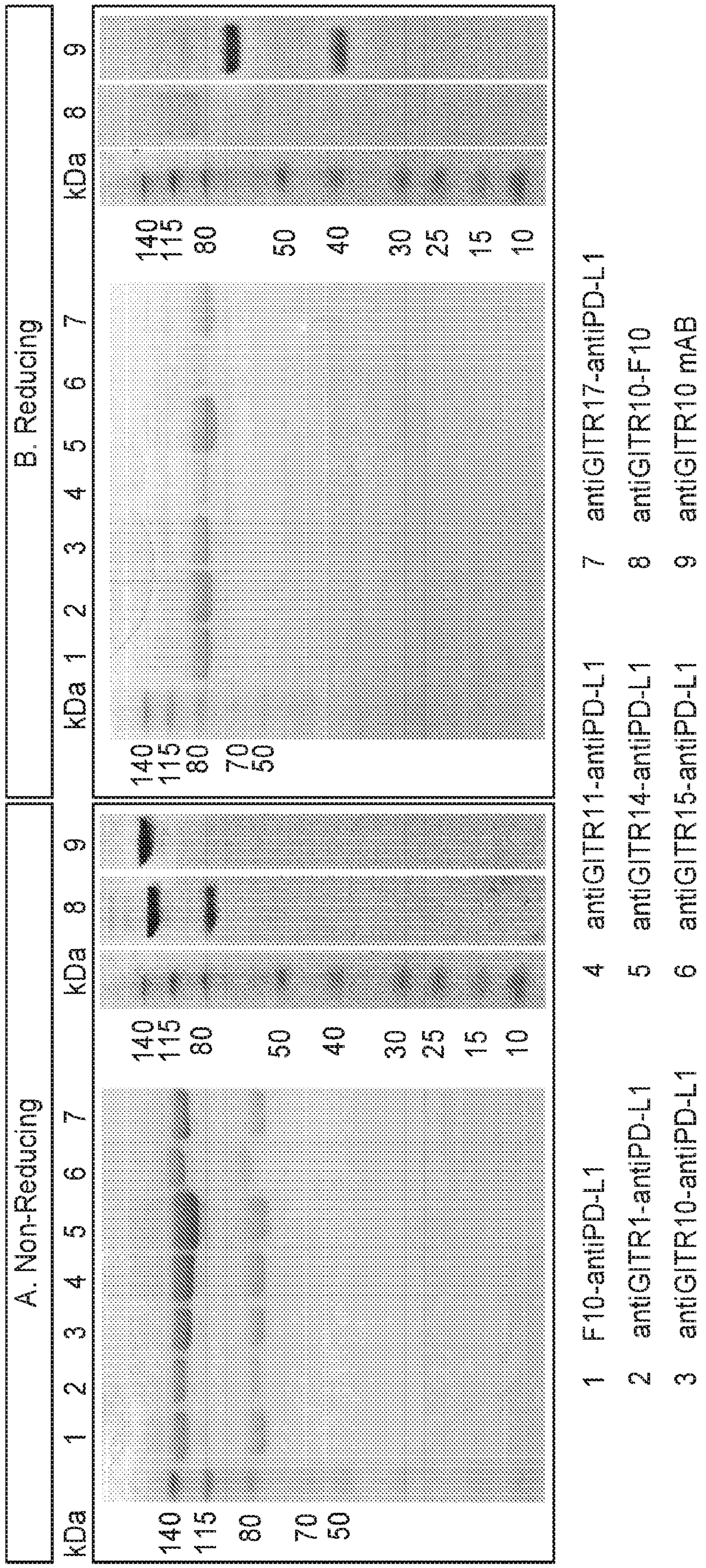

A. Non-Reducing
kDa
1
2
3
4
5
6
7
140
115
80
70
50
kDa
8
9
140
115
80
50
40
30
25
15
10
B. Reducing
kDa
1
2
3
4
5
6
7
140
115
80
70
50
kDa
8
9
140
115
80
50
40
30
25
15
10
1 F10-antiPD-L1
2 antiGITR1-antiPD-L1
3 antiGITR10-antiPD-L1
4 antiGITR11-antiPD-L1
5 antiGITR14-antiPD-L1
6 antiGITR15-antiPD-L1
7 antiGITR17-antiPD-L1
8 antiGITR10-F10
9 antiGITR10 mAB

Figure 19

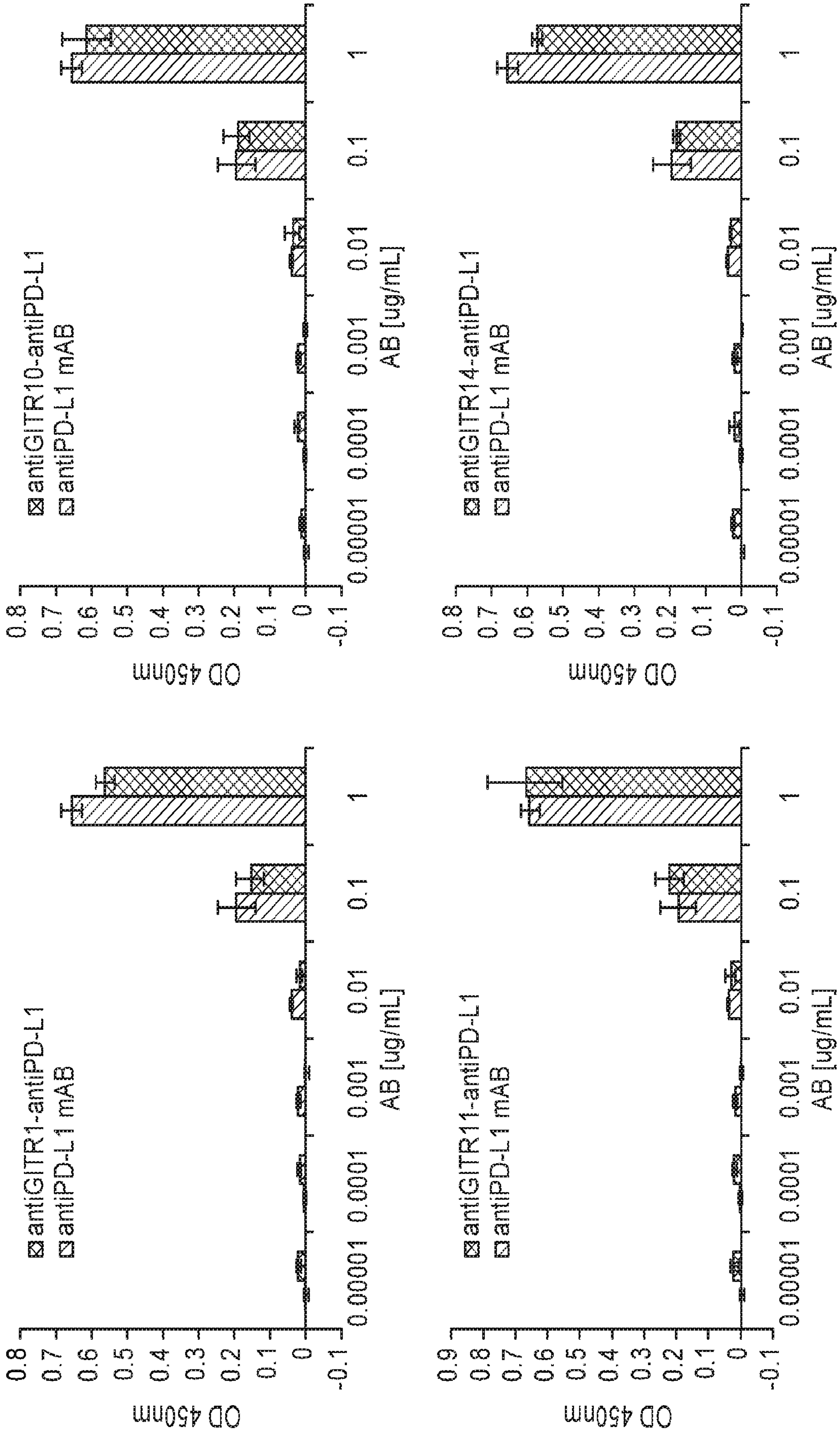

☒ antiGITR1-antiPD-L1
▨ antiPD-L1 mAB
OD 450nm
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.00001
0.0001
0.001
0.01
0.1
1
AB [ug/mL]
☒ antiGITR10-antiPD-L1
▨ antiPD-L1 mAB
OD 450nm
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.00001
0.0001
0.001
0.01
0.1
1
AB [ug/mL]
☒ antiGITR11-antiPD-L1
▨ antiPD-L1 mAB
OD 450nm
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.00001
0.0001
0.001
0.01
0.1
1
AB [ug/mL]
☒ antiGITR14-antiPD-L1
▨ antiPD-L1 mAB
OD 450nm
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.00001
0.0001
0.001
0.01
0.1
1
AB [ug/mL]

Figure 19 cont.

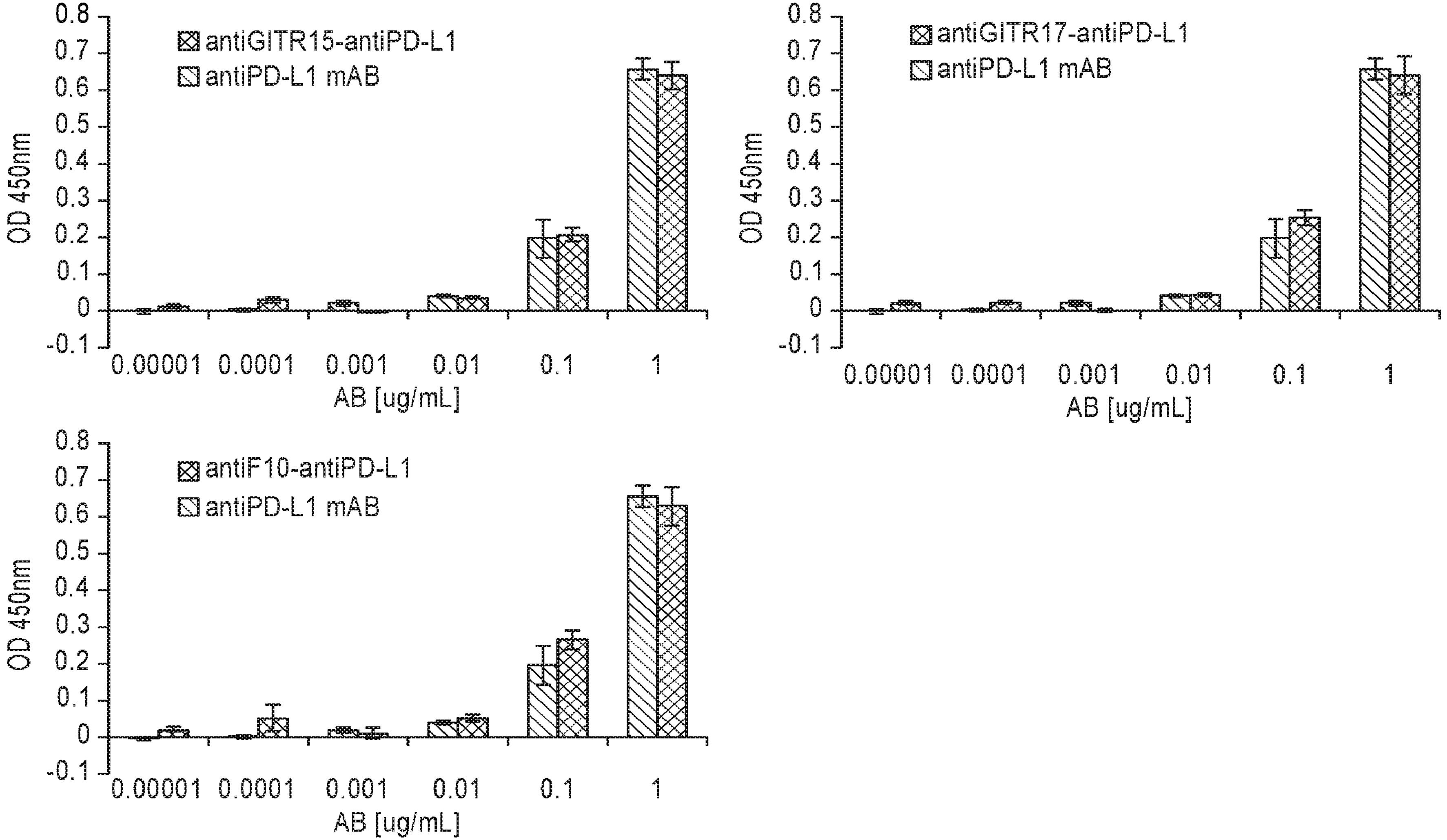


Figure 20

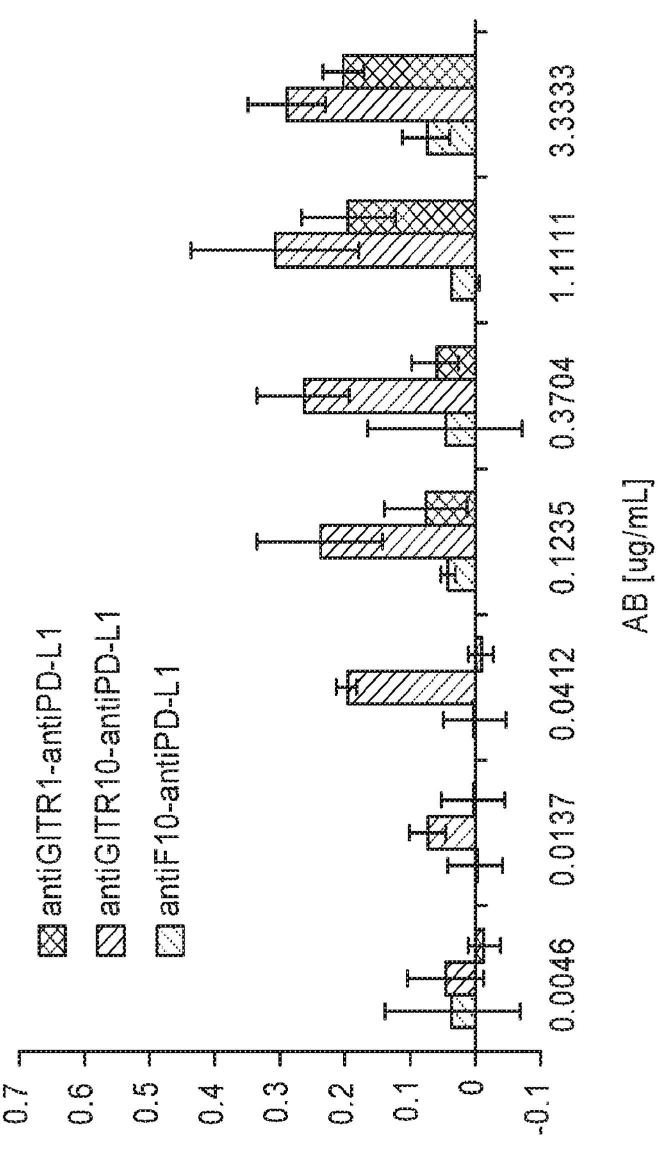

▨ antiGITR1-antiPD-L1
▨ antiGITR10-antiPD-L1
▨ antiF10-antiPD-L1
OD 450nm
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.0046
0.0137
0.0412
0.1235
0.3704
1.1111
3.3333
AB [ug/mL]

Figure 21

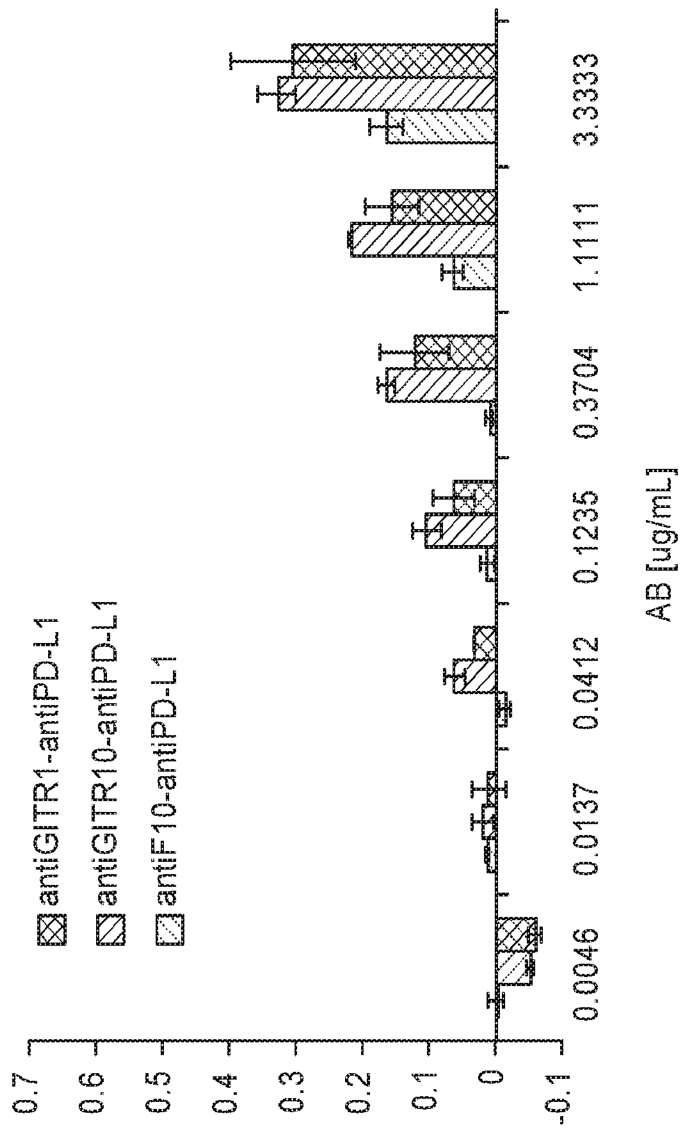

OD 450nm
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.0046
0.0137
0.0412
0.1235
0.3704
1.1111
3.3333
AB [ug/mL]
▨ antiGITR1-antiPD-L1
▨ antiGITR10-antiPD-L1
▨ antiF10-antiPD-L1

Figure 22

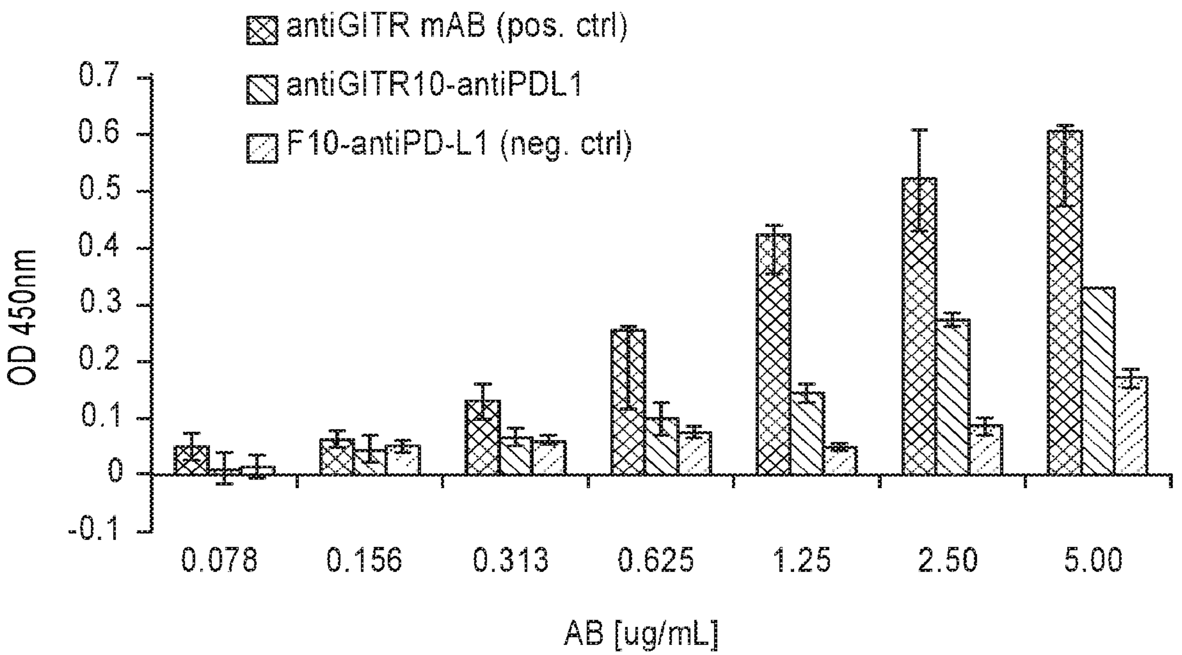

antiGITR mAB (pos. ctrl)
antiGITR10-antiPDL1
F10-antiPD-L1 (neg. ctrl)
OD 450nm
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
0.078
0.156
0.313
0.625
1.25
2.50
5.00
AB [ug/mL]

Figure 23A

αGITR10-αPD-L1

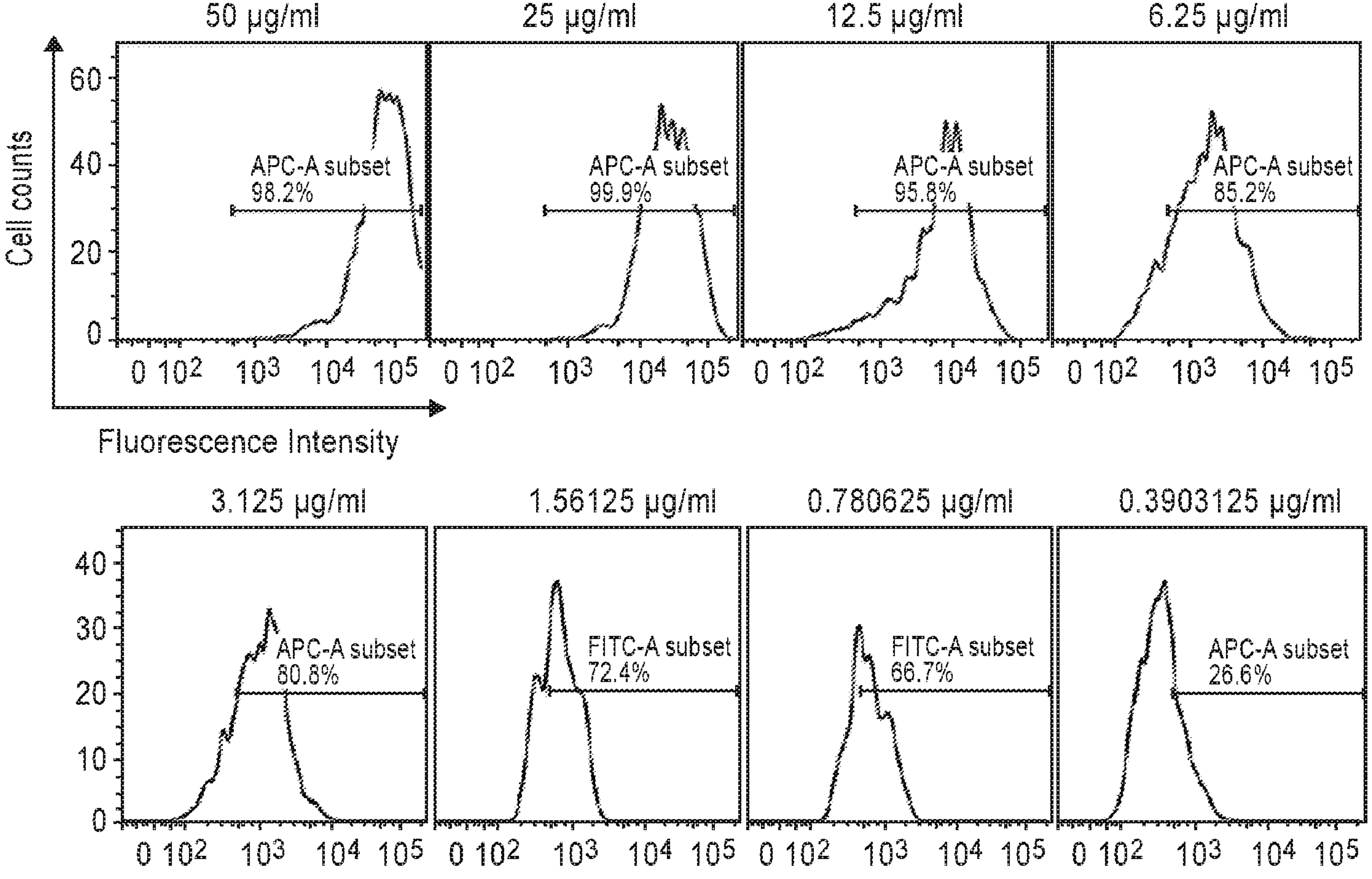


Figure 23B

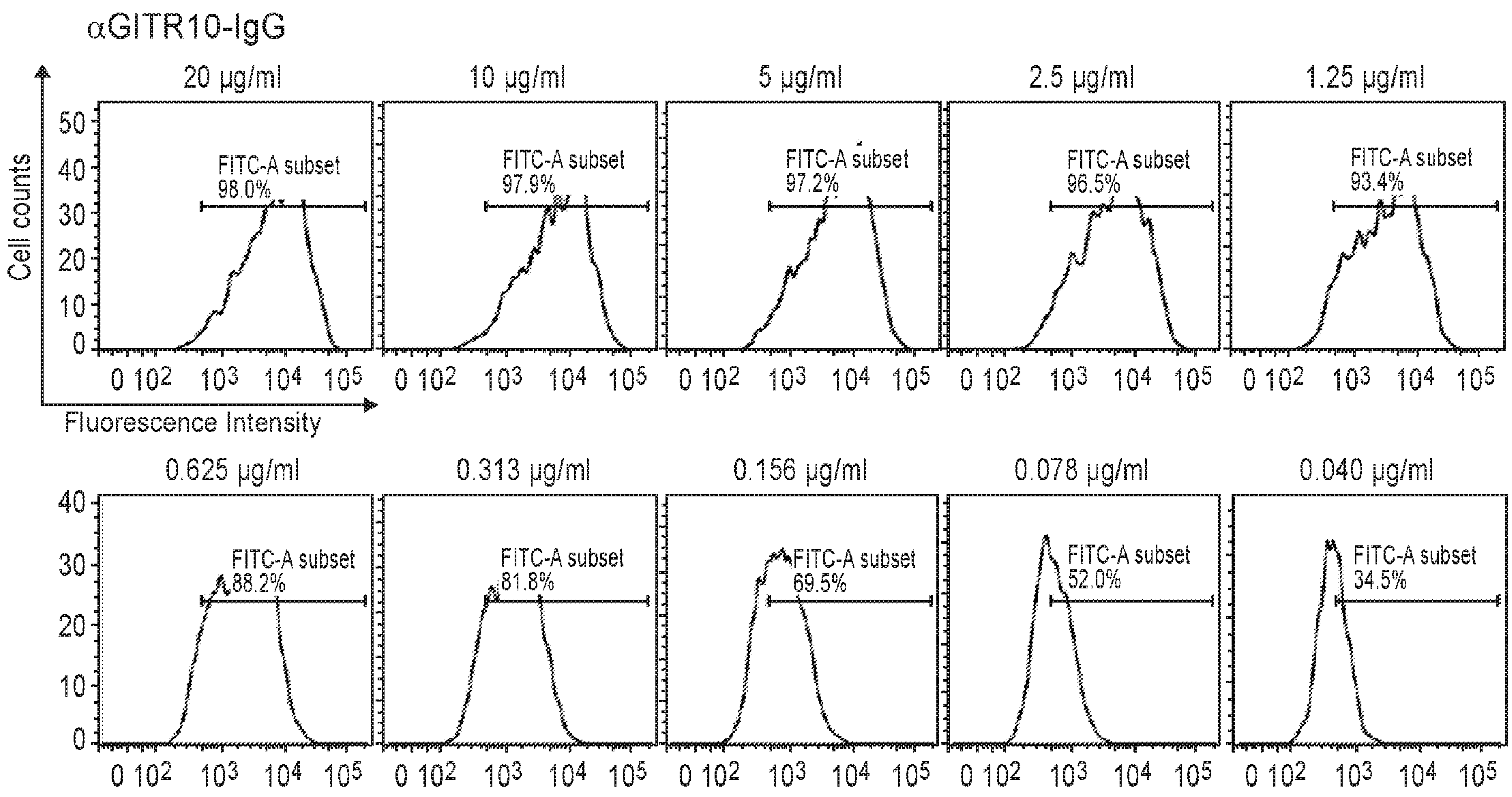

αGITR10-IgG
20 µg/ml
10 µg/ml
5 µg/ml
2.5 µg/ml
1.25 µg/ml
0.625 µg/ml
0.313 µg/ml
0.156 µg/ml
0.078 µg/ml
0.040 µg/ml
Cell counts
Fluorescence Intensity
FITC-A subset 98.0%
FITC-A subset 97.9%
FITC-A subset 97.2%
FITC-A subset 96.5%
FITC-A subset 93.4%
FITC-A subset 88.2%
FITC-A subset 81.8%
FITC-A subset 69.5%
FITC-A subset 52.0%
FITC-A subset 34.5%
0
10
20
30
40
50
0 10^2 10^3 10^4 10^5

Figure 24A

αGITR10-αPD-L1

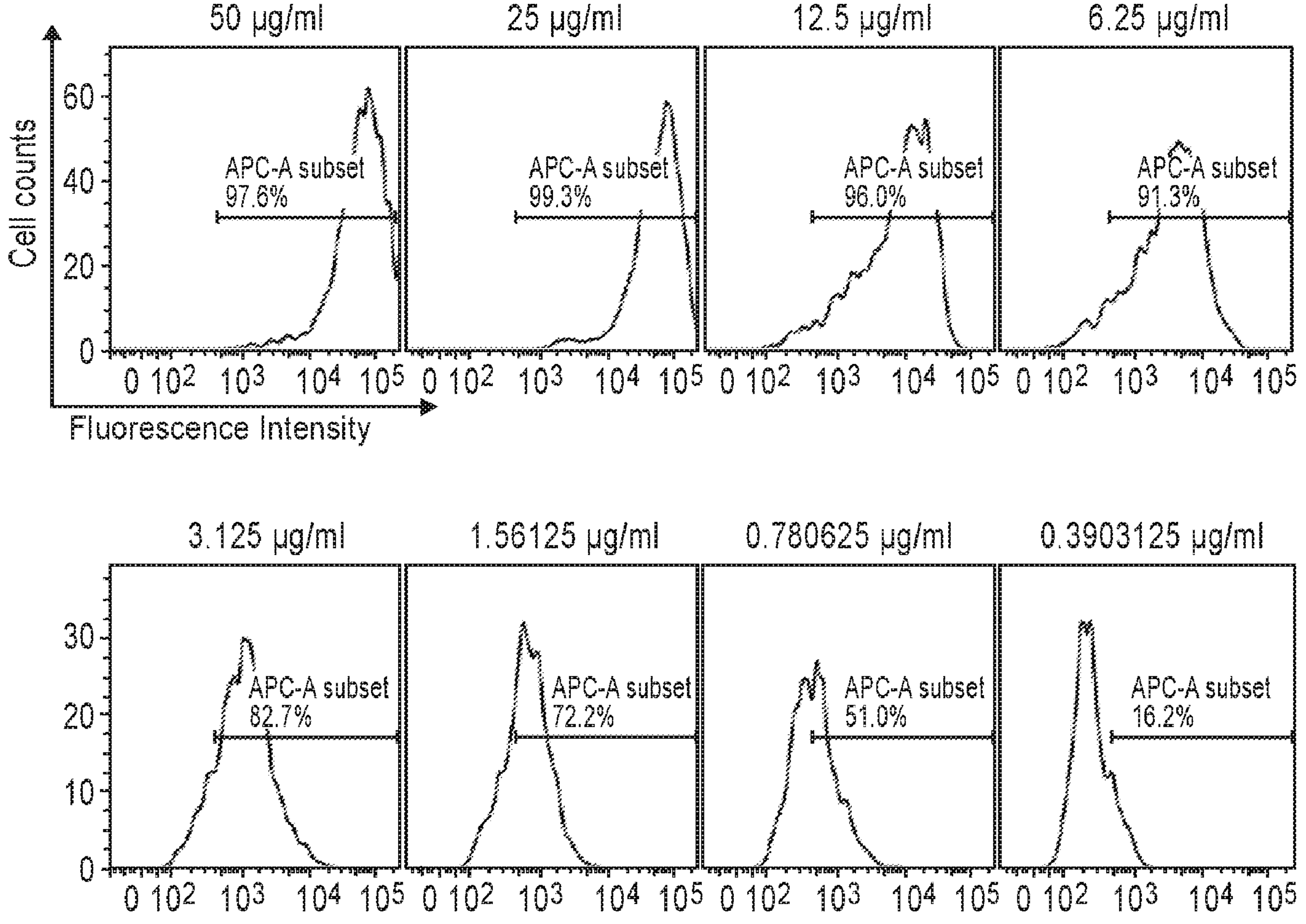


Figure 24B

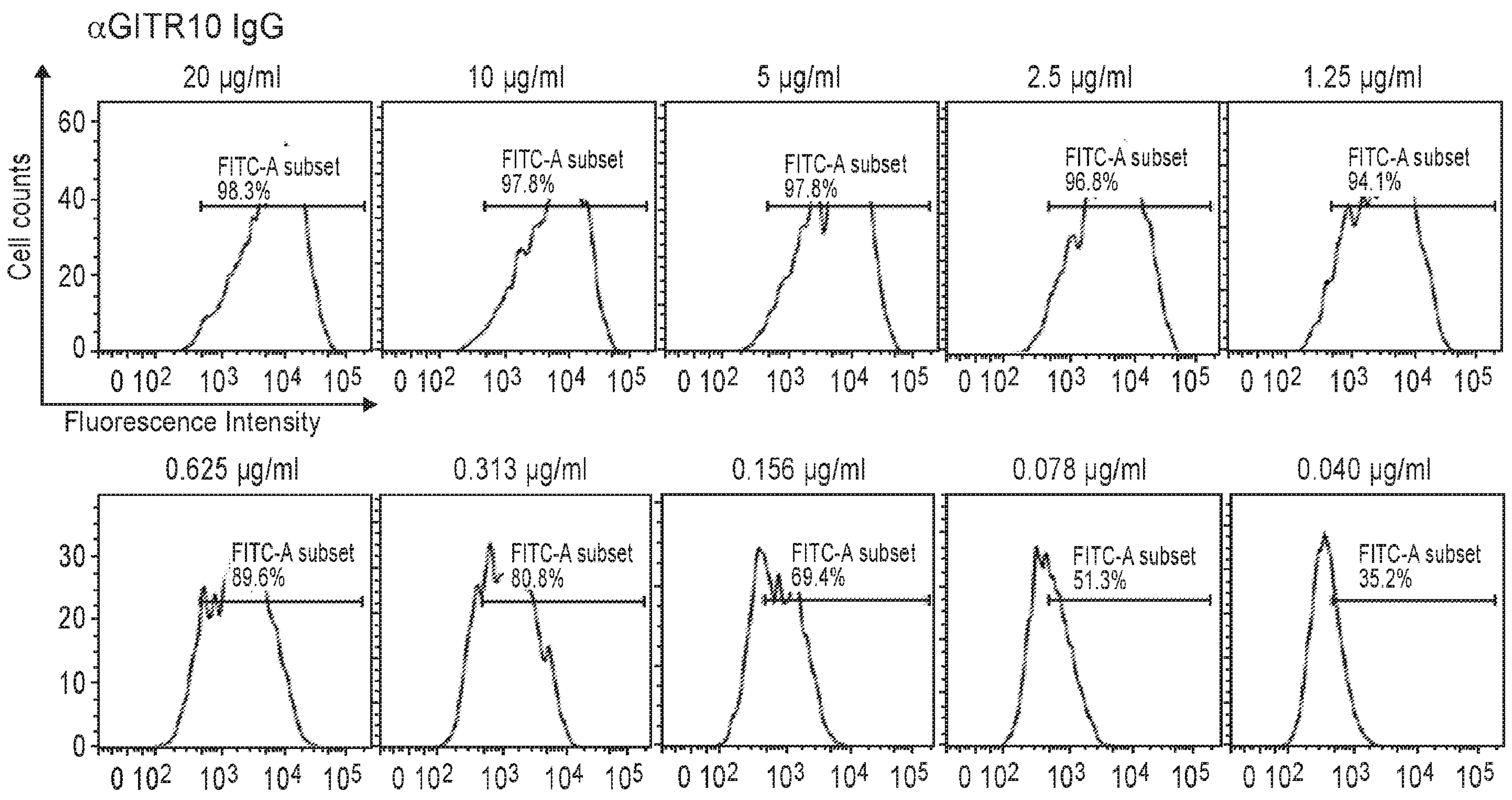

αGITR10 IgG
20 µg/ml
10 µg/ml
5 µg/ml
2.5 µg/ml
1.25 µg/ml
Cell counts
60
40
20
0
FITC-A subset
98.3%
FITC-A subset
97.8%
FITC-A subset
97.8%
FITC-A subset
96.8%
FITC-A subset
94.1%
0 10²
10³
10⁴
10⁵
Fluorescence Intensity
0.625 µg/ml
0.313 µg/ml
0.156 µg/ml
0.078 µg/ml
0.040 µg/ml
30
20
10
0
FITC-A subset
89.6%
FITC-A subset
80.8%
FITC-A subset
69.4%
FITC-A subset
51.3%
FITC-A subset
35.2%

Figure 25

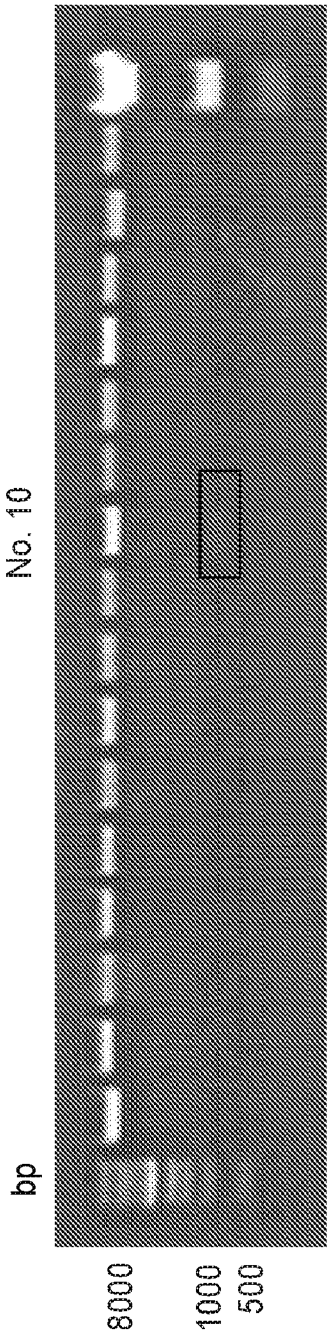


Figure 26

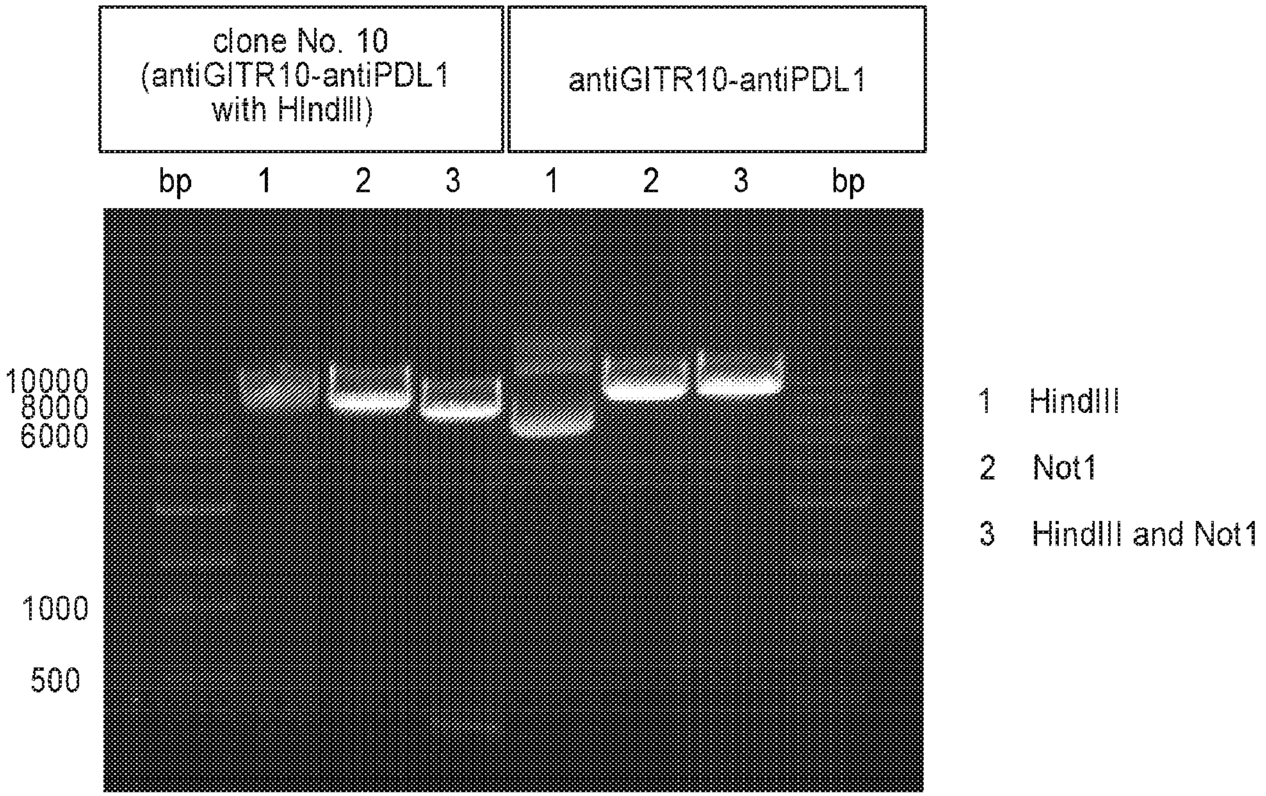

clone No. 10
(antiGITR10-antiPDL1
with HindIII)
antiGITR10-antiPDL1
bp
1
2
3
1
2
3
bp
10000
8000
6000
1000
500
1 HindIII
2 Not1
3 HindIII and Not1

Figure 27

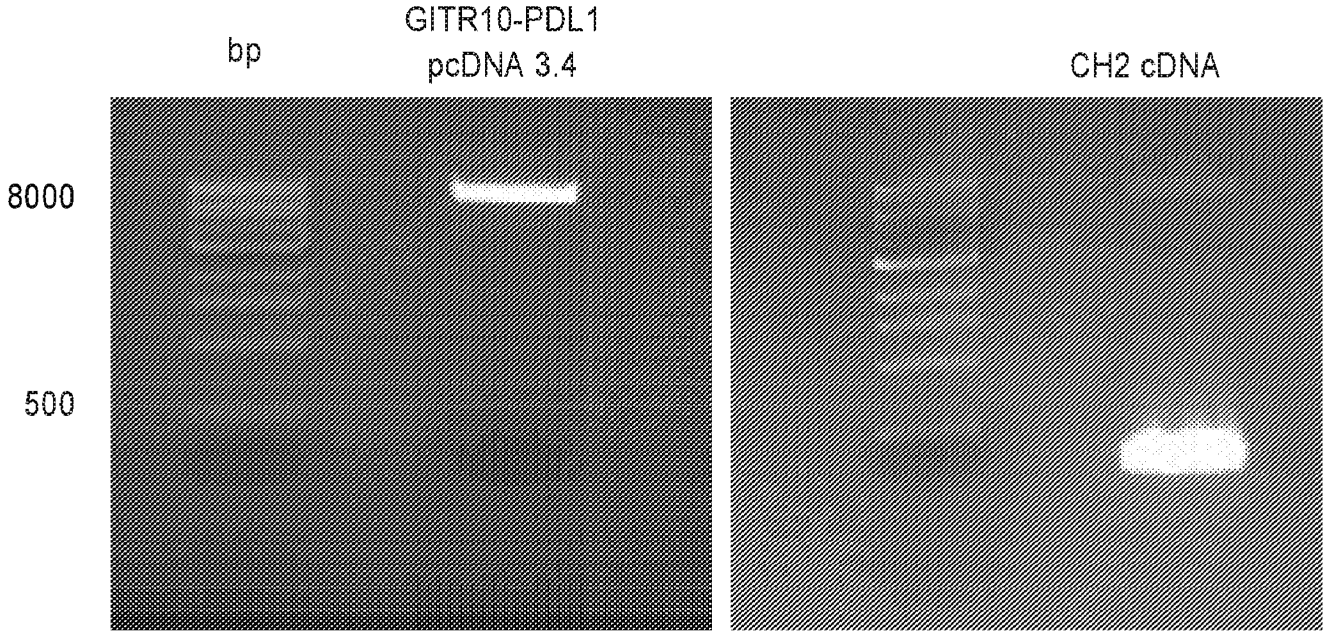


Figure 28

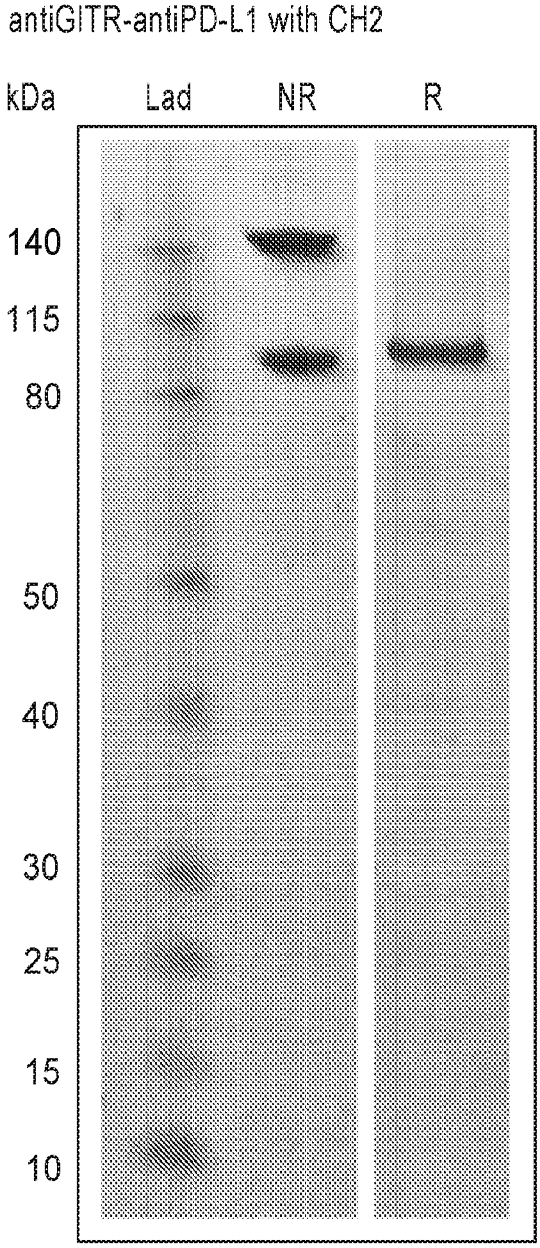

antiGITR-antiPD-L1 with CH2
kDa
Lad
NR
R
140
115
80
50
40
30
25
15
10

Figure 29

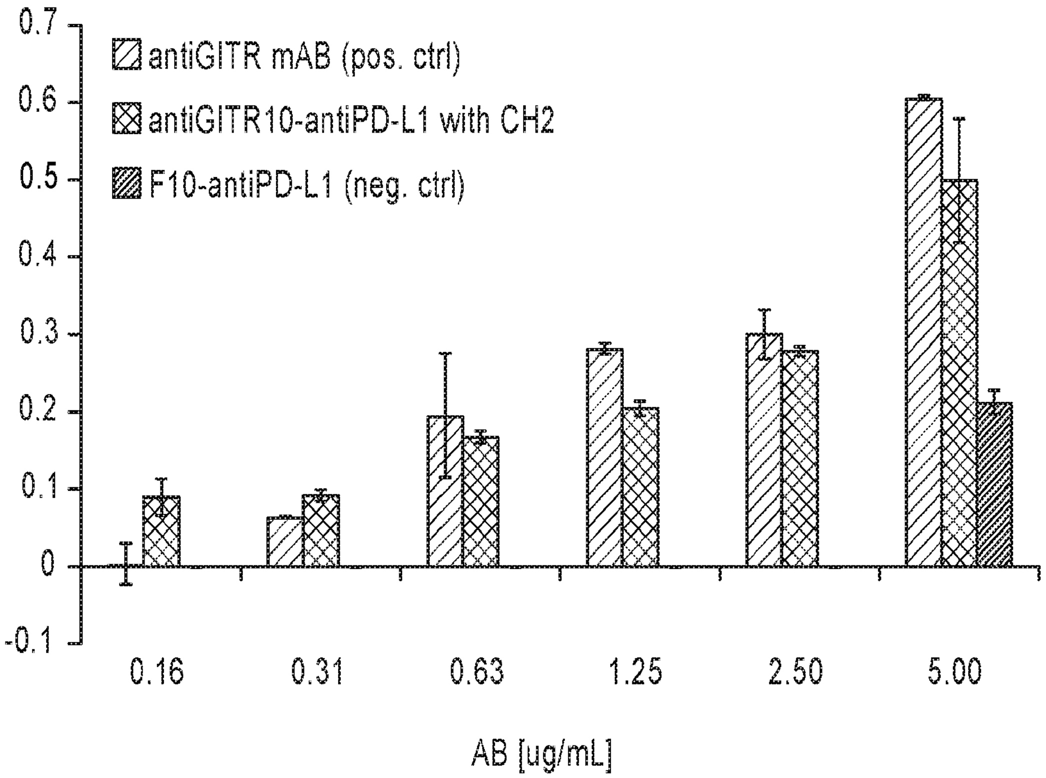

0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
antiGITR mAB (pos. ctrl)
antiGITR10-antiPD-L1 with CH2
F10-antiPD-L1 (neg. ctrl)
0.16
0.31
0.63
1.25
2.50
5.00
AB [ug/mL]

Figure 30

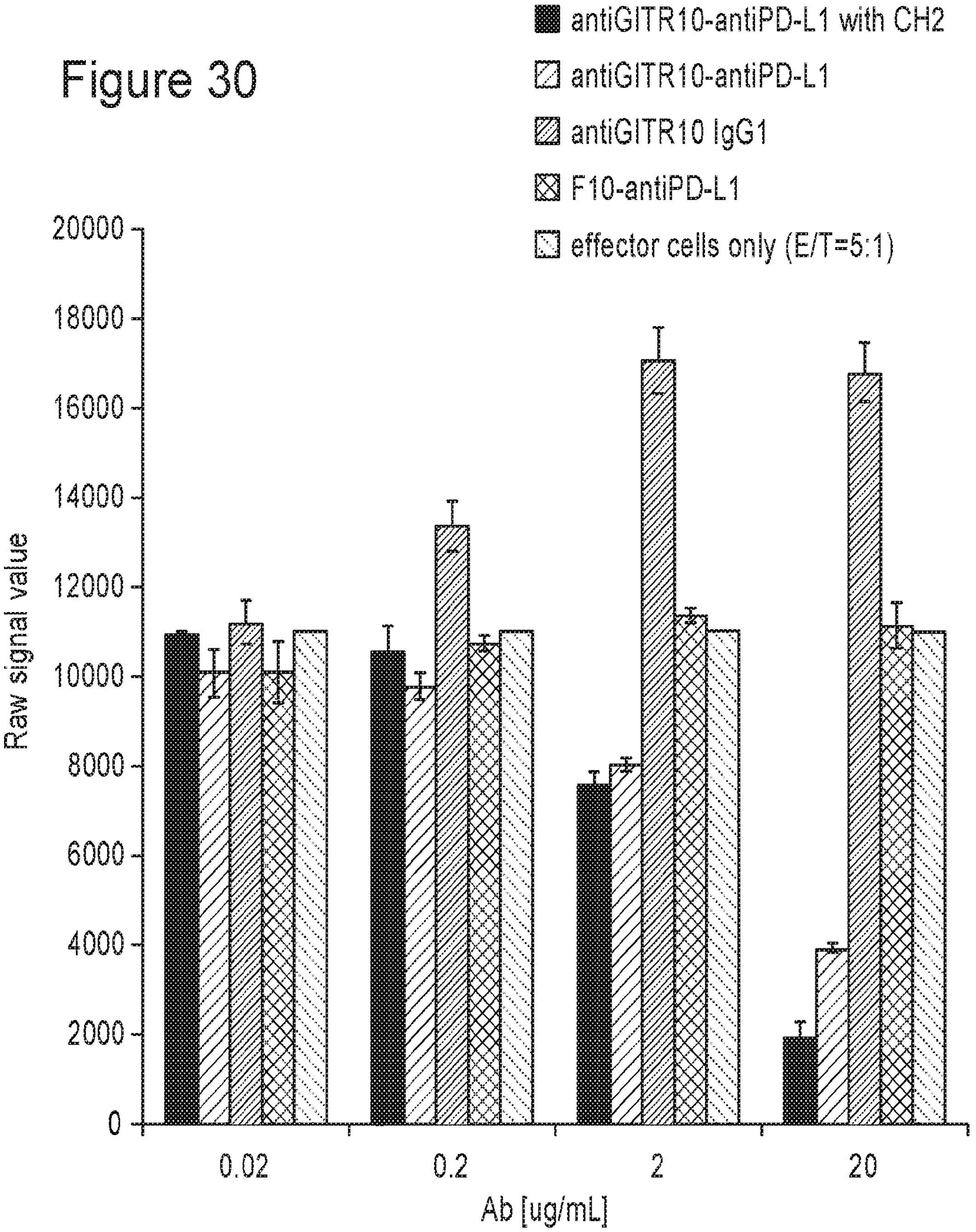

antiGITR10-antiPD-L1 with CH2
antiGITR10-antiPD-L1
antiGITR10 IgG1
F10-antiPD-L1
effector cells only (E/T=5:1)
Raw signal value
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
0.02
0.2
2
20
Ab [ug/mL]

Figure 31

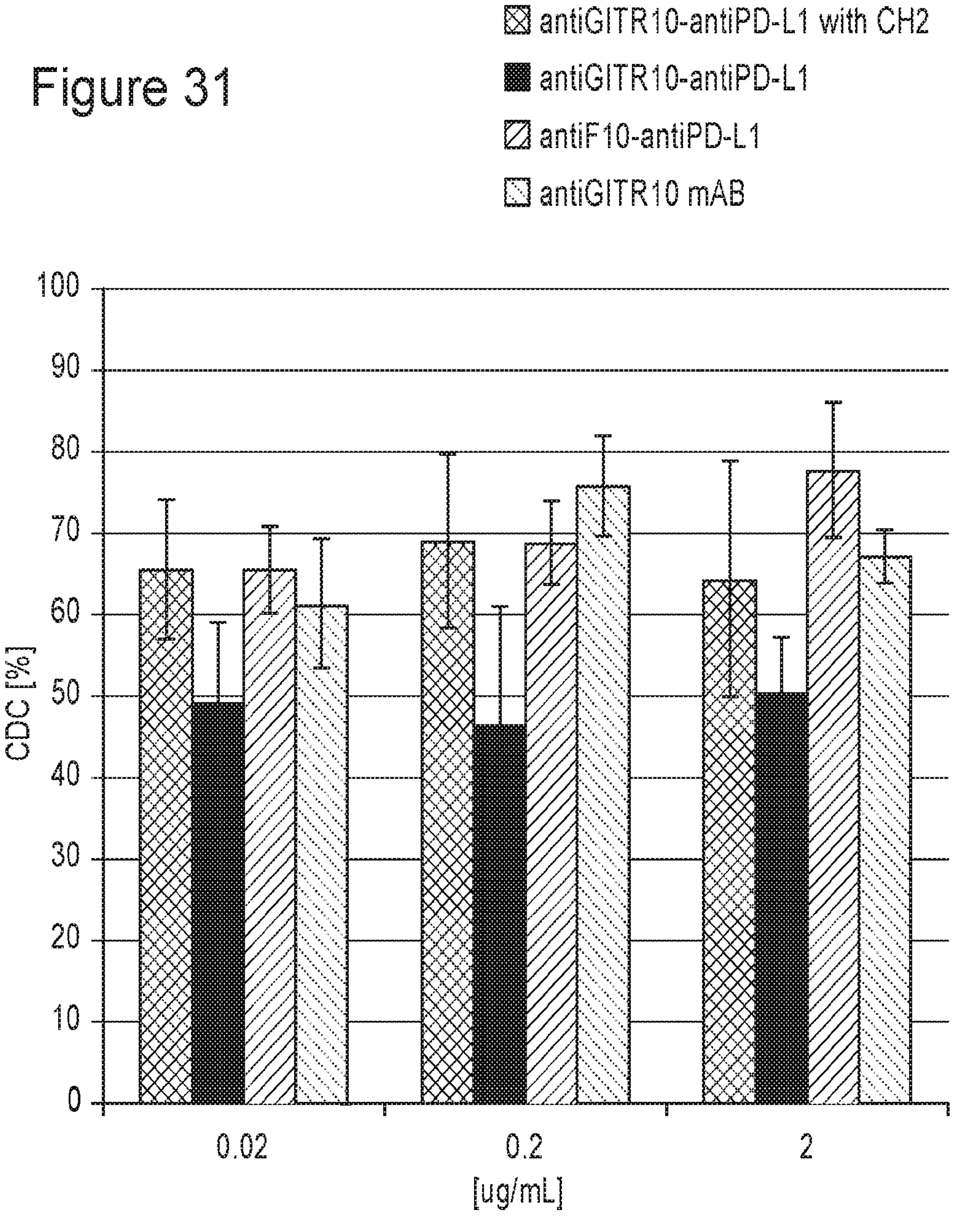

antiGITR10-antiPD-L1 with CH2
antiGITR10-antiPD-L1
antiF10-antiPD-L1
antiGITR10 mAB
100
90
80
70
60
50
40
30
20
10
0
CDC [%]
0.02
0.2
2
[ug/mL]

Figure 32

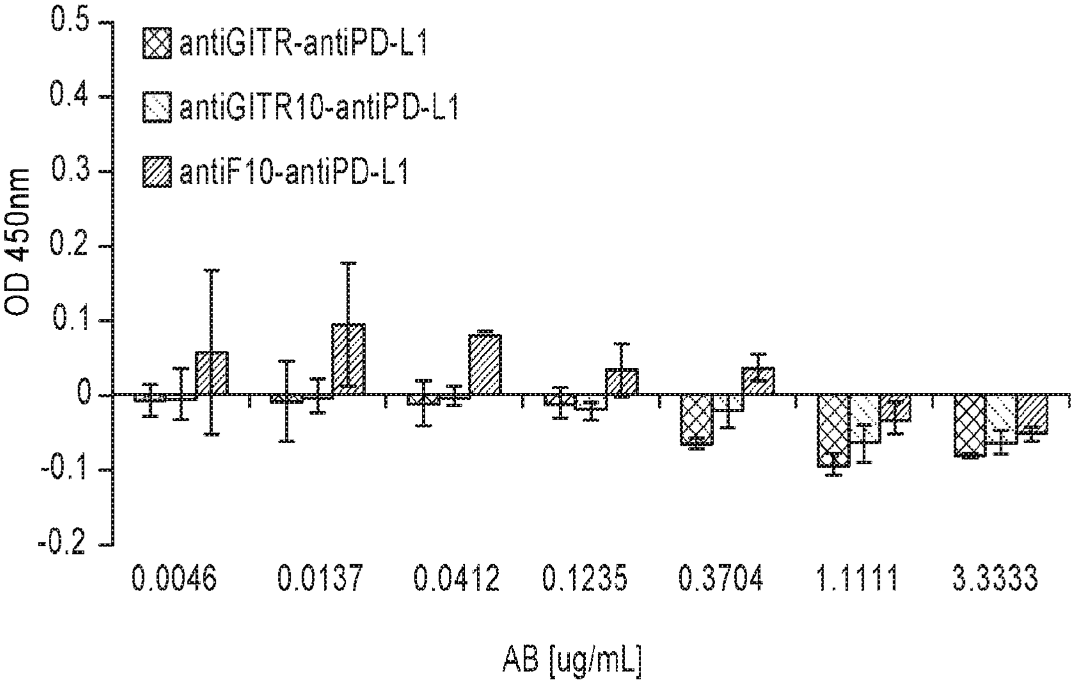

0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
OD 450nm
antiGITR-antiPD-L1
antiGITR10-antiPD-L1
antiF10-antiPD-L1
0.0046
0.0137
0.0412
0.1235
0.3704
1.1111
3.3333
AB [ug/mL]

Figure 33

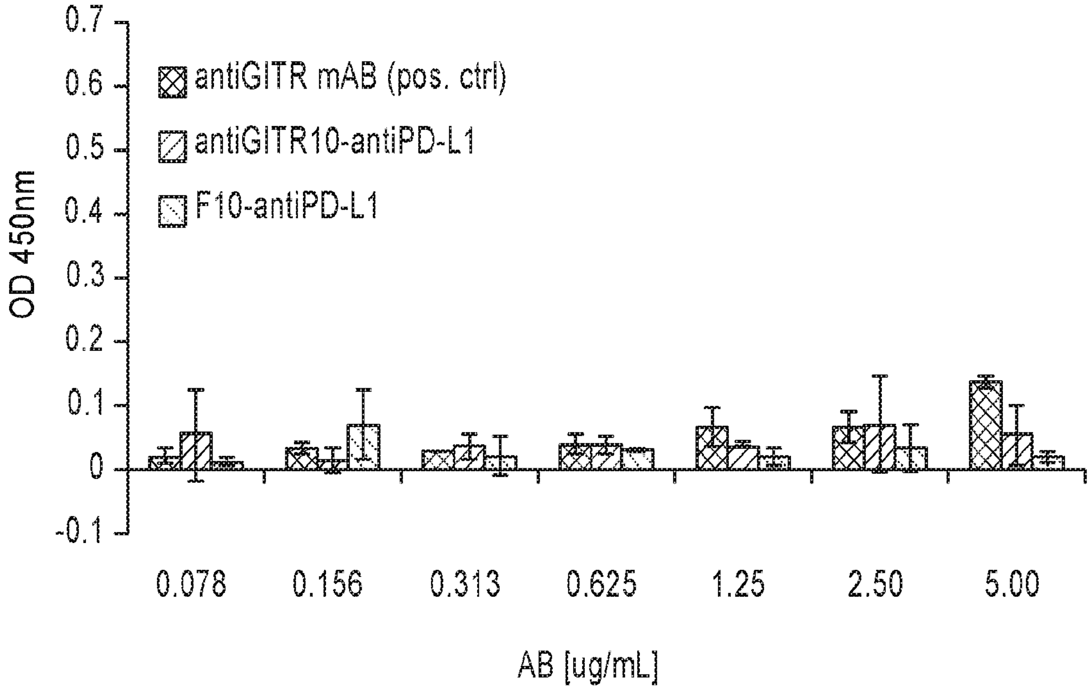

0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
OD 450nm
antiGITR mAB (pos. ctrl)
antiGITR10-antiPD-L1
F10-antiPD-L1
0.078
0.156
0.313
0.625
1.25
2.50
5.00
AB [ug/mL]

Figure 34

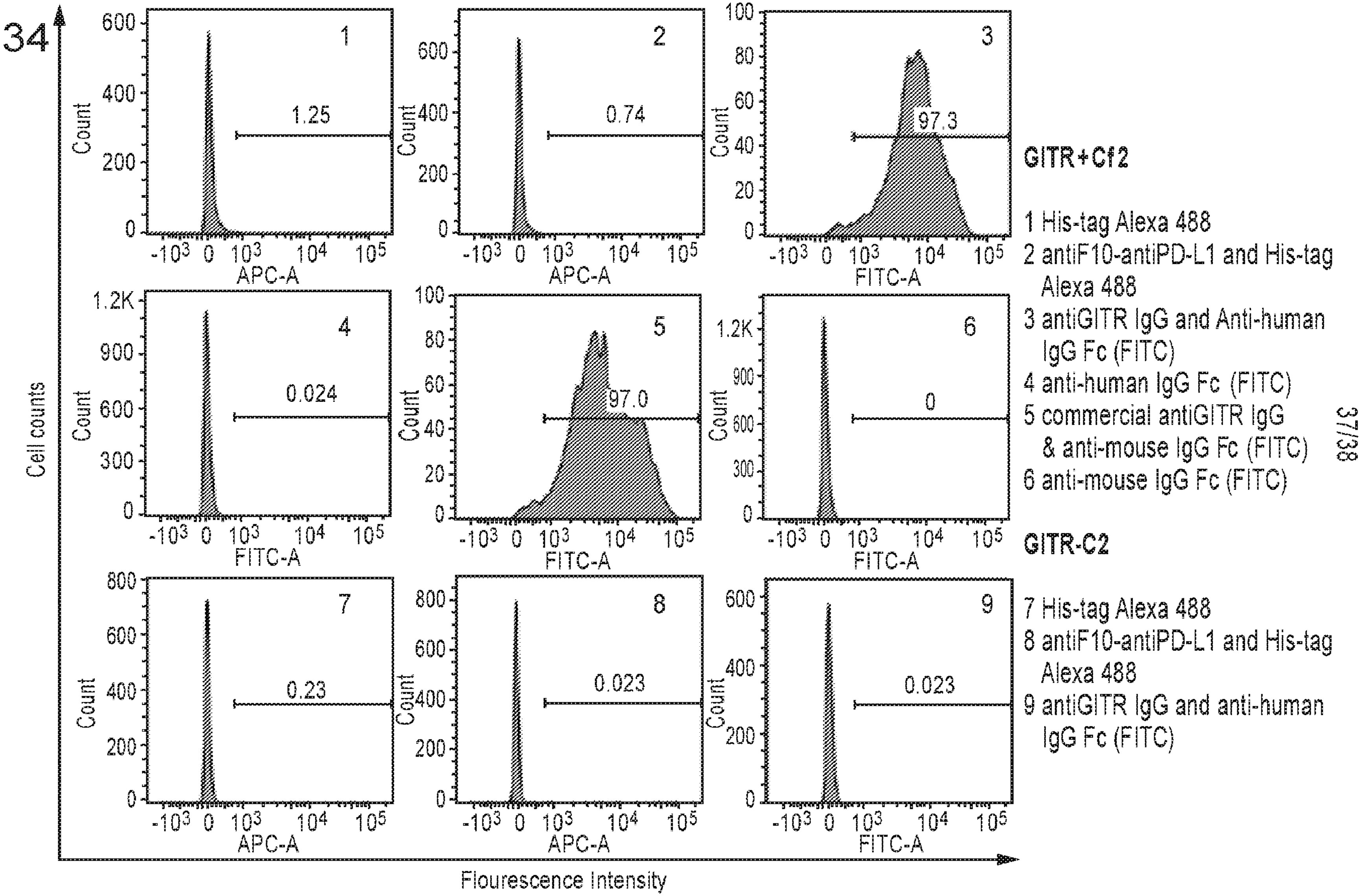
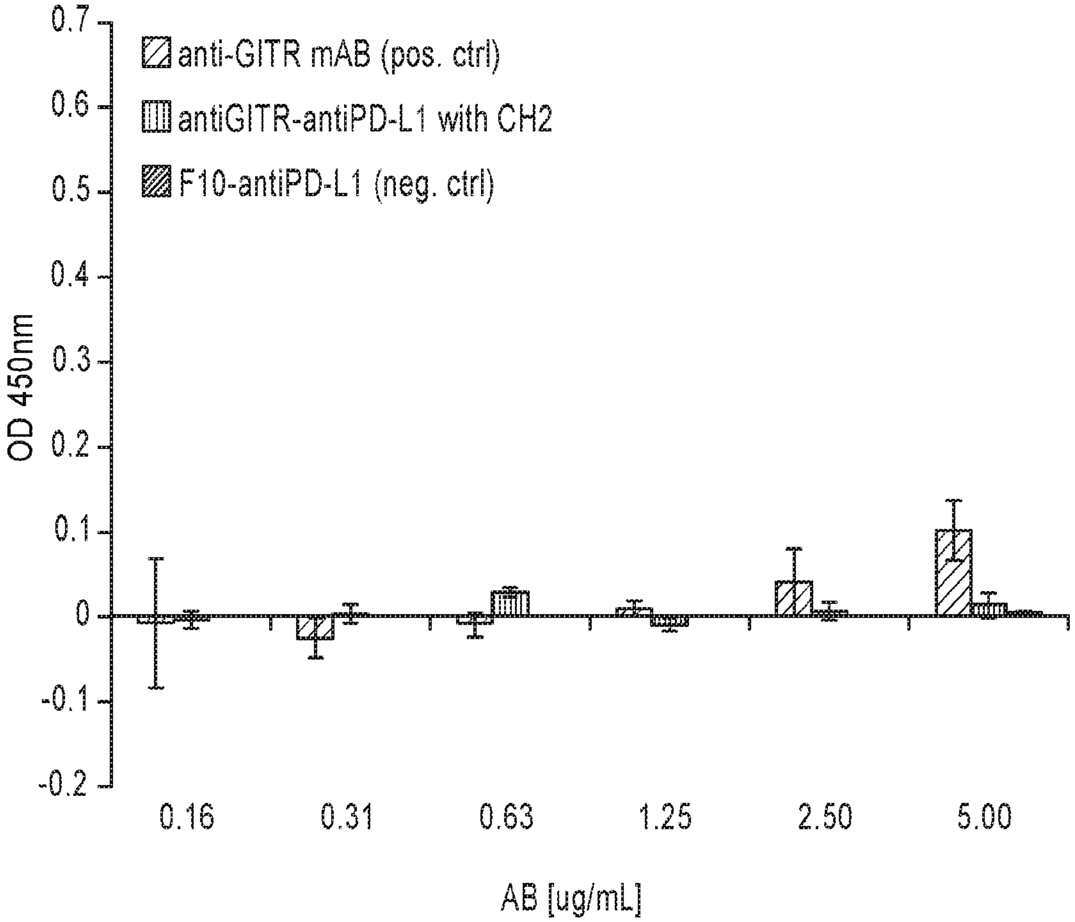

Cell counts
Count
600
400
200
0
1.2K
900
300
800
100
80
60
40
20
-10^3
0
10^3
10^4
10^5
APC-A
FITC-A
1
1.25
2
0.74
3
97.3
4
0.024
5
97.0
6
0
7
0.23
8
0.023
9
0.023
Flourescence Intensity
GITR+Cf2
1 His-tag Alexa 488
2 antiF10-antiPD-L1 and His-tag Alexa 488
3 antiGITR IgG and Anti-human IgG Fc (FITC)
4 anti-human IgG Fc (FITC)
5 commercial antiGITR IgG & anti-mouse IgG Fc (FITC)
6 anti-mouse IgG Fc (FITC)
GITR-C2
7 His-tag Alexa 488
8 antiF10-antiPD-L1 and His-tag Alexa 488
9 antiGITR IgG and anti-human IgG Fc (FITC)

Figure 35


anti-GITR mAB (pos. ctrl)
antiGITR-antiPD-L1 with CH2
F10-antiPD-L1 (neg. ctrl)
OD 450nm
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
-0.2
0.16
0.31
0.63
1.25
2.50
5.00
AB [ug/mL]

SEQUENCE LISTING

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<130>  DFCI-122_001WO - 322270-2813

<150>  US 62/408,271
<151>  2016-10-14

<160>  1905

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<210>  62
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<210>  67
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Val
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1               5                   10                  15


Asp Val



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1               5                   10                  15


Tyr



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1               5                   10                  15


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Asp Gln



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1               5                   10                  15
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Asp Leu



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<400>  89

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1               5                   10                  15


<210>  90
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<400>  90

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1               5                   10                  15


Leu



<210>  91
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<400>  91

Ala Arg Gly Tyr Ser Tyr Tyr Pro Gly Gly Gly Gly Gly Arg Asn Phe
1               5                   10                  15


Asp Tyr




<210>  92
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<400>  92

Ala Arg Ala Pro Thr Tyr Tyr Ala Ser Arg Asp Ser Tyr Asn Phe Asp
1               5                   10                  15


Tyr




<210>  93
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<220>
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<400>  93

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1               5                   10


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<213> Artificial Sequence

<220>
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<400> 94

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<210> 95
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<210> 96
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<400> 96

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1   5   10   15

Ile Phe Asp Val
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<400> 97

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<400>  98

Ala Arg Glu Tyr Leu Gly Asp Asp Tyr Ser Ser Gly Ser Tyr Phe Asp
1               5                   10                  15


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Ala Arg Glu Ser Gly Tyr Ser Gly Thr Gly Gln Phe Asp Val
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Ala Arg Gly Pro Gly Tyr Asp Pro Ser Ser Leu Arg Gly Phe Asp Val
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<400>  103

Ala Arg Gly Glu Glu Ala Tyr Tyr Asp Leu
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<400>  104

Ala Arg Gly Thr Ser Tyr Leu Pro Gly Arg Ser Gly Phe Asp Val
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Ala Arg Gly Arg Gly Tyr Asp Pro Ser Val Gly Gly Phe Asp Val
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<400>  106

Ala Arg Asp Ser Thr Pro Ser Val Thr Ser Ser Leu Tyr Arg Ile Pro
1               5                   10                  15


Ala Phe Asp Val
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<400>  107

Ala Arg Gly Pro Gly Tyr Tyr Pro Asp Ser Asn Asn Tyr Asp Leu
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Arg Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
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Asn Ile Gly Ser Lys Ser
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Gln Thr Val Ser Asn Tyr
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Ser Ser Asn Ile Gly Ser Asn Thr
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His Ile Gly Ser Lys Ser
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Ser Ser Asp Val Gly Gly Tyr Asn His
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Ser Gly Ser Ile Ala Ser Thr Tyr
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Ser Gly Ser Ile Ala Ser Asn Tyr
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<400> 120

Ser Gly Ser Ile Ala Ser Asn Tyr
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Asp Ile Gly Ser Lys Ser
1   5

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Ser Gly Ser Val Ser Thr Ser Asn Tyr
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Arg Ser Leu Phe Asp Ser Ser Asp Asn Lys Asn Tyr
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Arg Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
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Ser Ser Asn Ile Gly Val Asn Tyr
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Ser Ser Asn Ile Gly Ser Asn Thr
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Gln Ser Val Asp Arg Gly Tyr
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<400>  129

Ser Ser Asp Ile Gly Ala Tyr Asn Tyr
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Ala Leu Pro Lys Gln Tyr
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Ser Asp Asn Val Gly Asn Gln Gly
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Asn Asn Asn Val Gly Asn Gln Gly
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Gln Ser Val Asp Ser His
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Thr Ser Asn Val Gly Arg Asn Thr
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Arg Ser Asn Ile Gly Ser Asn Thr
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Arg Ser Asn Ile Gly Arg Asn Thr
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Gln Ser Val Ser Ser Phe
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Asn Gly Pro Ser Asn Tyr Ile
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Gln Ser Val Ser Ser Ser Tyr
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Ser Ser Asn Ile Gly Val Ser Phe
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Trp Ala Ser
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Ala Ala Ser
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Ser Asn Asn
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Ser Asn Asn
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Asp Val Ser
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Glu Val Thr
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Glu Asp His
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Glu Asp Asn
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Asp Asn Ser
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Glu Asp Asn
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Asp Asp Ile
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Ser Thr Asn
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Arg Asn Asn
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Trp Ala Ser
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Trp Ala Ser
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Arg Asn Asn
1


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Ser Asn Asn
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Gly Ala Ser
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Glu Val Ser
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Lys Asp Ser
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Arg Asp Asn
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Arg Asn Asn
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Glu Val Asn
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Gly Ala Ser
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Asn Asp Asn
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Ser Asn Asn
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Ser Asn Asn
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Lys Asn Asn
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Lys Asp Thr
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<400>  177

Glu Asp Asn
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Arg Asp Asp
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<400> 181

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<400> 182

Gln Val Trp Asp Arg Ser Ser Asp His Val Val
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<400> 183

Gln Gln Tyr Asp Asn Leu Pro Pro Val Thr
1 5 10

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<400> 184

Ser Ala Trp Asp Asp Ser Leu Gly Gly Glu Val
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<400> 185

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<400> 186

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1   5   10

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<400> 187

Ser Ser Tyr Ala Gly Gly Lys Trp Val
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<400> 188

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1   5   10

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Gln Ser Phe Asp Ala Ser Thr Leu Val
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<400> 192

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<400> 193

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<400>  194

Val Leu Tyr Met Gly Ser Gly Ile Ser Met
1               5                   10


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<400>  195

Ser Ala Trp Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


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<400>  196

Gln Gln Tyr Phe Ser Ser Pro Pro Ile Phe Thr
1               5                   10


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<220>
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<400> 197

Gln Gln Tyr Tyr Ser Thr Pro Pro Thr
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<400> 198

Gly Val Trp Asp Asp Ser Leu Asn Gly His Trp Val
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<400> 199

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<400> 200

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Gln Ala Trp Asp Ser Ser Thr Ala Val
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<210>  203
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<400>  203

Ser Ala Trp Asp Ser Ser Leu Thr Ala Val Val
1               5                   10


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<400>  204

Ser Ala Trp Asp Ser Ser Leu Ser Ala Trp Val
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1               5                   10


<210>  205
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<400>  205

Ala Ala Trp Asp Asp Ser Leu Asp Gly Pro Val
1               5                   10


<210>  206
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<400>  206

Gln Gln Arg Ser Met Trp Pro Leu Thr
1               5


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<400>  207

Ser Ser Trp Asp Asp Asp Leu Asn Gly Pro Val
1               5                   10


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<400>  208

Gln Ser Tyr Asp Ser Ser Val Val
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<400>  209

Ala Ala Trp Asp Val Ser Leu Asn Gly Gln Val
1               5                   10


<210>  210
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<400>  210

Ser Ala Trp Asp Ser Ser Leu Ser Asp Trp Val
1               5                   10


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<400>  211

Gln Gln Arg Phe Asn Trp Pro Pro Thr
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Gln Ser Ala Asp Ala Ser Glu Asn Ser Val
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Gly Val Thr Phe Ser Ser Tyr Ala
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Gly Gly Ile Phe Ser Ser Tyr Ala
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Gly Val Ile Phe Ser Ser Tyr Ala
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Gly Gly Thr Phe Ser Ser Tyr Ala
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Gly Gly Ile Phe Ser Ser Tyr Ala
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<210>  247
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<400>  262

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<400>  266

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<400>  269

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<400>  270

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<400>  273

Ile Ser Pro Ile Phe Gly Thr Ala
1               5


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<400>  274

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<400>  276

Ile Ser Pro Ile Phe Gly Thr Ala
1               5


<210>  277
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Gly Tyr Asp Leu
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<400>  280

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<220>
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<400> 283

Ala Arg Gly Gly Gly Gly Arg Phe Asp Val
1 5 10

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<400> 284

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<400> 285

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Asp Val

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1               5                   10                  15


<210>  287
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<400>  287

Ala Arg Gly Gly Ser Gly Ser Phe Asp Val
1               5                   10


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<400>  290

Ala Arg Val Arg Gly Gly Tyr Gly Pro Tyr Gly Asp Phe Asp Val
1               5                   10                  15


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<400>  291

Ala Arg Gly Arg Ser Tyr Ile Val Ser Val Ser Pro Gly Phe Asp Val
1               5                   10                  15


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<400>  292

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<210>  293
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<400>  293

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1               5                   10


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<400>  294

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<400>  295

Ala Arg Gly Gly Gly Tyr Tyr Pro Ala Gly Val Gly Arg Tyr Asp Val
1               5                   10                  15


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<400>  296

Ala Arg Gly Pro Thr Leu Tyr Ser Pro Pro Val Phe Asp Val
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Ala Arg Gly Ala Gly Val Ser Ala Gly Pro Ser Trp Pro Phe Asp Val
1   5   10   15

<210> 298
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<400> 298

Ala Arg Ser Arg Gly Tyr Asn Val Ala Ala Ser Phe Gly Phe Asp Val
1   5   10   15

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Ala Arg Gly Gly Gly Val Phe Asp Val
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<400>  301

Ala Arg Glu Gly Gly Tyr Ser Pro Gly Gly Val Asp Phe Asp Tyr
1               5                   10                  15


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<400>  302

Ala Arg Ser Pro Ala Tyr Tyr Phe Gly Pro Asn Met Asp Val
1               5                   10


<210>  303
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<213>  Artificial Sequence

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<400>  303

Ala Arg Gly Pro Gly Tyr His Pro Ala Gly Ala Ser Gly Gln Phe Phe
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Asp Leu
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<400> 304

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<400>  307

Ser Ser Asn Ile Gly Ser Asn Thr
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<210>  308
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<400>  308

Asn Ile Ala Thr Lys Ser
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<210>  309
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<212>  PRT
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<220>
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<400>  309

Asn Ile Ala Thr Lys Ser
1               5


<210>  310
<211>  8
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<400>  310

Ile Asn Asn Val Gly Asp Gln Gly
1               5


<210>  311
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<220>
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<400>  311

Asn Ile Gly Ser Lys Ser
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<210>  312
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<400>  312

Ser Asn Asn Val Gly Asn Gln Gly
1               5


<210>  313
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<400>  313

Thr Ser Asn Ile Gly Asn Asn Ala
1               5


<210>  314
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<400>  314

Gly Ser Asn Val Gly Ser Asn Val
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1   5

<210> 315
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<400> 315

Ser Ser Asn Ile Gly Arg Asn Asp
1   5

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<400> 316

Ser Ser Asn Ile Gly Ser Asn Thr
1   5

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<400> 317

Ser Ser Asn Leu Gly Ser Asn Tyr
1   5

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<400>  318

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<210>  319
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<220>
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<400>  319

Thr Gly Ala Val Thr Ser Gly Tyr Tyr
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<210>  320
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<400>  320

Ser Ser Asn Ile Gly Ser His Ser
1               5


<210>  321
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<212>  PRT
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<220>
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<400>  321

Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1               5


<210>  322
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<220>
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<400>  322

Ser Leu Arg Thr Ser Tyr
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<210>  323
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<400>  323

Ser Ser Asn Ile Gly Ser Asn Thr
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<400>  324

Ser Ser Asn Val Gly Asn Gln Gly
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<210>  325
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<220>
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<400>  325

Gln Asn Val Leu Tyr Ser Ser Asn Asn Lys Asn Asn
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<400>  326

Ser Gly Ser Val Ser Thr Thr Asn Tyr
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<210>  327
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<400>  327

Ser Asn Asn Val Gly Lys Gln Gly
1               5


<210>  328
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<212>  PRT
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<220>
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<400>  328

Gln Tyr Ile Asp Arg Ser
1               5


<210>  329
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<220>
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<400>  329
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Ser Gly Ser Val Ser Ser Phe Asn Tyr
1               5


<210>  330
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<220>
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<400>  330

Ser Ser Asn Ile Gly Asn Asn Ala
1               5


<210>  331
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<213>  Artificial Sequence

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<400>  331

Ser Gly Ser Ile Ala Ser Thr Tyr
1               5


<210>  332
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<220>
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<400>  332

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1               5


<210>  333
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<400>  333

Ser Asn Asn Val Gly Asn Gln Gly
1               5


<210>  334
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  334

Arg Ser Leu Phe Asp Ser Ser Asp Asn Lys Asn Tyr
1               5                   10


<210>  335
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<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  335

Ser Ser Asn Ile Gly Ser Asn Thr
1               5


<210>  336
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  336

Arg Ser Asn Ile Gly Ser Asn Thr
1               5


<210>  337
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<220>
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<400>  337

Ser Asn Asn
1


<210>  338
<211>  3
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<220>
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<400>  338

His Asp Ser
1


<210>  339
<211>  3
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<220>
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<400>  339

Arg Asn Ser
1


<210>  340
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<400>  340

Gly Ala Ser
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1

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<400> 341

Tyr Asp Ser
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<210> 342
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<400> 342

Arg Asn Asn
1

<210> 343
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<400> 343

Ser Leu Asn
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Arg Asn Asn
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<400>  345

Gly Arg Asp
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<210>  346
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<220>
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<400>  346

Ser Asn Asn
1


<210>  347
<211>  3
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<220>
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<400>  347

Arg Asn Ser
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<210>  348
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<400> 348

Gly Ala Thr
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<210> 349
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<400> 349

Ser Thr Ser
1

<210> 350
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<220>
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<400> 350

Gly Asn Ser
1

<210> 351
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<213> Artificial Sequence

<220>
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<400> 351

Glu Val Ser
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<210> 352
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<220>
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<400> 352

Gln Ser Thr
1

<210> 353
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<220>
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<400> 353

Ser Asn Asn
1

<210> 354
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<220>
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<400> 354

Arg Asn Asp
1

<210> 355
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<400> 355

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Trp Ala Ser
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<210>  356
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<220>
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<400>  356

Asn Thr Asn
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<210>  357
<211>  3
<212>  PRT
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<220>
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<400>  357

Arg Asn Asn
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<210>  358
<211>  3
<212>  PRT
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<220>
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<400>  358

Tyr Ala Ser
1


<210>  359
<211>  3
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<220>
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<400> 359

Asn Thr Asn
1

<210> 360
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<220>
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<400> 360

Tyr Asp Asp
1

<210> 361
<211> 3
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<220>
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<400> 361

Glu Asp His
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<210> 362
<211> 3
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<220>
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<400> 362

Asp Asn Ser
1

<210> 363

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<211>  3
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<220>
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<400>  363

Arg Asn Asn
1


<210>  364
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<220>
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<400>  364

Trp Ala Ser
1


<210>  365
<211>  3
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<220>
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<400>  365

Ser Asn Asn
1


<210>  366
<211>  3
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<400>  366

Ser Asn Asn
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1

<210> 367
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<220>
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<400> 367

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Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1               5                   10
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<210> 368
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<400> 368

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Ala Ala Trp Asp Asp Ser Leu Ser Gly Pro Trp Val
1               5                   10
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<210> 369
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<400> 369

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Ser Ala Trp Asp Ser Ser Leu Ser Asp Trp Val
1               5                   10
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<210> 370
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<212> PRT
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<220>
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<400>  370

Gln Gln Tyr Ser Ser Ser Pro Tyr Thr
1               5


<210>  371
<211>  11
<212>  PRT
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<220>
<223>  Synthetic Polypeptide

<400>  371

Gln Leu Trp Asp His Thr Asn Ser His Val Val
1               5                   10


<210>  372
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  372

Ser Ala Trp Asp Asn Thr Val Ser Gly Trp Val
1               5                   10


<210>  373
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  373

Glu Ala Trp Asp Asp Ser Leu Ser Gly Pro Val
1               5                   10


<210>  374
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<213> Artificial Sequence

<220>
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<400> 374

Ala Ala Trp Asp Asp Arg Leu Asn Gly Phe Val
1   5   10

<210> 375
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 375

Ala Ala Trp Asp Ala Ser Leu Met Ile Tyr Val
1   5   10

<210> 376
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 376

Ala Ala Trp Asp Asp Ser Leu Asn Gly Tyr Val
1   5   10

<210> 377
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<400> 377

Ala Ala Trp Asp Asp Ser Leu Asn Gly Val Val
1   5   10

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<210>  378
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<400>  378

Gln Gln Tyr Gly Ser Ser Pro Gln Thr
1               5


<210>  379
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<400>  379

Leu Leu Tyr Tyr Gly Gly Pro Trp Val
1               5


<210>  380
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<213>  Artificial Sequence

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<400>  380

Ala Ala Trp Asp Asp Gly Leu Ser Gly Trp Val
1               5                   10


<210>  381
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<400>  381
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Ala Ser Trp Asp Asp Ser Leu Asn Ala Tyr Val
1               5                   10


<210>  382
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<400>  382

Asn Ser Arg Gly Ser Gly Gly Asn Pro Tyr Val
1               5                   10


<210>  383
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<400>  383

Ala Ala Trp Asp Asp Ser Leu Asn Gly Arg Val
1               5                   10


<210>  384
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<400>  384

Ser Ala Trp Asp Asn Ser Leu Ser Ala Trp Val
1               5                   10


<210>  385
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<400>  385

Gln Gln Tyr Tyr Gly Lys Pro Phe Thr
1               5


<210>  386
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<220>
<223>  Synthetic Polypeptide

<400>  386

Val Leu Tyr Met Gly Arg Gly Ile Tyr Val
1               5                   10


<210>  387
<211>  11
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<213>  Artificial Sequence

<220>
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<400>  387

Ser Ala Trp Asp Ser Ser Leu Ser Val Trp Val
1               5                   10


<210>  388
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  388

His Gln Thr Ser Ser Leu Pro Trp Thr
1               5


<210>  389
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<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  389

Ala Leu Tyr Val Gly Gly Gly Ile Ser Val
1               5                   10


<210>  390
<211>  11
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<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  390

Ala Ala Trp Asp Asp Ser Leu Ser Gly Pro Val
1               5                   10


<210>  391
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<220>
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<400>  391

Gln Ser Phe Asp Ala Ser Thr Leu Val
1               5


<210>  392
<211>  11
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<220>
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<400>  392

Gln Ser Tyr Asp Ser Ser Leu Ser Val Val Val
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1               5                   10


<210>  393
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<400>  393

Ser Ala Trp Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


<210>  394
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  394

Gln Gln Tyr Phe Ser Ser Pro Pro Ile Phe Thr
1               5                   10


<210>  395
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<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  395

Ala Ala Trp Asp Asp Ser Leu Lys Gly Arg Val
1               5                   10


<210>  396
<211>  8
<212>  PRT
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<400> 396

Gln Ser Tyr Asp Ser Ser Val Val
1   5

<210> 397
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
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agctgtaagg cgagcggtgg cccattcagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tgtttggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagcacctc aaccgcctac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacgac   300

ggttacgctc ctagtggtgg tctgcgtgag tttgacgttt ggggccaggg gaccttagtc   360

actgtgtcta gc   372

<210> 398
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
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<400> 398
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atcaactgca agtccagccg gagtgtttta tacagctcca acaacaagaa ctacttagct   120

tggtaccaac aaaaaccggg acagcctcct aagttgctca tttattgggc ttctacccgg   180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc   240

atcagcagcc tgcaggctga agatgtggcg gtttattact gtcagcaata ttatagtggt   300

tcctggacat tcggccaagg gaccaaggtg gaaatcaaac   340

<210> 399
<211> 363
<212> DNA
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<220>
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cctggtcagg gcctcgaatg gatgggcggc attagcccta tctttggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagata aaagcacgaa taccgcctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt 300

ggtgcttaca tgggtcctag tatggatgtg tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 400
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
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<400> 400
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acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240

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ggagggacca agctgaccgt cctag 325

<210> 401
<211> 363
<212> DNA
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<400>  401
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cctggtcagg gcctcgaatg gatgggcggc atcagcccaa tctttggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagata aaagcacgtc aactgtgtat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgct      300

cgttactacg ctggtggtta cttcgatgtg tggggccagg ggaccttagt cactgtgtct      360

agc                                                                    363


<210>  402
<211>  325
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  402

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Ala Gly Thr Cys Thr Cys Cys Ala Gly Gly Cys Ala Cys Cys Cys Thr
            20                  25                  30


Gly Thr Cys Thr Thr Thr Gly Thr Cys Thr Cys Cys Ala Gly Gly Gly
        35                  40                  45


Gly Ala Ala Ala Gly Ala Gly Cys Cys Ala Cys Cys Cys Thr Cys Thr
    50                  55                  60


Cys Cys Thr Gly Cys Ala Gly Gly Gly Cys Cys Ala Gly Thr Cys Ala
65                  70                  75                  80


Gly Ala Cys Thr Gly Thr Thr Ala Gly Cys Ala Ala Cys Thr Ala Cys
                85                  90                  95
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Thr Thr Ala Gly Cys Cys Thr Gly Gly Thr Ala Thr Cys Ala Gly Cys
            100                 105                 110


Ala Gly Ala Gly Ala Cys Cys Thr Gly Gly Cys Cys Ala Gly Gly Cys
        115                 120                 125


Thr Cys Cys Cys Ala Gly Gly Cys Thr Cys Cys Thr Cys Ala Thr Cys
    130                 135                 140


Thr Ala Cys Gly Cys Thr Gly Cys Ala Thr Cys Cys Ala Cys Gly Cys
145                 150                 155                 160


Gly Gly Gly Cys Cys Ala Cys Thr Gly Gly Thr Gly Thr Cys Cys Cys
                165                 170                 175


Ala Gly Cys Cys Ala Gly Gly Thr Thr Cys Ala Gly Thr Gly Gly Cys
            180                 185                 190


Ala Gly Cys Gly Gly Gly Thr Cys Thr Gly Gly Gly Ala Cys Ala Gly
        195                 200                 205


Ala Gly Thr Thr Cys Ala Cys Thr Cys Thr Cys Ala Cys Cys Ala Thr
    210                 215                 220


Cys Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala Ala Thr Cys Thr
225                 230                 235                 240


Gly Ala Ala Gly Ala Thr Thr Thr Thr Gly Cys Ala Ala Thr Thr Thr
                245                 250                 255


Ala Thr Thr Ala Cys Thr Gly Thr Cys Ala Ala Cys Ala Gly Thr Ala
            260                 265                 270


Thr Gly Ala Thr Ala Ala Cys Thr Thr Gly Cys Cys Thr Cys Cys Gly
        275                 280                 285


Gly Thr Cys Ala Cys Thr Thr Thr Cys Gly Gly Cys Cys Cys Thr Gly
    290                 295                 300
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Gly Gly Ala Cys Cys Ala Cys Ala Gly Thr Gly Gly Ala Thr Ala Thr
305                 310                 315                 320


Cys Ala Ala Ala Cys
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<210>  403
<211>  375
<212>  DNA
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<220>
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<400>  403
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cctggtcagg gcctcgaatg gatgggcggc atcagcccaa tcttcggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatc agagtaccaa cactgtctac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacagt      300

ggtaattacg acggttacgg tcctggtagt cgtttcgacg tgtggggcca ggggacctta      360

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<210>  404
<211>  331
<212>  DNA
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<220>
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<400>  404
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tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta tttctgttca gcttgggatg acagcctggg tggcgaggtc      300
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ttcggaactg ggaccaaggt caacgtccta g                                   331


<210>  405
<211>  363
<212>  DNA
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<220>
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<400>  405
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agctgtaagg cgagcggagt gacctttagt tcttacgcca ttagctgggt gcgacaggct     120

cctggtcagg gcctcgaatg gatgggcggc attatgccta tgttcggcac tgcaaattat     180

gcccagaaat ttcagggtag agtcacaatt accgcagata agagtacgag cactgcctat     240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgagcgt     300

ggtagttgga gtttcggtta ctttgatgtg tggggccagg ggaccttagt cactgtgtct     360

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<210>  406
<211>  325
<212>  DNA
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<220>
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<400>  406
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acctgtgggg gagaccacat tggaagtaaa agtgtgcact ggtaccagcg gaagccgggc     120

caggcccctg tgctggtcat ctattctgac accgaccggc cctcagggat ccctgagcgg     180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg     240

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ggaggcacca agctgaccgt cctag                                           325


<210>  407
<211>  363
<212>  DNA
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<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  407
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagt gacctttagc tcttacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcagccctc tgtttggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtacgag caccgtgtat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcgt      300

acatacgctg acggtcgtac attcgacgtg tggggccagg ggaccttagt cactgtgtct      360

agc                                                                    363


<210>  408
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  408
cagtctgtgc tgactcagcc accctccgcg tccgggtctc ctggacagtc ggtcaccatc       60

tcctgcactg gaaccagtag tgacgttggt ggttataacc atgtctcctg gtaccaacag      120

cacccaggca aagcccccaa agtcctgatt tatgacgtca gtaagcggcc ctcaggggtc      180

ccagatcgct tctctggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc      240

caggctgagg atgaggctga ttattactgc acctcatatg caggcagcaa cagtttggtc      300

ttcggaactg ggaccgaggt caccgtccta g                                     331


<210>  409
<211>  372
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  409
```

```
Cys Ala Gly Gly Thr Thr Cys Ala Ala Thr Thr Ala Gly Thr Gly Cys
1               5                   10                  15


Ala Gly Thr Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Thr
            20                  25                  30


Gly Ala Ala Ala Ala Ala Gly Cys Cys Cys Gly Gly Cys Thr Cys Ala
        35                  40                  45


Ala Gly Thr Gly Thr Thr Ala Ala Ala Gly Thr Ala Ala Gly Cys Thr
    50                  55                  60


Gly Thr Ala Ala Gly Gly Cys Gly Ala Gly Cys Gly Gly Thr Gly Gly
65                  70                  75                  80


Cys Ala Cys Thr Thr Thr Cys Ala Gly Thr Thr Cys Ala Thr Ala Cys
                85                  90                  95


Gly Cys Cys Ala Thr Thr Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110


Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Thr Gly Gly Thr Cys Ala
        115                 120                 125


Gly Gly Gly Cys Cys Thr Cys Gly Ala Ala Thr Gly Gly Ala Thr Gly
    130                 135                 140


Gly Gly Cys Gly Gly Cys Ala Thr Cys Ala Gly Cys Cys Cys Ala Ala
145                 150                 155                 160


Thr Cys Thr Thr Thr Gly Gly Thr Ala Cys Thr Gly Cys Ala Ala Ala
                165                 170                 175


Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Ala Ala Ala Thr Thr Thr
            180                 185                 190


Cys Ala Gly Gly Gly Thr Ala Gly Ala Gly Thr Cys Ala Cys Ala Ala
        195                 200                 205
```

```
Thr Thr Ala Cys Cys Gly Cys Ala Gly Ala Cys Ala Ala Gly Ala Gly
    210                 215                 220


Cys Ala Cys Gly Ala Gly Cys Ala Cys Thr Gly Cys Cys Thr Ala Cys
225                 230                 235                 240


Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Gly Thr Ala Gly Cys Cys
                245                 250                 255


Thr Gly Cys Gly Thr Thr Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
            260                 265                 270


Ala Gly Cys Thr Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr
        275                 280                 285


Gly Cys Gly Cys Gly Cys Gly Ala Gly Cys Thr Gly Gly Gly Thr Thr
    290                 295                 300


Ala Cys Cys Thr Gly Gly Cys Thr Gly Gly Thr Ala Gly Thr Cys Cys
305                 310                 315                 320


Thr Ala Gly Thr Cys Cys Thr Gly Gly Thr Thr Thr Cys Gly Ala Thr
                325                 330                 335


Thr Ala Cys Thr Gly Gly Gly Gly Cys Cys Ala Gly Gly Gly Gly Ala
            340                 345                 350


Cys Cys Thr Thr Ala Gly Thr Cys Ala Cys Thr Gly Thr Gly Thr Cys
        355                 360                 365


Thr Ala Gly Cys
    370


<210>  410
<211>  328
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide
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```
<400>  410
cagtctgtgc tgactcagcc accctccgcg tccgggtctc ctggacagtc agtcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatcatt tatgaggtca ctaagcggcc ctcaggggtc      180

cctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccgt cgctgggctc      240

caggctgagg atgaggctga ttattactgc agctcgtatg caggcggcaa gtgggtcttc      300

ggaactggga ccaaggtcac cgtcctag                                          328


<210>  411
<211>  363
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  411

Cys Ala Gly Gly Thr Thr Cys Ala Ala Thr Thr Ala Gly Thr Gly Cys
1               5                   10                  15


Ala Gly Thr Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Thr
            20                  25                  30


Gly Ala Ala Ala Ala Ala Gly Cys Cys Cys Gly Gly Cys Thr Cys Ala
        35                  40                  45


Ala Gly Thr Gly Thr Thr Ala Ala Ala Gly Thr Ala Ala Gly Cys Thr
    50                  55                  60


Gly Thr Ala Ala Gly Gly Cys Gly Ala Gly Cys Gly Gly Ala Gly Gly
65                  70                  75                  80


Cys Ala Cys Thr Thr Thr Thr Ala Gly Cys Thr Cys Thr Thr Ala Cys
                85                  90                  95


Gly Cys Cys Ala Thr Thr Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110
```

```
Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Thr Gly Gly Thr Cys Ala
        115                 120                 125

Gly Gly Gly Cys Cys Thr Cys Gly Ala Ala Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Cys Gly Gly Cys Ala Thr Thr Ala Gly Cys Cys Cys Ala Ala
145                 150                 155                 160

Thr Cys Thr Thr Cys Gly Gly Cys Ala Cys Thr Gly Cys Ala Ala Ala
                165                 170                 175

Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Ala Ala Ala Thr Thr Thr
            180                 185                 190

Cys Ala Gly Gly Gly Thr Ala Gly Ala Gly Thr Cys Ala Cys Ala Ala
        195                 200                 205

Thr Thr Ala Cys Cys Gly Cys Ala Gly Ala Cys Ala Cys Cys Ala Gly
    210                 215                 220

Cys Ala Cys Cys Thr Cys Ala Ala Cys Cys Gly Cys Cys Thr Ala Cys
225                 230                 235                 240

Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Gly Thr Ala Gly Cys Cys
                245                 250                 255

Thr Gly Cys Gly Thr Thr Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
            260                 265                 270

Ala Gly Cys Thr Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr
        275                 280                 285

Gly Cys Gly Cys Gly Cys Ala Gly Thr Cys Gly Thr Cys Gly Thr Thr
    290                 295                 300

Ala Cys Thr Gly Gly Gly Cys Thr Gly Ala Cys Gly Gly Thr Gly Gly
305                 310                 315                 320
```

```
Thr Thr Thr Cys Gly Ala Thr Thr Ala Thr Thr Gly Gly Gly Gly Cys
                325                 330                 335


Cys Ala Gly Gly Gly Gly Ala Cys Cys Thr Thr Ala Gly Thr Cys Ala
            340                 345                 350


Cys Thr Gly Thr Gly Thr Cys Thr Ala Gly Cys
        355                 360


<210>  412
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  412
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatggga agaaataccg tcaactggta ccggcacctc      120

ccagggacgg cccccgaact cctcatctat gataatgatg agcgtccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaagatg agggtcatta ttactgtgct gcgtgggatg acagcctgaa tggtccggtg      300

ttcggcggag ggaccaagct gaccgtcctg g                                     331


<210>  413
<211>  366
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  413

Cys Ala Gly Gly Thr Thr Cys Ala Ala Thr Thr Ala Gly Thr Gly Cys
1               5                   10                  15


Ala Gly Thr Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Thr
            20                  25                  30
```

```
Gly Ala Ala Ala Ala Ala Gly Cys Cys Cys Gly Gly Cys Thr Cys Ala
        35                  40                  45


Ala Gly Thr Gly Thr Thr Ala Ala Ala Gly Thr Ala Ala Gly Cys Thr
    50                  55                  60


Gly Thr Ala Ala Gly Gly Cys Gly Ala Gly Cys Gly Gly Ala Gly Gly
65                  70                  75                  80


Thr Ala Cys Thr Thr Thr Thr Ala Gly Thr Thr Cys Thr Thr Ala Cys
                85                  90                  95


Gly Cys Cys Ala Thr Thr Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110


Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Thr Gly Gly Thr Cys Ala
        115                 120                 125


Gly Gly Gly Cys Cys Thr Cys Gly Ala Ala Thr Gly Gly Ala Thr Gly
    130                 135                 140


Gly Gly Cys Gly Gly Cys Ala Thr Thr Ala Gly Cys Cys Cys Thr Ala
145                 150                 155                 160


Thr Gly Thr Thr Cys Gly Gly Thr Ala Cys Thr Gly Cys Ala Ala Ala
                165                 170                 175


Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Ala Ala Ala Thr Thr Thr
            180                 185                 190


Cys Ala Gly Gly Gly Thr Ala Gly Ala Gly Thr Cys Ala Cys Ala Ala
        195                 200                 205


Thr Thr Ala Cys Cys Gly Cys Ala Gly Ala Cys Ala Ala Ala Ala Gly
    210                 215                 220


Thr Ala Cys Cys Ala Gly Cys Ala Cys Thr Gly Cys Cys Thr Ala Cys
225                 230                 235                 240
```

Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Gly Thr Ala Gly Cys Cys
245 250 255

Thr Gly Cys Gly Thr Thr Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
260 265 270

Ala Gly Cys Thr Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr
275 280 285

Gly Cys Gly Cys Gly Cys Gly Ala Gly Gly Gly Thr Gly Gly Thr Thr
290 295 300

Ala Cys Ala Gly Thr Cys Cys Thr Gly Gly Thr Gly Gly Thr Gly Thr
305 310 315 320

Thr Gly Ala Cys Thr Thr Cys Gly Ala Cys Thr Ala Cys Thr Gly Gly
325 330 335

Gly Gly Cys Cys Ala Gly Gly Gly Gly Ala Cys Cys Thr Thr Ala Gly
340 345 350

Thr Cys Ala Cys Thr Gly Thr Gly Thr Cys Thr Ala Gly Cys
355 360 365

<210> 414
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 414
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60

tcctgcaccc gcagcagtgg cagcattgcc agcacctatg tgcagtggta ccggcagcgc 120

ccgggcagtg cccccaccac tgtgatctat gaggatcatc agagaccctc tggggtccct 180

gatcggttct ccggctccct cgacagctcc tccaactctg cctccctcac catctctgga 240

ctgaggactg aggacgcggc aacctactac tgtcagtctt ttgatgccag cactctggtg 300 ttcggcggcg ggaccaagct gaccgtcctc g 331

<210> 415
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 415

Cys Ala Gly Gly Thr Thr Cys Ala Ala Thr Thr Ala Gly Thr Gly Cys
1 5 10 15

Ala Gly Thr Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Thr
20 25 30

Gly Ala Ala Ala Ala Ala Gly Cys Cys Cys Gly Gly Cys Thr Cys Ala
35 40 45

Ala Gly Thr Gly Thr Thr Ala Ala Ala Gly Thr Ala Ala Gly Cys Thr
50 55 60

Gly Thr Ala Ala Gly Gly Cys Gly Ala Gly Cys Gly Gly Thr Gly Thr
65 70 75 80

Thr Ala Cys Thr Thr Thr Thr Ala Gly Thr Thr Cys Thr Thr Ala Cys
85 90 95

Gly Cys Cys Ala Thr Thr Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
100 105 110

Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Thr Gly Gly Thr Cys Ala
115 120 125

Gly Gly Gly Cys Cys Thr Cys Gly Ala Ala Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Cys Gly Gly Cys Ala Thr Cys Ala Gly Cys Cys Cys Ala Ala
145 150 155 160

```
Thr Cys Thr Thr Thr Gly Gly Thr Ala Cys Thr Gly Cys Ala Ala Ala
                165                 170                 175


Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Ala Ala Ala Thr Thr Thr
            180                 185                 190


Cys Ala Gly Gly Gly Thr Ala Gly Ala Gly Thr Cys Ala Cys Ala Ala
        195                 200                 205


Thr Thr Ala Cys Cys Gly Cys Ala Gly Ala Cys Gly Ala Ala Ala Gly
    210                 215                 220


Thr Ala Cys Gly Ala Ala Thr Ala Cys Thr Gly Thr Gly Thr Ala Thr
225                 230                 235                 240


Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Gly Thr Ala Gly Cys Cys
                245                 250                 255


Thr Gly Cys Gly Thr Thr Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
            260                 265                 270


Ala Gly Cys Thr Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr
        275                 280                 285


Gly Cys Gly Cys Gly Cys Gly Gly Thr Ala Cys Ala Ala Cys Ala Thr
    290                 295                 300


Ala Cys Ala Gly Thr Ala Cys Ala Gly Cys Thr Cys Gly Thr Thr Ala
305                 310                 315                 320


Cys Thr Thr Cys Gly Ala Cys Gly Thr Thr Thr Gly Gly Gly Gly Cys
                325                 330                 335


Cys Ala Gly Gly Gly Gly Ala Cys Cys Thr Thr Ala Gly Thr Cys Ala
            340                 345                 350


Cys Thr Gly Thr Gly Thr Cys Thr Ala Gly Cys
        355                 360
```

<210> 416
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 416
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60

tcctgcaccc gcagaagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc 120

ccgggcagtg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct 180

gatcgcttct ctggctccat cgacaggtcc tccaactctg cctccctcac catctctgga 240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgacagcga caatcatgaa 300

gtgatattcg gcggagggac caagctgacc gtcctag 337

<210> 417
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 417
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagt gacttttcgt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcagcggta tctttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgtc aaccgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcct 300

gcttactact tcggtcctaa tatggacgtg tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 418
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 418
cagtctgtgc tgactcagcc accctcagtg tctggggccc cagggcagag ggtcaccatc   60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcaa   120

cttccaggaa cagtccccaa actcatcatc tatgataata gcaatcggcc ctcaggggtc   180

cctgcccgat tctctggctc caagtctggc acctcagcct ccctggccat cagtgggctc   240

cagtctgagg atgaggccgc atattattgc cagtcgtatg acagcagcct gagtgttgtg   300

gtattcggcg gtgggaccaa gctgtccgtc ctag   334

<210> 419
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 419
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggagg cacttttagt tcttacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc atcagcccta tgtttggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtacgag cactgcctac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtagt   300

cgttacgctc ctagtgacag tacaaatttt gatcaatggg gccaggggac cttagtcact   360

gtgtctagc   369

<210> 420
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 420
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc   60

tcctgcaccg gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc   120

ccgggcagtg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct   180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga   240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgataccag caatcggaag   300

gttttcggcg gagggaccaa gctgaccgtc ctag   334

<210> 421
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 421
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg cccatttagt tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attagcggta tctttggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgtc aaccgcatat   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgac   300

cgtttctacg ttggtgagcg tttcgatgtg tggggccagg ggaccttagt cactgtgtct   360

agc   363

<210> 422
<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 422
cagtctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccagaatt   60

acctgtgggg gaaatgacat tggaagtaaa agtgtccact ggtaccagca gaagccaggc   120

caggcccctg tgctggtcgt ctatgatgat atcgaccggc cctcagggat ccctgagcga   180

ttctctggct ccaactatgg ggacacggcc accctgacca tcagctgggt cgaggccggg   240

```
gatgaggccg actattactg tcaggtgtgg gatactaata gtgatcccgt ctttgtcttc      300

ggaagtggga ccaaggtcac cgtccttg                                         328


<210>  423
<211>  375
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  423

Cys Ala Gly Gly Thr Thr Cys Ala Ala Thr Thr Ala Gly Thr Gly Cys
1               5                   10                  15


Ala Gly Thr Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Thr
            20                  25                  30


Gly Ala Ala Ala Ala Ala Gly Cys Cys Cys Gly Gly Cys Thr Cys Ala
        35                  40                  45


Ala Gly Thr Gly Thr Thr Ala Ala Ala Gly Thr Ala Ala Gly Cys Thr
    50                  55                  60


Gly Thr Ala Ala Gly Gly Cys Gly Ala Gly Cys Gly Gly Thr Gly Gly
65                  70                  75                  80


Cys Ala Cys Cys Thr Thr Cys Ala Gly Cys Thr Cys Thr Thr Ala Cys
                85                  90                  95


Gly Cys Cys Ala Thr Thr Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110


Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Thr Gly Gly Thr Cys Ala
        115                 120                 125


Gly Gly Gly Cys Cys Thr Cys Gly Ala Ala Thr Gly Gly Ala Thr Gly
    130                 135                 140


Gly Gly Cys Gly Gly Cys Ala Thr Thr Ala Gly Cys Cys Cys Ala Ala
```

145 150 155 160

Thr Cys Thr Thr Cys Gly Gly Thr Ala Cys Thr Gly Cys Ala Ala Ala
165 170 175

Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Ala Ala Ala Thr Thr Thr
180 185 190

Cys Ala Gly Gly Gly Thr Ala Gly Ala Gly Thr Cys Ala Cys Ala Ala
195 200 205

Thr Thr Ala Cys Cys Gly Cys Ala Gly Ala Cys Cys Ala Gly Ala Gly
210 215 220

Cys Ala Cys Gly Ala Gly Cys Ala Cys Thr Gly Cys Cys Thr Ala Cys
225 230 235 240

Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Gly Thr Ala Gly Cys Cys
245 250 255

Thr Gly Cys Gly Thr Thr Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
260 265 270

Ala Gly Cys Thr Gly Thr Gly Thr Ala Thr Thr Ala Cys Thr Gly Thr
275 280 285

Gly Cys Gly Cys Gly Cys Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly
290 295 300

Thr Thr Gly Gly Thr Cys Gly Thr Ala Thr Cys Thr Gly Gly Ala Thr
305 310 315 320

Cys Gly Cys Thr Gly Gly Thr Thr Ala Cys Gly Gly Thr Thr Thr Cys
325 330 335

Gly Ala Thr Cys Ala Gly Thr Gly Gly Gly Gly Cys Cys Ala Gly Gly
340 345 350

Gly Gly Ala Cys Cys Thr Thr Ala Gly Thr Cys Ala Cys Thr Gly Thr

```
        355                 360                 365


Gly Thr Cys Thr Ala Gly Cys
    370                 375


<210>  424
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  424
cagactgtgg tgactcagga gccatcgttc tcagtgtccc ctggagggac agttaccctc        60

acttgtggct tgagctctgg ctcagtctcc actagtaact accccagctg gtaccagcag       120

accccaggcc agcctccacg cacgctcatc tacagcacaa acactcgctc ttctggggtc       180

cctgatcgct tctctggctc catccttggg aacaaagctg ccctcaccat cacgggggcc       240

caggcagatg atgaatctga ttattactgt gtcctatata tgggtagtgg catttcgatg       300

ttcggcggag ggaccaagtt gaccgtccta g                                      331


<210>  425
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  425
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta        60

agctgtaagg cgagcggtgg tacttttagt tcatacgcca ttagctgggt gcgacaggct       120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tctttggtac tgcaaattat       180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagcaccag cactgtgtac       240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcct       300

ggttaccacc ctgctggtgc tagtggtcaa ttctttgatc tttggggcca ggggacctta       360

gtcactgtgt ctagc                                                        375
```

<210> 426
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 426
tcctatgagc tgactcagcc accctcggtg tccaaggact tgagacagac cgccacactc 60

acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac 120

cagggccacc ctcccaaact cctatcctac aggaataacc accggccctc agggatctca 180

gacagatcat ctgcatccag gtcaggagac acagcctccc tgaccattac tggactccag 240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgcttgggtg 300

ttcggcggag ggaccaagct gaccgtccta g 331

<210> 427
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 427
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggtgt gaccttcagc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcaccaa caccgcctat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt 300

ggttacgctc ctgacgctct gacaaatttt gacgtttggg gccaggggac cttagtcact 360

gtgtctagc 369

<210> 428
<211> 346
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 428
gaaattgtgc tgactcagtc tccagactcc ctggctatgt ctctgggcga gagggccacc   60

gtcaactgca agtccagccg gagtcttttc gacagctccg acaataagaa ctacttagct   120

tggtaccaga agaaaccagg acagcctcct caattgctca tttactgggc atctacccga   180

caatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc   240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttttagtagt   300

cctcccatat tcaccttcgg ccctgggacc aaagtggaga tcaaac   346

<210> 429
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 429
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggagt gacttttagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attacccccta tgtttggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagata aaagtacgag caccgtctat   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt   300

ggttacatcg ctgttgctgg tgacatggac gtgtggggcc aggggacctt agtcactgtg   360

tctagc   366

<210> 430
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 430
gacatccaga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc   60

atcaactgca agtccagtcg gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaagcagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

cctccgacgt tcggccaagg gaccaaggtg gaaatcaaac 340

<210> 431
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 431
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agctgtaagg cgagcggtgt taccttcagt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccac tgttcggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagata agagcacgag cactgcctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgac 300

gcttactacg ttggtggtgg tgctcgtcct tttgacctct ggggccaggg gaccttagtc 360

actgtgtcta gc 372

<210> 432
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 432
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tcttgttctg gaggcagctc caacatcgga gttaattatg tatactggta tcaggtggtc 120

ccaggagcgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tggactccag 240

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tctgaggatg aggctgacta ttactgtgga gtatgggatg acagcctgaa tggtcattgg      300

gtgttcggcg gagggaccga cctgaccgtc ctgg                                  334


<210>  433
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  433
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agctgtaagg cgagcggtgg tccatttagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcacgtc aaccgtgtac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggttac      300

agttactacc ctggtggtgg tggtggtcgt aatttcgact actggggcca ggggacctta      360

gtcactgtgt ctagc                                                       375


<210>  434
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  434
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tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgagggtg aggctgatta ttactgtgca gcatgggatg acagcctgaa aggtcgggtg      300

ttcggcggag ggaccaaggt gaccgtccta g                                     331


<210>  435
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<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 435
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agctgtaagg cgagcggagg tccattcagt tcttacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc atcagccctc tgtttggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcacgtc aaccgcctac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgctcct   300

acatactacg ctagtcgtga cagttacaat ttcgattatt ggggccaggg gaccttagtc   360

actgtgtcta gc   372

<210> 436
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 436
gaaacgacac tcacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc   60

ctctcctgca gggccagtca gagtgttgac agaggctact tagcctggta tcagcagaag   120

cctggccagg ctcccaggct cctcatctat ggtgcatccc acagggccgc tggcatccca   180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag   240

cctgaggatt ttgcagtata tttctgtcag cagtatggta gttcacgcct ctctttcggc   300

ggagggacca aggtggagat ccaac   325

<210> 437
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 437
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agctgtaagg cgagcggtgt gactttcagt tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgttcggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagcacgaa tactgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacaca 300

acatacatcg ctggtggtca cttcgacgtt tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 438
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 438
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tcctgcactg gaaccagcag tgacattggt gcttataact atgtctcctg gtaccaacaa 120

cacccagaca aagcccccaa gctcatcatt tatgaggtca gtaagcggcc ctcaggggtc 180

cctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc 240

caggctgagg atgaggctga ttattactgc agctcctatg caggcagcaa caatgtggta 300

ttcggcggag ggaccaagct gaccgtccta g 331

<210> 439
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 439
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agctgtaagg cgagcggtgg taccttcagc tcatacgcca ttagctgggt gcgacaggct 120

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cctggtcagg gcctcgaatg gatgggcggc atcagccctc tgtttggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagtaccaa tactgcctat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgctagt      300

ggttacttca caggttgggg tacattcgac tactggggcc aggggacctt agtcactgtg      360

tctagc                                                                 366


<210>  440
<211>  319
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  440
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acctgctctg gagatgcatt gccaaagcaa tatgcttatt ggtaccagca gaagccaggc      120

caggcccctg tgctggtgat atataaagac agtgagaggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctttg      240

gatgaggctg actattactg tcaggcgtgg gacagcagca ctgctgtctt cggaactggg      300

accaaggtca ccgtcctag                                                   319


<210>  441
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  441
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agctgtaagg cgagcggagg tacttttagt tcttacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcagcccta tctttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagcacgag caccgcctac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt      300
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tactactaca cagttggtgt ttatgacgtt tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 442
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 442
tcctatgagc tgactcagcc accctcggtg tccaagggct tgagacagac cgccaccctc 60

acctgcattg ggacagcga caatgttggc aaccaaggag taggttggct gcagcagcac 120

cagggccacc ctcccaaact cctgtcctac agggataaca cccggccctc aggcatctca 180

gagagattct ctgcatccag gtcaggaaac acagcctccc tgaccattac tggactccag 240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcac tgccgtggtg 300

ttcggcggag ggaccaagct ggccgtccta g 331

<210> 443
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 443
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agctgtaagg cgagcggtgt taccttcagt tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tctttggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagata aaagtacctc aaccgtctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt 300

ggttacagtg ctgacggtgg tgctggtaat aatacaatct tcgacgtttg gggccagggg 360

accttagtca ctgtgtctag c 381

<210> 444

<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 444
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acctgtactg ggaacaacaa caatgttggc aaccaaggag cagcctggct gcagcagcac 120

cagggccacc ctcccaaact cctatccgac aggaataaca accggccctc agggatctca 180

gagagattat ctgcatccag gtcaggaaat acagcctccc tgaccattac tggactccag 240

gctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgcttgggtg 300

ttcggcggag ggaccaagct gaccgtccta a 331

<210> 445
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 445
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agctgtaagg cgagcggagt tacttttagc tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagccctc tgtttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagtacctc aactgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgagcgt 300

ggttacacag ttggtggtgg tggtatggac gtgtggggcc aggggacctt agtcactgtg 360

tctagc 366

<210> 446
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 446
cagtctgccc tgactcagcc tccctccgcg tccgggtctc ctggacagtc agtcaccatc 60

tcctgcactg gaaccagcag tgacgttggt gctcacaact ttgtctcctg gtaccaacaa 120

cacccagaca aagcccccaa actcatcatt tatgaggtca ataggcggcc ctcaggggtc 180

cctgatcgct tctctggctc caagtctggc acctcagcct ccctggccat cagtggtctc 240

cagtctgacg atgaggctga ctattactgt gcagcatggg acgacagtct cgatggtccg 300

gtgttcggcg gagggaccaa gctgaccgtc ctag 334

<210> 447
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 447
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agctgtaagg cgagcggagt tacttttagc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcagcccaa tctttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagcacgaa cactgtgtac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgagtac 300

ctgggtgacg actacagtag tggtagttac ttcgatgtgt ggggccaggg gaccttagtc 360

actgtgtcta gc 372

<210> 448
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 448
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ctctcctgta gggccagtca gagtgttgat agtcacttag cctggtacca acaaaaaggt 120

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc      180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcaatgg cctagagcct      240

gaggattttg caatttattt ctgtcagcag cgcagcatgt ggcccctcac tttcggcgga      300

gggaccaagg tggagatcaa ac                                               322


<210>  449
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  449
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agctgtaagg cgagcggagg tactttcagt tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtacctc aactgcatat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgagagt      300

ggttacagtg gtacaggtca atttgacgtg tggggccagg ggaccttagt cactgtgtct      360

agc                                                                    363


<210>  450
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  450
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tcctgttttg ggagaacctc caacgtcgga cgaaacactg ttaactggta ccaacaattg      120

cccggagcgg cccccaagat cctcattttt aacgataatc aacggccctc gggggtccct      180

gaccgcttct ctggctccaa gtctggcacc gccgcctccc tgaccataag taggctccag      240

tccgcggatg aggctgatta ctattgttca tcatgggatg acgacctgaa cggtccggtc      300
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ttcggcggag ggaccaagct gagcgtcgta g                                    331


<210>  451
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  451
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agctgtaagg cgagcggagg tatctttagt tcttacgcca ttagctgggt gcgacaggct     120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tcttcggtac tgcaaattat     180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa caccgcctat     240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtggt     300

ggttactacg actacggtgt tggttacgac caatggggcc aggggacctt agtcactgtg     360

tctagc                                                                366


<210>  452
<211>  322
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  452
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tcttgttctg gaggcaggtc caacatcgga agtaatactg ttaactggta ccagcagctc     120

ccaggaacgg cccccaaact cctcatctat agtaataatc accggccctc aggggtccct     180

gatcgcttct ctggctccaa gtctggcaac acggcctccc tgaccatctc tgggctccag     240

gcggaggatg aggctgatta ttactgccag tcctatgaca gcagcgttgt attcggcgga     300

gggaccaagc tgaccgtcct ag                                              322


<210>  453
<211>  366
<212>  DNA
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<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 453
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agctgtaagg cgagcggtgg taccttcagc tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attaccccta tctttggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagacg agagtaccag cactgcctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtggt 300

ggttacagtc ctagtatcgg tggtttcgac gtttggggcc aggggacctt agtcactgtg 360

tctagc 366

<210> 454
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 454
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tcttgttctg gaagcaggtc caatatcgga agaaatactg taaactggta ccagcaactc 120

ccaggaacgg cccccaaact cctcatctat agtaacaatc agcggccctc aggggtccct 180

gaccgagtct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

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ttcggaactg ggaccaaggt caccgtccta g 331

<210> 455
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 455

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agctgtaagg cgagcggagg tacctttagt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcagcccaa tctttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatc gcagtacgag caccgcctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcct 300

ggttacgacc ctagtagtct gcgtggtttt gacgtttggg gccaggggac cttagtcact 360

gtgtctagc 369

<210> 456
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 456
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acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac 120

cagggccacc ctcccaaact cctattctac aagaataaca accggccctc agggatttca 180

gagagattat ctgcatccag gtcaggaaac acagcctccc tgaccattac tggactccag 240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgattgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 457
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 457
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agctgtaagg cgagcggtgg cacttttagc tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcattccaa tctttggtac tgcaaattat 180 gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa tactgcctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgag 300

gaggcttact acgacctttg gggccagggg accttagtca ctgtgtctag c 351

<210> 458
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 458
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgct gggccagtca gagtgttagc agcttcttag cctggtacca acacaaacct 120

ggccaggttc ccaggctcct catctatgat gcatccaata gggccactgg catcccagcc 180

aggttctctg gcagtgggtc tgggacacac ttcactctca ctatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag cgtttcaatt ggcctccgac gttcggccaa 300

gggaccaagg tggaaagcaa ac 322

<210> 459
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 459
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agctgtaagg cgagcggagg tacttttagt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcaccccta tgttcggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtacgag caccgcctat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtaca 300

agttacctgc ctggtcgtag tggttttgat gtttggggcc aggggacctt agtcactgtg 360

tctagc 366

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<210>  460
<211>  322
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  460
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acctgctctg cagatgcatt gccaaagcaa tatgcttatt ggtaccagca gaggccaggc       120

caggcccctg tgttgctgat atataaagac actgagaggc ccccagggat ccctgagcga       180

ttctctggct ccagctcagg gacaacagtc acgttgacca tcagtggagt ccaggcagaa       240

gacgaggctg actactattg tcaatcagca gacgctagtg aaaattctgt cttcggaggt       300

gggaccaagg tcaccgtcct ag                                                322


<210>  461
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  461
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agctgtaagg cgagcggtgt tacttttcgt tcatacgcca ttagctgggt gcgacaggct       120

cctggtcagg gcctcgaatg gatgggcggc atcagcgcaa tgtttggtac tgcaaattat       180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagtacgaa caccgcatat       240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt       300

ggttacgacc ctagtgttgg tggttttgat gtgtggggcc aggggacctt agtcactgtg       360

tctagc                                                                  366


<210>  462
<211>  331
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Synthetic Polynucleotide

<400> 462
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtcagcatc   60

tcctgcaccg gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc   120

ccgggcagtg cccccgccac tgtgatctat gaggataacc aaagaccctc tggggtccct   180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga   240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgataccag caatctggta   300

ttcggcgtag ggaccaagct gaccgtccta g   331

<210> 463
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 463
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg tacctttagt tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attattccta tcttcggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagacg atagcacgtc aaccgcatac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacagt   300

acacctagtg ttacaagtag tctgtaccgt atccctgctt ttgatgtgtg gggccagggg   360

accttagtca ctgtgtctag c   381

<210> 464
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 464
ctgcctgtgc tgactcaatc atcctctgcc tctgcttccc tgggatcctc ggtcaagctc   60

acctgcagtc tgaccaatgg gcccagtaac tacatcatcg catggcatca gcagcagcca 120

gagaagggcc ctcggtactt gatgaagctt aacagtgatg gcagccacag caagggggac 180

gggatccctg atcgcttctc aggctccagc tctggggctg agcgctacct caccatctcc 240

aaccttaagt ctgaggatga ggctgattat tactgtgaga cctgggacag taacactcat 300

gtggtattcg gcggagggac caagctgacc gtcctag 337

<210> 465
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 465
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagg tacctttagt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attaccccaa tgtttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagaca agagcacgtc aactacatac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcct 300

ggttactacc ctgacagtaa taattatgat ctctggggcc aggggacctt agtcactgtg 360

tctagc 366

<210> 466
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 466
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagt agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcaa gtagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

```
cctgaagatt ttgcaaccta ctattgtcaa caggttaaca gcttccctcg aacttttggc      300

caggggacca agctggagat gaaac                                            325


<210>  467
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  467
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggtgt gacctttagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tgtttggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagacc agagcacgaa caccgcctat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt      300

acatacagtc ctggtggtac atactttgat gtttggggcc aggggacctt agtcactgtg      360

tctagc                                                                 366


<210>  468
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  468
cagcctgtgc tgactcagcc accctcagcg tctgcgaccc ccggacagac ggtgaccatc       60

tcttgttctg gcagcagttc caacatcggc gtgagctttg tctactggta tcaacaattt      120

ccaggaacgg cccccaagct cctcatttac agggatgata tgaggcagtc aggggtccct      180

gaccgatttt ctggcttcaa gtctggctcc tcagcctccc tgaccatctc tgggctccag      240

tccgaagatg aggccactta ttattgttcc gcgtgggatg agagcctgag tagtgtgttg      300

ttcggcggag ggaccaaggt caccgtccta g                                     331


<210>  469
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<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 469

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 Pro Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln 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 Asp Asp Gly Tyr Ala Pro Ser Gly Gly Leu Arg Glu Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 470
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 470

Asp Ile Gln 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 Arg Ser Val Leu Tyr Ser
            20                  25                  30


Ser Asn Asn Lys Asn Tyr Leu Ala 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 Gln
                85                  90                  95


Tyr Tyr Ser Gly Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110


Lys



<210>  471
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  471

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 Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn 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 Arg Gly Ala Tyr Met Gly Pro Ser Met Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  472
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  472

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45


Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Asp His
```

```
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  473
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  473

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys 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 Gly Ala Arg Tyr Tyr Ala Gly Gly Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  474
<211>  108
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 474

```
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ser Asn Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80


Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
                85                  90                  95


Val Thr Phe Gly Pro Gly Thr Thr Val Asp Ile Lys
            100                 105
```

<210> 475
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 475

```
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 Val Thr Phe Ser Ser Tyr
            20                  25                  30
```

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Asn 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 Asp Ser Gly Asn Tyr Asp Gly Tyr Gly Pro Gly Ser Arg Phe
            100   105   110

Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 476
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 476

Gln Pro Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln

```
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ser Ala Trp Asp Asp Ser Leu
                85                  90                  95


Gly Gly Glu Val Phe Gly Thr Gly Thr Lys Val Asn Val Leu
            100                 105                 110


<210>  477
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Met Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Glu Arg Gly Ser Trp Ser Phe Gly Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 478
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 478

Leu Pro Val Leu Thr Gln Pro Pro Ser Met Ser Ala Ala Pro Gly Gln
1   5   10   15

Thr Ala Arg Ile Thr Cys Gly Gly Asp His Ile Gly Ser Lys Ser Val
            20   25   30

His Trp Tyr Gln Arg Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45

Ser Asp Thr Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65   70   75   80

Asp Glu Ala Asp Tyr Phe Cys Gln Val Trp Asp Ser Ser Asn Asp His
                85   90   95

Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 479
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 479

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys 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 Arg Thr Tyr Ala Asp Gly Arg Thr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  480
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  480

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Leu Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys 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 Arg Thr Tyr Ala Asp Gly Arg Thr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  481
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  481

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Glu Leu Gly Tyr Leu Ala Gly Ser Pro Ser Pro Gly Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  482
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  482

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Ile Ile Tyr Glu Val Thr Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ala Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Gly
                85                  90                  95


Lys Trp Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  483
<211>  121
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Synthetic Polypeptide

<400>  483

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Thr 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 Arg Arg Tyr Trp Ala Asp Gly Gly Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  484
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  484

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Met Gly Arg Asn
```

            20   25   30

Thr Val Asn Trp Tyr Arg His Leu Pro Gly Thr Ala Pro Glu Leu Leu
        35   40   45

Ile Tyr Asp Asn Asp Glu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Gly His Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 485
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 485

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 Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln 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 Glu Gly Gly Tyr Ser Pro Gly Gly Val Asp Phe Asp Tyr Trp
            100   105   110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 486
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 486

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Thr
            20   25   30

Tyr Val Gln Trp Tyr Arg Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35   40   45

Ile Tyr Glu Asp His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Leu Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

Leu Arg Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Phe Asp Ala
                85   90   95

Ser Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 487

<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 487

```
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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Thr Thr Tyr Ser Thr Ala Arg Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 488
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 488

```
Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
```

```
1               5                   10                  15


Thr Val Thr Ile Ser Cys Thr Arg Arg Ser Gly Ser Ile Ala Ser Asn
            20                  25                  30


Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45


Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Ile Asp Arg Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85                  90                  95


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


<210>  489
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  489

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 Val Thr Phe Arg Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Gly Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Pro Ala Tyr Tyr Phe Gly Pro Asn Met Asp Val Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 490
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 490

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Val Pro Lys Leu
        35   40   45

Ile Ile Tyr Asp Asn Ser Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65   70   75   80

Gln Ser Glu Asp Glu Ala Ala Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Val Val Val Phe Gly Gly Gly Thr Lys Leu Ser Val Leu

```
            100                 105                 110


<210>  491
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  491

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Ser Ser Arg Tyr Ala Pro Ser Asp Ser Thr Asn Phe Asp Gln
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  492
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
```

<400> 492

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Thr Gly Ser Ser Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr
85 90 95

Ser Asn Arg Lys Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 493
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 493

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 Pro Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

```
Gly Gly Ile Ser Gly Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Asp Arg Phe Tyr Val Gly Glu Arg Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  494
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  494

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asn Asp Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45


Asp Asp Ile Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Tyr Gly Asp Thr Ala Thr Leu Thr Ile Ser Trp Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Thr Asn Ser Asp Pro
```

```
                85                  90                  95


Val Phe Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  495
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  495

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Gln 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 Gly Val Gly Arg Ile Trp Ile Ala Gly Tyr Gly Phe
            100                 105                 110


Asp Gln Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  496
<211>  110
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 496

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Ser
            20   25   30

Asn Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Pro Pro Arg Thr
        35   40   45

Leu Ile Tyr Ser Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Met Gly Ser
                85   90   95

Gly Ile Ser Met Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 497
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 497

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 Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Pro Gly Tyr His Pro Ala Gly Ala Ser Gly Gln Phe Phe
            100   105   110

Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 498
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 498

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Asp Leu Arg Gln
1   5   10   15

Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20   25   30

Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35   40   45

Ser Tyr Arg Asn Asn His Arg Pro Ser Gly Ile Ser Asp Arg Ser Ser
    50   55   60

Ala Ser Arg Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln

65 70 75 80

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
85 90 95

Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 499
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 499

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 Val Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Arg Gly Tyr Ala Pro Asp Ala Leu Thr Asn Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 500
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 500

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Met Ser Leu Gly
1               5                   10                  15


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


Ser Asp Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Gly Gln
        35                  40                  45


Pro Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln 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 Gln
                85                  90                  95


Tyr Phe Ser Ser Pro Pro Ile Phe Thr Phe Gly Pro Gly Thr Lys Val
            100                 105                 110


Glu Ile Lys
        115
```

<210> 501
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 501

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 Val Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Thr Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys 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 Gly Arg Gly Tyr Ile Ala Val Ala Gly Asp Met Asp Val Trp
            100   105   110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 502
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 502

Asp Ile Gln 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 Arg Ser Val Leu Tyr Ser
            20   25   30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Ala 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 Gln
                85                  90                  95


Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110


Lys



<210>  503
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  503

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln 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 Asp Ala Tyr Tyr Val Gly Gly Gly Ala Arg Pro Phe Asp
            100                 105                 110


Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  504
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  504

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Glu Thr Pro Gly Gln
1               5                   10                  15


Asn Val Ile Ile Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Val Asn
            20                  25                  30


Tyr Val Tyr Trp Tyr Gln Val Val Pro Gly Ala Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly His Trp Val Phe Gly Gly Gly Thr Asp Leu Thr Val Leu
            100                 105                 110


<210>  505
```

```
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  505

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 Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Tyr Ser Tyr Tyr Pro Gly Gly Gly Gly Gly Arg Asn Phe
            100                 105                 110


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  506
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  506

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
```

1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Gly Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Lys Gly Arg Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 507
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 507

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 Pro Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Ala Pro Thr Tyr Tyr Ala Ser Arg Asp Ser Tyr Asn Phe Asp
            100   105   110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 508
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 508

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asp Arg Gly
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser His Arg Ala Ala 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 Phe Cys Gln Gln Tyr Gly Ser Ser Arg
                85   90   95

Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Gln

```
            100                 105


<210>  509
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  509

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn 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 Asp Thr Thr Tyr Ile Ala Gly Gly His Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  510
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
```

```
<400>  510

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly Ala Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Asp Lys Ala Pro Lys Leu
        35                  40                  45


Ile Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
                85                  90                  95


Asn Asn Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  511
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  511

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Gly Ile Ser Pro Leu Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Ala Ser Gly Tyr Phe Thr Gly Trp Gly Thr Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  512
<211>  106
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  512

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
            20                  25                  30


Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Lys Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Leu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
```

                85   90   95

Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105

<210> 513
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 513

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 Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln 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 Arg Tyr Tyr Tyr Thr Val Gly Val Tyr Asp Val Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 514
<211> 110
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 514

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1   5   10   15

Thr Ala Thr Leu Thr Cys Ile Gly Asp Ser Asp Asn Val Gly Asn Gln
            20   25   30

Gly Val Gly Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35   40   45

Ser Tyr Arg Asp Asn Thr Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
    50   55   60

Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65   70   75   80

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85   90   95

Thr Ala Val Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu
            100   105   110

<210> 515
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 515

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 Val Thr Phe Ser Ser Tyr
            20   25   30

```
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys 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 Gly Gly Gly Tyr Ser Ala Asp Gly Gly Ala Gly Asn Asn Thr
            100                 105                 110


Ile Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  516
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  516

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Asn Asn Asn Val Gly Asn Gln
            20                  25                  30


Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Asp Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
```

```
65                  70                  75                  80


Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85                  90                  95


Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  517
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  517

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Glu Arg Gly Tyr Thr Val Gly Gly Gly Gly Met Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

```
<210>  518
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  518

Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ala His
            20                  25                  30


Asn Phe Val Ser Trp Tyr Gln Gln His Pro Asp Lys Ala Pro Lys Leu
        35                  40                  45


Ile Ile Tyr Glu Val Asn Arg Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80


Gln Ser Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
                85                  90                  95


Leu Asp Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  519
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  519

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


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


Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  520
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  520

Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Asp Ser His
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Gly Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Thr 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 Asn Gly Leu Glu Pro
65   70   75   80

Glu Asp Phe Ala Ile Tyr Phe Cys Gln Gln Arg Ser Met Trp Pro Leu
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 521
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 521

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 Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln 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 Glu Ser Gly Tyr Ser Gly Thr Gly Gln Phe Asp Val Trp Gly
            100   105   110

```
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  522
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  522

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Ala Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Phe Gly Arg Thr Ser Asn Val Gly Arg Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Lys Ile Leu
        35                  40                  45


Ile Phe Asn Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Thr Ile Ser Arg Leu Gln
65                  70                  75                  80


Ser Ala Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Trp Asp Asp Asp Leu
                85                  90                  95


Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Ser Val Val
            100                 105                 110


<210>  523
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  523
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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 Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Gly Tyr Tyr Asp Tyr Gly Val Gly Tyr Asp Gln Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  524
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  524

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Gly Arg Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
```

```
        35                  40                  45


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


Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln
65                  70                  75                  80


Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Val
                85                  90                  95


Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  525
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  525

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Gly Tyr Ser Pro Ser Ile Gly Gly Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  526
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  526

Gln Pro Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Arg Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Val Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Val Ser Leu
                85                  90                  95


Asn Gly Gln Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  527
<211>  123
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  Synthetic Polypeptide

<400>  527

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Arg 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 Pro Gly Tyr Asp Pro Ser Ser Leu Arg Gly Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  528
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  528

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Asp Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
```

```
            20                  25                  30


Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Phe Tyr Lys Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85                  90                  95


Ser Asp Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  529
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  529

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Glu Glu Ala Tyr Tyr Asp Leu Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  530
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  530

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Trp Ala Ser Gln Ser Val Ser Ser Phe
            20                  25                  30


Leu Ala Trp Tyr Gln His Lys Pro Gly Gln Val 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 His 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 Phe Asn Trp Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ser Lys
            100                 105


<210>  531
```

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

<220>
<223>  Synthetic Polypeptide

<400>  531

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Thr Ser Tyr Leu Pro Gly Arg Ser Gly Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  532
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  532

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
```

```
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Ser Ala Asp Ala Leu Pro Lys Gln Tyr Ala
            20                  25                  30


Tyr Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Leu Ile Tyr
        35                  40                  45


Lys Asp Thr Glu Arg Pro Pro Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ala Ser Glu Asn Ser
                85                  90                  95


Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  533
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  533

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 Val Thr Phe Arg Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Ala Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn 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 Arg Gly Tyr Asp Pro Ser Val Gly Gly Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  534
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  534

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15


Thr Val Ser Ile Ser Cys Thr Gly Ser Ser Gly Ser Ile Ala Ser Asn
            20                  25                  30


Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Ala Thr Val
        35                  40                  45


Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr
                85                  90                  95


Ser Asn Leu Val Phe Gly Val Gly Thr Lys Leu Thr Val Leu
```

            100   105   110

<210> 535
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 535

```
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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Asp 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 Asp Ser Thr Pro Ser Val Thr Ser Ser Leu Tyr Arg Ile Pro
            100                 105                 110


Ala Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 536
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

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<400>  536

Leu Pro Val Leu Thr Gln Ser Ser Ser Ala Ser Ala Ser Leu Gly Ser
1               5                   10                  15


Ser Val Lys Leu Thr Cys Ser Leu Thr Asn Gly Pro Ser Asn Tyr Ile
            20                  25                  30


Ile Ala Trp His Gln Gln Gln Pro Glu Lys Gly Pro Arg Tyr Leu Met
        35                  40                  45


Lys Leu Asn Ser Asp Gly Ser His Ser Lys Gly Asp Gly Ile Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65                  70                  75                  80


Asn Leu Lys Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp
                85                  90                  95


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


<210>  537
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  537

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Gly Ile Thr Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Thr 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 Pro Gly Tyr Tyr Pro Asp Ser Asn Asn Tyr Asp Leu Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  538
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  538

Glu Thr Thr Leu Thr Gln Ser Pro Gly 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 Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys 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 Thr Tyr Tyr Cys Gln Gln Val Asn Ser Phe Pro
```

```
                85                  90                  95


Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Met Lys
            100                 105


<210>  539
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  539

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Asn 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 Thr Tyr Ser Pro Gly Gly Thr Tyr Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  540
<211>  110
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 540

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Ala Thr Pro Gly Gln
1   5   10   15

Thr Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Val Ser
            20   25   30

Phe Val Tyr Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Arg Asp Asp Met Arg Gln Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Phe Lys Ser Gly Ser Ser Ala Ser Leu Thr Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Thr Tyr Tyr Cys Ser Ala Trp Asp Glu Ser Leu
                85   90   95

Ser Ser Val Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 541
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 541
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggagg tacttttagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attatcacaa tctttggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtacctc aaccgcatac   240

```
atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgct      300

acaggtttct acgacgtttg gggccagggg accttagtca ctgtgtctag c               351


<210>  542
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  542
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtccggta      300

ttcggcggag ggaccaagct gaccgtccta g                                     331


<210>  543
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  543
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagt tactttcagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tcttcggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcacgtc aactgcatac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt      300

gagtactacg ctagtaatgg tgacagtttc gatgtttggg gccaggggac cttagtcact      360

gtgtctagc                                                              369


<210>  544
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<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 544
cagcctgtgc tgactcagcc accctcggtg tcagtggccc caggaaagac ggccagcatt   60

tcctgtgagg gaaacaacat tgcgactaaa agtgtgcact ggtaccagca gaagtcaggc   120

cacgcccctg tggtggtcgt ctatcatgat agcgaccggc cctcaggggt ccctgaccga   180

ttctctggct ccaagtctgg cacctcagcc tccctggcca tcagtgggct ccggtccgag   240

gatgaggctg attattactg tgcagcatgg gatgacagcc tgagtggtcc ttgggtgttc   300

ggcggaggga ccaagctgac cgtcctag   328

<210> 545
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 545
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggagg tacctttagt tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attagcgcaa tcttcggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgcg caccgcatac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtagt   300

ggttactacg ttgctgctag tggtgctttc gacgtgtggg gccaggggac cttagtcact   360

gtgtctagc   369

<210> 546
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 546
cagcctgggc tgactcagcc accctcggtg tcaaagggct tgagacagac cgccacactc 60

acctgcactg ggaacatcaa caatgttggc gaccaaggag caggttggct gcagcagcac 120

cagggccgcc ctcccaaact cctgtcgtac aggaatagca accggccctc aggtgtctca 180

gagagattct ctgcatccag gtcaggaaat acagcctccc tgaccattac tggactccag 240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgattgggtg 300

ttcggcggag ggaccaagct gaccgtccta g 331

<210> 547
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 547
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggtgg catcttcagc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcaccccaa tcttcggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagcacgcg taccgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacctg 300

agtcgtgaca gtctgaatct gcctggtagt agtcctggtt acgatctctg gggccagggg 360

accttagtca ctgtgtctag c 381

<210> 548
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 548
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccaggaga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtgtatta ctgtcagcag tatagtagtt ctccctacac ttttggccag 300

gggaccaaac tggagatcaa ac 322

<210> 549
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 549
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagt gattttcagc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tcttcggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgtc aaccgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcgt 300

ggttacgctc ctggtacaag tttccactac gatgtgtggg gccaggggac cttagtcact 360

gtgtctagc 369

<210> 550
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 550
ctgcctgtgc tgactcaggc accctcaatg tcagtggccc caggaaagac ggccagtatt 60

acctgtgggg gagacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat gtattatgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240

gatgaggccg actatttctg ccagctgtgg gatcatacta attctcatgt ggtcttcggc 300 ggaaggacca aactgaccgt cctag 325

<210> 551
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 551
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggtgg cacctttagt tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tctttggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt acctcagatg agagtaccag cactgcatac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgaccaa 300

ggtggtacac gtggtaatta cttcgacgtt tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 552
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 552
cagcctgtgc tgactcagcc accctcggtg tccaagggct tgagacagac cgccacagtc 60

acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac 120

cagggccacc ctcccaaact cctatcctac aggaataaca accggccctc agggatttca 180

gagagattat ctgcatccag gtcaggaaac acagcctccc tgaccattgc tggactccag 240

cctgaggacg aggctgacta ttactgctca gcatgggaca acaccgtcag tggttgggtg 300

ttcggcggag ggaccagggt gaccgtccta g 331

<210> 553
<211> 351
<212> DNA

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<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  553
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta        60

agctgtaagg cgagcggtgg tactttcagt tcatacgcca ttagctgggt gcgacaggct       120

cctggtcagg gcctcgaatg gatgggcggc attatcacaa tcttcggtac tgcaaattat       180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa caccgcctac       240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt       300

ggtggtcgtt ttgacgtttg gggccagggg accttagtca ctgtgtctag c                351


<210>  554
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  554
tcctatgagc tgactcagcc accctcagtg tctgggaccc ccgggcagag ggtcaccatc        60

tcttgttctg gaagcacctc caacatcgga aataatgctc taaactggta ccagaaactc       120

ccagggacgg cccccaaact cctcatctat agtcttaatc agcgtccctc aggggtccct       180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag       240

tctgaggatg aggctgatta ttactgtgaa gcatgggatg acagcctgag tggtccggtg       300

ttcggcggag ggaccaaggt gaccgtccta g                                      331


<210>  555
<211>  351
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  555
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta        60
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agctgtaagg cgagcggagg tccatttcgc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attatcccaa tcttcggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagtacgtc aactgcatac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt 300

gtttacagtt ttgatgtgtg gggccagggg accttagtca ctgtgtctag c 351

<210> 556
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 556
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tcttgttctg gaagcggctc caacgtcgga agtaatgttg taaattggta ccagcatctc 120

ccaggaacgg cccccaaact cctcatctat cgtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttattgtgca gcatgggatg acagactgaa tggctttgtc 300

tttggtactg ggacgaaggt caccgtcctg a 331

<210> 557
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 557
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggtgt tcctttcagt tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcagcccac tgtttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagacc agagcacgtc aaccgtctac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtctg 300

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ggtacataca gtcctagtct gtaccctcgt ggtatggacg tttggggcca ggggacctta      360

gtcactgtgt ctagc                                                       375


<210>  558
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  558
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccggacagag tgtcaccatc       60

tcttgttctg gaagcagctc caacatcggc agaaatgatg ttaactggta ccagcaattc      120

ccgggaaggg cccccaaact cctcatctat ggtcgtgatg agcggccctt cggggtccct      180

gcccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgct gcatgggatg ccagtctgat gatctatgtc      300

ttcggaactg ggaccacggt caccgtcctg g                                     331


<210>  559
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  559
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagt gacctttagt tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcagcccta tgttcggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagtacgaa tactgtctat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt      300

gcttacctga gtgttcgtgg tagtttcgac gtgtggggcc aggggacctt agtcactgtg      360

tctagc                                                                 366


<210>  560
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<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 560
tcctatgagc tgactcagcc accctcagtg tctgggaccc ccgggcagag ggtcaccatc   60

tcttgttctg gaagcagctc caacatcgga agtaacactg taaactggta ccagcagctc   120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct   180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag   240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggttatgtc   300

ttcggaactg ggaccaaggt caccgtccta g   331

<210> 561
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 561
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgt gattttcagt tcttacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc atcatcccaa tctttggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagata aaagtacgtc aactgcctat   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt   300

agtggtagtt tcgacgtttg gggccagggg accttagtca ctgtgtctag c   351

<210> 562
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 562

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cagcctgggc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagttc caacctcgga agtaattatg tcttctggta ccagcacctc      120

ccaggagcgg cccccaaact cctcatctat agaaatagtc agcggccctc tggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtgtggta      300

ttcggcggag ggaccaagct gaccgtccta g                                     331


<210>  563
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  563
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagt gactttcagc tcttacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcagccctg tgtttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg atagtacgaa taccgcctac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcgt      300

ggttacacag ttagtagtct ggctggtcgt tacttcgacc agtggggcca ggggacctta      360

gtcactgtgt ctagc                                                       375


<210>  564
<211>  325
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  564
gaaacgacac tcacgcagtc tccaggcacc ctgtccttgt ctccagggga aagagcctcc       60

ctctcctgca aggccagtga gagtctttgc agcacttgct tggcctggta ccagcagaaa      120

cctggccagg ctcccaggct catcgtctat ggtgcaacca gcagggccac tggcatccca      180
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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctca gacgttcggc 300

caagggacca aggtggaaat caaac 325

<210> 565
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 565
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagg cacttttagc tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcgtgccac tgtttggcac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagtaccag cactgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtctg 300

ggtctgtact ttgacgtgtg gggccagggg accttagtca ctgtgtctag c 351

<210> 566
<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 566
cagactgtgg tgactcagga gccctcactg actgtgtccc caggagagac agtcactctc 60

acctgtgctt ccagcactgg agcagtcacc agtggttact atccaaactg gttccagcag 120

aaacctggac aagcacccag ggcactgatt tatagtacaa gcaacaaaca ctcctggacc 180

cctgcccggt tctcaggctc cctccttggg ggcaaagctg ccctgacact gtcaggtgtg 240

cagcctgagg acgaggctga gtattattgt ctgctctact atggtggtcc ttgggtgttc 300

ggcggaggga ccaagttgac cgtcctgg 328

<210> 567

<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 567
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg tactttcagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attatcccaa tcttcggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagcacgaa caccgcctac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgttcgt   300

ggtggttacg gtccttacgg tgactttgac gtttggggcc aggggacctt agtcactgtg   360

tctagc   366

<210> 568
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 568
cagcctgggc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc   60

tcttgttctg gaagcagctc caacatcgga agtcattctg tgaactggta ccggcagctc   120

ccaggaacgg ccccccaact cctcatctat ggtaacagca atcggccctc aggggtccct   180

gaccgattct ctggctccaa gtctggcacc tcagcgtccc tggccatcag tgggctccag   240

tctgaggatg aggctgatta tttctgtgcg gcatgggatg acggcctgag tggttgggtg   300

ttcggcggag ggaccaaatt gaccgtccta g   331

<210> 569
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 569
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg ccccttttagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tcttcggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagata agagtacgaa caccgcatac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt   300

agttacatcg ttagtgttag tcctggtttt gacgtgtggg gccaggggac cttagtcact   360

gtgtctagc   369

<210> 570
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 570
cagtctgtgc tgactcagcc accctccgcg tccgggtctc ctggacagtc agtcaccatc   60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag   120

tacccaggca aagcccccaa actcatgatt tatgaggtca gtaagcggcc ctcaggggtc   180

cctgatcgtt tctctggctc caagtctggc acctcagcct ccctggccat cagtgagctc   240

caatctgagg atgaggctga ttattactgt gcatcatggg atgacagcct gaatgcttat   300

gtcttcggaa gtgggaccaa ggtcaccgtc ctgg   334

<210> 571
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 571
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggagg cattttcagt tcatacgcca ttagctgggt gcgacaggct   120

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cctggtcagg gcctcgaatg gatgggcggc atcagcgcaa tctttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagtaccag caccgcatat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgacagt      300

ggtatcgcta gtggttacac agcttacatg gattattggg gccaggggac cttagtcact      360

gtgtctagc                                                              369


<210>  572
<211>  325
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  572
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc       60

acatgccaag gagacagcct cagaacctct tacgcaagct ggtaccagca gaagccaggc      120

cagtcccctg tactggtcat ctatcaaagt actaagcggc cctcagggat ccctgagcga      180

ttctctgcct ccagctcagg aaacacagct tccctgacca tcactggggc tcaggcggaa      240

gatgaggctg actattactg taactcccgg ggcagcgggg gtaaccccta tgtcttcgga      300

actgggacca aggtcaccgt ccttg                                            325


<210>  573
<211>  351
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  573
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggtgg cattttccgt tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attatcccaa tgttcggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagtacgac tactgtctat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgct      300
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ggtagtacat ttgatgtgtg gggccagggg accttagtca ctgtgtctag c             351


<210>  574
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  574
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120

ccaggaacgg cccccagact cctcatctat agtaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtcgggtg      300

ttcggcggag ggaccaagct gaccgtccta g                                     331


<210>  575
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  575
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggtgg taccttcagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attaacccta tctttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa tactgcctac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgag      300

agtgcttact acagtcgtaa ttacgatgtg tggggccagg ggaccttagt cactgtgtct      360

agc                                                                    363


<210>  576
<211>  331
<212>  DNA
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<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 576
tcctatgagc tgactcagcc accctcggtg tccaagggct tgagacagac cgccacactc   60

acctgcactg ggaacagcag caatgttggc aaccaaggag catcttggct gcagcagcac   120

cagggccacc ctcccaaact cctatcctac aggaatgaca accggccctc agggatctca   180

gagagattct ctgcatccag gtcaggaaat acagcctccc tgaccattac tggactccag   240

cctgaggacg aggctgacta ttactgctca gcatgggaca acagcctcag tgcttgggtg   300

ttcggtggag ggaccaagct gaccgtccta g   331

<210> 577
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 577
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgt gacttttagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc atcagcccaa tgttcggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa taccgcatat   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt   300

ggttactacc ctgctggtgt tggtcgttat gatgtttggg gccaggggac cttagtcact   360

gtgtctagc   369

<210> 578
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 578

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gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc        60

atcaactgca agtccagcca gaatgtttta tacagctcca acaataagaa taacttagct       120

tggtaccaac aaagaccagg acagcctcct aaagtgctcc tttattgggc atctacccgg       180

gcatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc       240

atcaacagcc ttcaggctga agatgtggca ctttattact gtcaacaata ttatggtaaa       300

cccttcactt tcggccctgg gaccaaagtg gagatcaaac                             340


<210>  579
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  579
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta        60

agctgtaagg cgagcggagg tacctttagc tcatacgcca ttagctgggt gcgacaggct       120

cctggtcagg gcctcgaatg gatgggcggc attacccctc tgttcggcac tgcaaattat       180

gcccagaaat ttcagggtag agtcacaatt accgcagacg atagtacgtc aactgcatat       240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcct       300

acactgtaca gtcctcctgt ttttgatgtg tggggccagg ggaccttagt cactgtgtct       360

agc                                                                     363


<210>  580
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  580
cagactgtgg tgactcagga gccatcgttc tcagtgtccc ctggagggac aatcaccctc        60

acttgtggct tgagttctgg ctcagtctct actactaatt atcccagctg gtaccagcag       120

accccaggcc gaactccacg cacgctcatc tacaacacaa acactcgctc ttctggggtc       180
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cctgatcgct tctctggctc catccttggg aacaaagctg ccctcaccat cacgggggcc      240

caggcaggtg atgaatctga ttattactgt gttttatata tgggtcgtgg catttatgtc      300

ttcggaagtg ggaccaaggt ctccgtcctg g                                     331


<210>  581
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  581
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagg cacttttcgc tcttacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcatgccaa tctttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagacg agagtacgac aaccgtgtac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtgct      300

ggtgttagtg ctggtcctag ttggcctttt gacgtttggg gccaggggac cttagtcact      360

gtgtctagc                                                              369


<210>  582
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  582
cagcctgggc tgactcagcc accctcggtg tccaaggact tgaggcagac cgccacactc       60

acctgcactg ggaacagcaa caatgttggc aaacaaggag ctacttggct gcagcagcac      120

cagggccacc ctcccaaact cctatcctac aggaataaca accggccctc agggatctca      180

gagagattct ctgcatccag gtcaggagac acagcctccc tgaccattac tggcctccag      240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgtatgggtg      300

ttcggcggag ggaccaagct gaccgtccta g                                     331
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<210> 583
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 583
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg taccttcagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgtc aaccgtgtac   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcgt   300

ggttacaatg ttgctgctag tttcggtttc gatgtgtggg gccaggggac cttagtcact   360

gtgtctagc   369

<210> 584
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 584
gaaattgtgt tgacgcagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc gggccagtca gtacattgat cgtagcttac actggtacca gcagaaacca   120

gatcagtctc caaagctcct catcaagtat gcttctcagt ccatctcagg ggtcccctcg   180

aggttcagtg gcagtggatc tgggacagat ttcagcctca ccatcaatag cctggaaact   240

gaagatgctg caacctatta ctgccatcag accagtagtt tgccgtggac attcggccaa   300

gggaccacgg tggaaatcaa ac   322

<210> 585
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 585
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

agctgtaagg cgagcggtgg cccatttagc tcatacgcca ttagctgggt gcgacaggct   120

cctggtcagg gcctcgaatg gatgggcggc atcatcccta tcttcggcac tgcaaattat   180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagtacgtc aaccgcctat   240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtaca   300

gactacagtg gttaccgtgg ttttgacgtt tggggccagg ggaccttagt cactgtgtct   360

agc   363

<210> 586
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 586
cagactgtgg tgactcagga gccatcgttc tcagtgtccc ctggagggac agtcacactc   60

acctgtgctt tgagttctgg ctcagtctcc agttttaact acgccagctg gtaccagcag   120

accccaggcc aggcgccacg cacactcatc tccaacacaa acactcgctc ttctggggtc   180

cctgatcgct tctctggctc catccttggg aacaaagcta ccctcaccat cacgggggcc   240

caggcagatg atgaatctca ttattactgt gcactgtatg tgggtggtgg catttccgtg   300

ttcggcggag ggaccaagtt gaccgtccta g   331

<210> 587
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 587
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta   60

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agctgtaagg cgagcggtgt tacttttagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc atcaccccaa tctttggcac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatc agagtacgag cactgcatac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtggt      300

ggtgttttcg acgtttgggg ccaggggacc ttagtcactg tgtctagc                   348


<210>  588
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  588
tcctatgagc tgactcagcc accctcggtg tctggagccc cccgacagag ggtcaccatc       60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc      120

ccaggaaagg ctcccaaact cctcatctat tatgatgata tgctgccctc aggggtctct      180

gaccgattct ctggctccaa gtctggctcc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgacta ttattgtgca gcatgggatg acagcctgag cggtccggtt      300

ttcggcggag ggaccaacct gaccgtccta g                                     331


<210>  589
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  589
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggagg tacttttagt tcttacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgttcggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagaca aaagtaccag cactgcctac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcgagggt      300
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ggttacagtc ctggtggtgt tgacttcgac tactggggcc aggggacctt agtcactgtg 360

tctagc 366

<210> 590
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 590
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60

tcctgcaccc gcagcagtgg cagcattgcc agcacctatg tgcagtggta ccggcagcgc 120

ccgggcagtg cccccaccac tgtgatctat gaggatcatc agagaccctc tggggtccct 180

gatcggttct ccggctccct cgacagctcc tccaactctg cctccctcac catctctgga 240

ctgaggactg aggacgcggc aacctactac tgtcagtctt ttgatgccag cactctggtg 300

ttcggcggcg ggaccaagct gaccgtcctc g 331

<210> 591
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 591
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagt gacttttcgt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc atcagcggta tctttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgtc aaccgcatat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtcct 300

gcttactact tcggtcctaa tatggacgtg tggggccagg ggaccttagt cactgtgtct 360

agc 363

<210> 592

<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 592
cagtctgtgc tgactcagcc accctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcaa 120

cttccaggaa cagtccccaa actcatcatc tatgataata gcaatcggcc ctcaggggtc 180

cctgcccgat tctctggctc caagtctggc acctcagcct ccctggccat cagtgggctc 240

cagtctgagg atgaggccgc atattattgc cagtcgtatg acagcagcct gagtgttgtg 300

gtattcggcg gtgggaccaa gctgtccgtc ctag 334

<210> 593
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 593
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggtgg tacttttagt tcatacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tctttggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagacg aaagcaccag cactgtgtac 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcct 300

ggttaccacc ctgctggtgc tagtggtcaa ttctttgatc tttggggcca ggggacctta 360

gtcactgtgt ctagc 375

<210> 594
<211> 331
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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<400>  594
tcctatgagc tgactcagcc accctcggtg tccaaggact tgagacagac cgccacactc       60

acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac      120

cagggccacc ctcccaaact cctatcctac aggaataacc accggccctc agggatctca      180

gacagatcat ctgcatccag gtcaggagac acagcctccc tgaccattac tggactccag      240

cctgaggacg aggctgacta ttactgctca gcatgggaca gcagcctcag tgcttgggtg      300

ttcggcggag ggaccaagct gaccgtccta g                                     331


<210>  595
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  595
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggtgt gaccttcagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcaccaa caccgcctat      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggtcgt      300

ggttacgctc ctgacgctct gacaaatttt gacgtttggg gccaggggac cttagtcact      360

gtgtctagc                                                              369


<210>  596
<211>  346
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  596
gaaattgtgc tgactcagtc tccagactcc ctggctatgt ctctgggcga gagggccacc       60

gtcaactgca agtccagccg gagtcttttc gacagctccg acaataagaa ctacttagct      120
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tggtaccaga agaaaccagg acagcctcct caattgctca tttactgggc atctacccga      180

caatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttttagtagt      300

cctcccatat tcaccttcgg ccctgggacc aaagtggaga tcaaac                     346


<210>  597
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  597
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta       60

agctgtaagg cgagcggtgg tccatttagc tcatacgcca ttagctgggt gcgacaggct      120

cctggtcagg gcctcgaatg gatgggcggc attagcccta tgtttggtac tgcaaattat      180

gcccagaaat ttcagggtag agtcacaatt accgcagatg aaagcacgtc aaccgtgtac      240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcggttac      300

agttactacc ctggtggtgg tggtggtcgt aatttcgact actggggcca ggggacctta      360

gtcactgtgt ctagc                                                       375


<210>  598
<211>  331
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  598
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgagggtg aggctgatta ttactgtgca gcatgggatg acagcctgaa aggtcgggtg      300
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ttcggcggag ggaccaaggt gaccgtccta g 331

<210> 599
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 599
caggttcaat tagtgcagtc tggtgctgaa gtgaaaaagc ccggctcaag tgttaaagta 60

agctgtaagg cgagcggagg tatctttagt tcttacgcca ttagctgggt gcgacaggct 120

cctggtcagg gcctcgaatg gatgggcggc attagcccaa tcttcggtac tgcaaattat 180

gcccagaaat ttcagggtag agtcacaatt accgcagatg agagcacgaa caccgcctat 240

atggaactga gtagcctgcg ttccgaagat acagctgtgt attactgtgc gcgcagtggt 300

ggttactacg actacggtgt tggttacgac caatggggcc aggggacctt agtcactgtg 360

tctagc 366

<210> 600
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 600
cagcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaggcaggtc caacatcgga agtaatactg ttaactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc accggccctc aggggtccct 180

gatcgcttct ctggctccaa gtctggcaac acggcctccc tgaccatctc tgggctccag 240

gcggaggatg aggctgatta ttactgccag tcctatgaca gcagcgttgt attcggcgga 300

gggaccaagc tgaccgtcct ag 322

<210> 601
<211> 117
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  601

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Thr Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Ala Thr Gly Phe Tyr Asp Val Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  602
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  602

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  603
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  603

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Arg Glu Tyr Tyr Ala Ser Asn Gly Asp Ser Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  604
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  604

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1               5                   10                  15


Thr Ala Ser Ile Ser Cys Glu Gly Asn Asn Ile Ala Thr Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Ser Gly His Ala Pro Val Val Val Val Tyr
        35                  40                  45


His Asp Ser Asp Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


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


Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Ser Gly
                85                  90                  95


Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

```
<210>  605
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  605

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Ala Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Arg 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 Ser Gly Tyr Tyr Val Ala Ala Ser Gly Ala Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  606
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  606
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Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ile Asn Asn Val Gly Asp Gln
            20                  25                  30


Gly Ala Gly Trp Leu Gln Gln His Gln Gly Arg Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Ser Asn Arg Pro Ser Gly Val Ser Glu Arg Phe Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85                  90                  95


Ser Asp Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  607
<211>  127
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  607

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 Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Arg 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 Asp Leu Ser Arg Asp Ser Leu Asn Leu Pro Gly Ser Ser Pro
            100                 105                 110


Gly Tyr Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  608
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  608

Glu Thr Thr Leu Thr Gln Ser Pro Gly 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 Asn
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Ser Ser Pro Tyr
                85                  90                  95
```

```
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  609
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  609

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 Val Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Arg Gly Tyr Ala Pro Gly Thr Ser Phe His Tyr Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  610
<211>  108
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Synthetic Polypeptide

<400>  610

Leu Pro Val Leu Thr Gln Ala Pro Ser Met Ser Val Ala Pro Gly Lys
1               5                   10                  15


Thr Ala Ser Ile Thr Cys Gly Gly Asp Asn Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Met Tyr
        35                  40                  45


Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Phe Cys Gln Leu Trp Asp His Thr Asn Ser His
                85                  90                  95


Val Val Phe Gly Gly Arg Thr Lys Leu Thr Val Leu
            100                 105


<210>  611
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  611

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

```
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ser Asp Glu 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 Asp Gln Gly Gly Thr Arg Gly Asn Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  612
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  612

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Val Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20                  25                  30


Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Ala Gly Leu Gln
65                  70                  75                  80
```

```
Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asn Thr Val
                85                  90                  95


Ser Gly Trp Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
            100                 105                 110


<210>  613
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  613

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Thr Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Gly Arg Phe Asp Val Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  614
```

<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 614

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20   25   30

Ala Leu Asn Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Ser Leu Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Ala Trp Asp Asp Ser Leu
                85   90   95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 615
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 615

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 Pro Phe Arg Ser Tyr

```
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Val Tyr Ser Phe Asp Val Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  616
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  616

Gln Ser Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Gly Ser Asn Val Gly Ser Asn
            20                  25                  30


Val Val Asn Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
```

```
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Arg Leu
                85                  90                  95


Asn Gly Phe Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  617
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  617

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 Val Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Ile Thr Ala Asp Gln 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 Gly Leu Gly Thr Tyr Ser Pro Ser Leu Tyr Pro Arg Gly Met
            100                 105                 110


Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
```

```
        115                 120                 125


<210>  618
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  618

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Arg Asn
            20                  25                  30


Asp Val Asn Trp Tyr Gln Gln Phe Pro Gly Arg Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Gly Arg Asp Glu Arg Pro Phe Gly Val Pro Ala Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Ala Ser Leu
                85                  90                  95


Met Ile Tyr Val Phe Gly Thr Gly Thr Thr Val Thr Val Leu
            100                 105                 110


<210>  619
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  619

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Arg Ala Tyr Leu Ser Val Arg Gly Ser Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  620
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  620

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45
```

```
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  621
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  621

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 Val Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Ser Gly Ser Phe Asp Val Trp Gly Gln Gly Thr Leu
```

```
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  622
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  622

Gln Pro Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Leu Gly Ser Asn
            20                  25                  30


Tyr Val Phe Trp Tyr Gln His Leu Pro Gly Ala Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Arg Asn Ser Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  623
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
```

```
<400>  623

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Asn 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 Arg Gly Tyr Thr Val Ser Ser Leu Ala Gly Arg Tyr Phe
            100                 105                 110


Asp Gln Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  624
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  624

Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Ser Leu Ser Cys Lys Ala Ser Glu Ser Leu Cys Ser Thr
            20                  25                  30
```

Cys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Ile
35 40 45

Val Tyr Gly Ala Thr 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 Gly Ser Ser Pro
85 90 95

Gln Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 625
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 625

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 Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Leu Gly Leu Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  626
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  626

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Glu
1               5                   10                  15


Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
            20                  25                  30


Tyr Tyr Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala
        35                  40                  45


Leu Ile Tyr Ser Thr Ser Asn Lys His Ser Trp Thr Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65                  70                  75                  80


Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly
                85                  90                  95


Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  627
<211>  122
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 627

```
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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Val Arg Gly Gly Tyr Gly Pro Tyr Gly Asp Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 628
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 628

```
Gln Pro Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser His
            20                  25                  30


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


Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ala Ala Trp Asp Asp Gly Leu
                85                  90                  95


Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  629
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  629

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 Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn 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 Arg Ser Tyr Ile Val Ser Val Ser Pro Gly Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 630
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 630

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Glu Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Ser
85 90 95

Leu Asn Ala Tyr Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu
100 105 110

```
<210>  631
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  631

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 Ile Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Ala Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Asp Ser Gly Ile Ala Ser Gly Tyr Thr Ala Tyr Met Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  632
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  632
```

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Thr Ser Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45


Gln Ser Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Ala Ser
    50                  55                  60


Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Gly Ser Gly Gly Asn Pro
                85                  90                  95


Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  633
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  633

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 Ile Phe Arg Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr 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 Gly Ala Gly Ser Thr Phe Asp Val Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  634
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  634

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95
```

```
Asn Gly Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  635
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  635

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Asn Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Glu Ser Ala Tyr Tyr Ser Arg Asn Tyr Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  636
<211>  110
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Synthetic Polypeptide

<400>  636

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Ser Asn Val Gly Asn Gln
            20                  25                  30


Gly Ala Ser Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Asp Asn Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asn Ser Leu
                85                  90                  95


Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  637
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  637

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

```
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Tyr Tyr Pro Ala Gly Val Gly Arg Tyr Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  638
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  638

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 Asn Val Leu Tyr Ser
            20                  25                  30


Ser Asn Asn Lys Asn Asn Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
        35                  40                  45


Pro Pro Lys Val Leu Leu Tyr Trp Ala Ser Thr Arg Ala 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 Asn Ser Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
                85                  90                  95


Tyr Tyr Gly Lys Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110


Lys



<210>  639
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  639

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Leu Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Asp 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 Pro Thr Leu Tyr Ser Pro Pro Val Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
```

```
        115                 120


<210>  640
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  640

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Ile Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Thr
            20                  25                  30


Asn Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Arg Thr Pro Arg Thr
        35                  40                  45


Leu Ile Tyr Asn Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Gly Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Met Gly Arg
                85                  90                  95


Gly Ile Tyr Val Phe Gly Ser Gly Thr Lys Val Ser Val Leu
            100                 105                 110


<210>  641
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  641

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 Thr Phe Arg Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Met Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr 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 Gly Ala Gly Val Ser Ala Gly Pro Ser Trp Pro Phe Asp Val
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 642
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 642

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Asp Leu Arg Gln
1   5   10   15

Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Lys Gln
            20   25   30

Gly Ala Thr Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35   40   45

```
Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85                  90                  95


Ser Val Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  643
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  643

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Arg Gly Tyr Asn Val Ala Ala Ser Phe Gly Phe Asp Val
```

```
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120



<210>  644
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  644

Glu Ile Val Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Tyr Ile Asp Arg Ser
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Thr
65                  70                  75                  80


Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Thr Ser Ser Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys
            100                 105


<210>  645
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
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<400>  645

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 Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Thr Asp Tyr Ser Gly Tyr Arg Gly Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  646
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  646

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Ala Leu Ser Ser Gly Ser Val Ser Ser Phe
            20                  25                  30
```

```
Asn Tyr Ala Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr
        35                  40                  45


Leu Ile Ser Asn Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Ile Leu Gly Asn Lys Ala Thr Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Asp Asp Glu Ser His Tyr Tyr Cys Ala Leu Tyr Val Gly Gly
                85                  90                  95


Gly Ile Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  647
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  647

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Gln 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 Gly Val Phe Asp Val Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  648
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  648

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


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30


Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Tyr Asp Asp Met Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Ser Gly Pro Val Phe Gly Gly Gly Thr Asn Leu Thr Val Leu
            100                 105                 110


<210>  649
<211>  122
<212>  PRT
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<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  649

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Glu Gly Gly Tyr Ser Pro Gly Gly Val Asp Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  650
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  650

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15
```

```
Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Thr
            20                  25                  30


Tyr Val Gln Trp Tyr Arg Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45


Ile Tyr Glu Asp His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Leu Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Arg Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Phe Asp Ala
                85                  90                  95


Ser Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  651
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  651

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 Val Thr Phe Arg Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Gly Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Pro Ala Tyr Tyr Phe Gly Pro Asn Met Asp Val Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 652
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 652

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Val Pro Lys Leu
        35   40   45

Ile Ile Tyr Asp Asn Ser Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65   70   75   80

Gln Ser Glu Asp Glu Ala Ala Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Val Val Val Phe Gly Gly Gly Thr Lys Leu Ser Val Leu
            100   105   110

```
<210>  653
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  653

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Pro Gly Tyr His Pro Ala Gly Ala Ser Gly Gln Phe Phe
            100                 105                 110


Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  654
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  654
```

```
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Asp Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20                  25                  30


Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Asn His Arg Pro Ser Gly Ile Ser Asp Arg Ser Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
                85                  90                  95


Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  655
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  655

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 Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Arg Gly Tyr Ala Pro Asp Ala Leu Thr Asn Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  656
<211>  115
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  656

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


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


Ser Asp Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Gly Gln
        35                  40                  45


Pro Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln 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 Gln
                85                  90                  95
```

```
Tyr Phe Ser Ser Pro Pro Ile Phe Thr Phe Gly Pro Gly Thr Lys Val
            100                 105                 110


Glu Ile Lys
        115


<210>  657
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  657

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 Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Tyr Ser Tyr Tyr Pro Gly Gly Gly Gly Gly Arg Asn Phe
            100                 105                 110


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  658
```

```
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  658

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Gly Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Lys Gly Arg Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  659
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  659

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 Ile Phe Ser Ser Tyr
```

```
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Gly Tyr Tyr Asp Tyr Gly Val Gly Tyr Asp Gln Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  660
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  660

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Gly Arg Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60
```

```
Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln
65                  70                  75                  80


Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Val
                85                  90                  95


Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  661
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide


<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (8)..(8)
<223>  Xaa can be any naturally occurring amino acid

<400>  661

Cys Ala Arg Xaa Xaa Gly Tyr Xaa Pro
1               5


<210>  662
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide


<220>
<221>  misc_feature
<222>  (4)..(6)
<223>  Xaa can be any naturally occurring amino acid
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```
<400>  662

Cys Ala Arg Xaa Xaa Xaa Tyr Tyr
1               5


<210>  663
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  663
tggacaaggg cttgagtgga t                                                 21


<210>  664
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  664
ccctggaact tctgtgcgta gt                                                22


<210>  665
<211>  18
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  665

Cys Cys Thr Ala Thr Cys Cys Thr Thr Gly Gly Thr Ala Thr Ala Gly
1               5                   10                  15


Cys Ala



<210>  666
<211>  21
<212>  DNA
<213>  Artificial Sequence
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<220>
<223>  Synthetic Oligonucleotide

<400>  666
tggacaaggg cttgagtgga t                                                 21


<210>  667
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  667
ccctggaact tctgtgcgta gt                                                22


<210>  668
<211>  18
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  668
ccctatcttt ggtacagc                                                     18


<210>  669
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  669

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1               5                   10


<210>  670
<211>  20
<212>  PRT
<213>  Artificial Sequence

<220>
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```
<223>  Synthetic Polypeptide

<400>  670

Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
1               5                   10                  15


Thr Val Ser Ser
            20


<210>  671
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  671

Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1               5                   10


<210>  672
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  672

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1               5                   10                  15


<210>  673
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  673

Ile Ile Pro Ile Phe Gly Thr Ala
1               5
```

```
<210>  674
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  674

Ile Ser Pro Ile Phe Gly Thr Ala
1               5


<210>  675
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  675

Ile Ile Pro Met Phe Gly Thr Ala
1               5


<210>  676
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  676

Ile Ile Pro Ile Phe Arg Thr Ala
1               5


<210>  677
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide
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<400>  677
caggtgcagc tggtgcagtc tgggggaggc gtggtccaac ctgggaggtc cctgagactc       60

tcctgtgtag cctctgagtt caccttcaat acttatggca tgcactgggt ccgccaggct      120

ccaggcaagg gactggagtg ggtggcagct atttcatatg atggaactaa gaaattttat      180

gcagactccc tgaagggccg attcaccatc tccagagaca attccaagaa cacgttgtat      240

ctccaaatga acagcctgag atctgaggac acggccgtgt attactgtgc gagaagtggt      300

gactccgatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ctca            354


<210>  678
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  678

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Phe Thr Phe Asn Thr Tyr
            20                  25                  30


Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Gly Asp Ser Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110
```

Met Val Thr Val Ser Ser
        115

<210> 679
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 679
tcctatgagc tgactcagcc accctcagtg tccgtgtccc caggacagac agccaccatc   60

acctgctctg gagatgaatt gggggataaa tttgctttct ggtatcaaca aaagccaggc   120

cagtcccctg tgctggtcat ctatcaagat agtaagaggc cctcagggat ccctgagcga   180

ttctctggct ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctctg   240

gatgaggctg actattactg tcaggcgtgg gacagcaaca gttatgtctt cggaactggg   300

accaaggtca ccgtcctagg t   321

<210> 680
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 680

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1   5   10   15

Thr Ala Thr Ile Thr Cys Ser Gly Asp Glu Leu Gly Asp Lys Phe Ala
            20   25   30

Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35   40   45

Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Leu
65   70   75   80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Asn Ser Tyr Val
                85   90   95

Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105

<210> 681
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 681
gaggtgcagc tggtgcagtc tggggctgag gtgaaggagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttctggggg caccttcggc agttatgcta tcaactgggt gcgacaggcc   120

cctggacaaa ggcttgagtg gatgggatgg atcgacgctg ccaatggtaa cacaaaatat   180

tcacagaagt tccagggcag agtcaccatt accggagaca catccgcgag cacagcctac   240

atggaactga gcagcctgag atctgaagac acggctgtgt attactgtgc gagagatagg   300

tggatgacta cgcgggcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca   360

<210> 682
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 682

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Glu Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Ser Tyr
            20   25   30

```
Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Ala Ala Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Gly Asp Thr 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 Asp Arg Trp Met Thr Thr Arg Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110


Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  683
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  683
cagcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga agtaattatg ttttctggta ccagcagctc      120

ccagggatgg cccccaaact cctcatctct aggaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggccccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgcg tggtcccgtg      300

ttcggcggag ggaccagggt gaccgtccta ggt                                   333


<210>  684
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Synthetic polypeptide

<400> 684

```
Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Tyr Val Phe Trp Tyr Gln Gln Leu Pro Gly Met Ala Pro Lys Leu Leu
        35                  40                  45


Ile Ser Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Pro Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Arg Gly Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
            100                 105                 110
```

<210> 685
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial polynucleotide

<400> 685

```
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cgtctggagg cactttcagc agctatgcag tcagctgggt gcgacaggcc      120

cctggacaag gtcttgagtg ggtgggaagg ataatcccta tttttggtaa ggcaaactac      180

gcacagaagt tccagggcag agtcacgata accgcggaca aatccacgag cacagcctat      240

atggaactga gcagcctgag acctgaagac acggccgtat attactgtgc gagagatcag      300

gggatttcgg ccaatttcaa agatgctttt gatatctggg gccaagggac cacggtcacc      360
```

gtctcctca   369

<210> 686
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 686

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 Thr Phe Ser Ser Tyr
            20   25   30

Ala Val Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35   40   45

Gly Arg Ile Ile Pro Ile Phe Gly Lys Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln 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 Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

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

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 687
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

```
<223>  Synthetic polynucleotide

<400>  687
gaaacgacac tcacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc       60

ctctcctgca gggccagtga gagtgttggc agcaacttag cctggtacca gcagaaacct      120

ggccaggctc ccagcctcct catctatggt gcatccacca gggccactgg tatcccagac      180

agattcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct      240

gaagattttg cagcttatta ttgtcagcag tataataact ggccactcac cttcggccct      300

gggaccaaag tggaaatcaa a                                                321


<210>  688
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  688

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


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Gly Ser Asn
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ser Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80


Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
                85                  90                  95


Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 689
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 689

```
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc        60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac       180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac       240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagggtagga       300

tattgtagta gtaccagctg tcacatcggc gcttttgata tctggggcca agggaccacg       360

gtcaccgtct cctca                                                        375
```

<210> 690
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 690

```
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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln 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 Val Gly Tyr Cys Ser Ser Thr Ser Cys His Ile Gly Ala Phe
            100                 105                 110


Asp Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  691
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  691
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca gggccagtca gagtgttagc agcagcatag cctggtatca gcagaaacct      120

gggcaggctc ccaggctcct catgtttgat tcatccacca gggccactgg tatcccagac      180

aggttcagtg gcagtgggtc tgggacagac ttcactctca acatcagcag cctagagcct      240

gaagattttg cagtgtatta ctgtcagcag tatagtagct caccttacac ttttggccag      300

gggaccaaac tggagatcaa a                                                321


<210>  692
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  692

Glu Thr Thr Leu Thr Gln Ser Pro Gly 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 Ser
            20                  25                  30


Ile Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met
        35                  40                  45


Phe Asp Ser Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Ser Ser Leu Glu Pro
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Ser Ser Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  693
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  693
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagcctca      300

tattgtagta ctaccagctg cgctagtggt gcttttgata tctggggcca aggcaccctg      360

gtcaccgtct cctca                                                       375


<210>  694
<211>  125
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Synthetic polypeptide

<400> 694

```
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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Ala Ser Tyr Cys Ser Thr Thr Ser Cys Ala Ser Gly Ala Phe
            100                 105                 110


Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 695
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 695

```
gacatccaga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc       60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct      120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctgcccgg      180
```

```
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240

atcagcagcc tgcagcctga agatgtggca atttattact gtcagcaata ttatagtgtt      300

ccattcactt tcggccctgg gaccaaagtg gagatcaaa                             339


<210>  696
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  696

Asp Ile Gln 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 Val Leu Tyr Ser
            20                  25                  30


Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala 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 Pro Glu Asp Val Ala Ile Tyr Tyr Cys Gln Gln
                85                  90                  95


Tyr Tyr Ser Val Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110


Lys



<210>  697
<211>  363
```

```
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  697
gaggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtt        60

tcctgcaagg cttctggata caccttcaat gtatatgcta tcaactgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac       180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac       240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagattac       300

tatggttcgg gagctagggg ctttgactac tggggccagg gcaccctggt caccgtctcc       360

tca                                                                     363


<210>  698
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  698

Glu 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 Asn Val Tyr
            20                  25                  30


Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Asp Tyr Tyr Gly Ser Gly Ala Arg Gly Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  699
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  699
cagcctgggc tgactcagcc accctcggtg tccaagggct tgagacagac cgccacactc       60

acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac      120

cagggccacc ctcccaaact cctatcctac acgaataaca accggccctc agggatctca      180

gagagattat ctgcatccag gtcaggaaac acagcctccc tggccattac tggactccag      240

cctgaggacg aggcagacta ttactgtgca tcatgggaca gcagcctcag tgtttgggtg      300

atcggcggag ggaccaagtt gaccgtccta ggt                                   333


<210>  700
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide

<400>  700

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20                  25                  30
```

```
Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Thr Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Ser Ser Leu
                85                  90                  95


Ser Val Trp Val Ile Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  701
<211>  378
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  701
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtat agcaaactac      180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagctctaat      300

tactatggtt cagggagtta ttatccgcga agtgcttttg atatctgggg ccaagggacc      360

acggtcaccg tctcctca                                                    378


<210>  702
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic polypeptide
```

```
<400>  702

Glu 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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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 Ser Ser Asn Tyr Tyr Gly Ser Gly Ser Tyr Tyr Pro Arg Ser Ala
            100                 105                 110


Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  703
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic polynucleotide

<400>  703
gaaacgacac tcacgcagtc tccagccacc ctgtctgtgt ctccagggga aagggccatc       60

ctctcctgca gggccagtca gagtataagc aatgacttag cctggtacca gcagaaacct      120

ggccaggctc ccaggctcct catctatggt gcatccagca gggccactgg catcccagac      180

aggttcagtg gcagtgggtc tgggacggac ttcaccttca ccatcagcag actggagtct      240

gaagattttg cagtgtatta ctgtcagcag tatggtgttt cacctctcac tttcggcggg      300
```

gggaccaagg tggagatcaa a   321

<210> 704
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 704

```
Glu Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asp
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Arg Leu Glu Ser
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Val Ser Pro Leu
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 705
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 705

Glu Phe Thr Phe Asn Thr Tyr Gly
1   5

<210> 706
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 706

Ile Ser Tyr Asp Gly Thr Lys Lys
1   5

<210> 707
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 707

Ala Arg Ser Gly Asp Ser Asp Ala Phe Asp Ile
1   5   10

<210> 708
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 708

Gly Gly Thr Phe Gly Ser Tyr Ala
1   5

<210> 709
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

```
<223>  Synthetic oligopeptide

<400>  709

Ile Asp Ala Ala Asn Gly Asn Thr
1               5


<210>  710
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  710

Ala Arg Asp Arg Trp Met Thr Thr Arg Ala Phe Asp Ile
1               5                   10


<210>  711
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  711

Gly Gly Thr Phe Ser Ser Tyr Ala
1               5


<210>  712
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  712

Ile Ile Pro Ile Phe Gly Lys Ala
1               5


<210>  713
<211>  16
```

```
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  713

Ala Arg Asp Gln Gly Ile Ser Ala Asn Phe Lys Asp Ala Phe Asp Ile
1               5                   10                  15


<210>  714
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  714

Gly Gly Thr Phe Ser Ser Tyr Ala
1               5


<210>  715
<211>  18
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  715

Ala Arg Val Gly Tyr Cys Ser Ser Thr Ser Cys His Ile Gly Ala Phe
1               5                   10                  15


Asp Ile



<210>  716
<211>  18
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide
```

```
<400>  716

Ala Arg Ala Ser Tyr Cys Ser Thr Thr Ser Cys Ala Ser Gly Ala Phe
1               5                   10                  15


Asp Ile




<210>  717
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  717

Gly Tyr Thr Phe Asn Val Tyr Ala
1               5


<210>  718
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  718

Ile Ile Pro Ile Leu Gly Ile Ala
1               5


<210>  719
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  719

Ala Arg Asp Tyr Tyr Gly Ser Gly Ala Arg Gly Phe Asp Tyr
1               5                   10
```

```
<210>  720
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  720

Ile Ile Pro Ile Phe Gly Ile Ala
1               5


<210>  721
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  721

Ala Ser Ser Asn Tyr Tyr Gly Ser Gly Ser Tyr Tyr Pro Arg Ser Ala
1               5                   10                  15


Phe Asp Ile



<210>  722
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  722

Glu Leu Gly Asp Lys Phe
1               5


<210>  723
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Synthetic oligopeptide

<400> 723

Gln Asp Ser
1

<210> 724
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 724

Gln Ala Trp Asp Ser Asn Ser Tyr Val
1   5

<210> 725
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 725

Ser Ser Asn Ile Gly Ser Asn Tyr
1   5

<210> 726
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 726

Arg Asn Asn
1

<210> 727
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 727

```
Ala Ala Trp Asp Asp Ser Leu Arg Gly Pro Val
1               5                   10
```

<210> 728
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 728

```
Glu Ser Val Gly Ser Asn
1               5
```

<210> 729
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 729

```
Gly Ala Ser
1
```

<210> 730
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 730

```
Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1               5
```

```
<210>  731
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  731

Gln Ser Val Ser Ser Ser
1               5


<210>  732
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  732

Asp Ser Ser
1


<210>  733
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  733

Gln Gln Tyr Ser Ser Ser Pro Tyr Thr
1               5


<210>  734
<211>  1255
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  734

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
```

```
1               5                   10                  15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20                  25                  30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35                  40                  45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50                  55                  60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65                  70                  75                  80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
                85                  90                  95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100                 105                 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
        115                 120                 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
    130                 135                 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145                 150                 155                 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
                165                 170                 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180                 185                 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
        195                 200                 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
```

```
    210                 215                 220


Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225                 230                 235                 240


Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
                245                 250                 255


Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
            260                 265                 270


Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
        275                 280                 285


Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
    290                 295                 300


Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305                 310                 315                 320


Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
                325                 330                 335


Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
            340                 345                 350


Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
        355                 360                 365


Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
    370                 375                 380


Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385                 390                 395                 400


Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
                405                 410                 415


Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
```

```
            420                 425                 430


Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
        435                 440                 445


Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
    450                 455                 460


Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465                 470                 475                 480


Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
                485                 490                 495


Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
            500                 505                 510


Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
        515                 520                 525


Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
    530                 535                 540


Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545                 550                 555                 560


Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565                 570                 575


Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
            580                 585                 590


Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
        595                 600                 605


Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
    610                 615                 620


Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
```

```
625                 630                 635                 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
                645                 650                 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
            660                 665                 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
        675                 680                 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690                 695                 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705                 710                 715                 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725                 730                 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740                 745                 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
        755                 760                 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
    770                 775                 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785                 790                 795                 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
                805                 810                 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820                 825                 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
```

```
        835                 840                 845


Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
    850                 855                 860


Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865                 870                 875                 880


Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
                885                 890                 895


Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900                 905                 910


Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
        915                 920                 925


Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
    930                 935                 940


Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945                 950                 955                 960


Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                965                 970                 975


Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
            980                 985                 990


Gln Leu Ile Arg Ala Ala Glu Ile  Arg Ala Ser Ala Asn  Leu Ala Ala
        995                 1000                1005


Thr Lys  Met Ser Glu Cys Val  Leu Gly Gln Ser Lys  Arg Val Asp
    1010                1015                1020


Phe Cys  Gly Lys Gly Tyr His  Leu Met Ser Phe Pro  Gln Ala Ala
    1025                1030                1035


Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro Ser Gln
```

1040 1045 1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
1055 1060 1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
1070 1075 1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
1085 1090 1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
1100 1105 1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
1115 1120 1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
1130 1135 1140

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
1145 1150 1155

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
1160 1165 1170

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
1175 1180 1185

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
1190 1195 1200

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
1205 1210 1215

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
1220 1225 1230

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys

```
    1235                1240                1245


Gly Val  Lys Leu His Tyr Thr
    1250                1255


<210>  735
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  735

Ile Ile Pro Ile Phe Gly Thr Ala
1               5


<210>  736
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  736

Ser Asn Asn Val Gly Asn Gln Gly
1               5


<210>  737
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  737

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1               5                   10


<210>  738
<211>  3
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 738

Trp Ala Ser
1

<210> 739
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 739

Gln Gln Tyr Tyr Ser Val Pro Phe Thr
1   5

<210> 740
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 740

Gln Ser Ile Ser Asn Asp
1   5

<210> 741
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 741

Gln Gln Tyr Gly Val Ser Pro Leu Thr
1   5

```
<210>  742
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  742

Thr Asn Asn
1


<210>  743
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  743

Ala Ser Trp Asp Ser Ser Leu Ser Val Trp Val
1               5                   10


<210>  744
<211>  96
<212>  PRT
<213>  Homo sapiens

<400>  744

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln 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


<210>  745
<211>  96
<212>  PRT
<213>  Homo sapiens

<400>  745

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln 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


<210>  746
<211>  96
<212>  PRT
<213>  Homo sapiens

<400>  746

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 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 Asn 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


<210>  747
<211>  96
<212>  PRT
<213>  Homo sapiens

<400>  747

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


Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr 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


<210>  748
<211>  87
<212>  PRT
```

```
<213>  Homo sapiens

<400>  748

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15


Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
            20                  25                  30


Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45


Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys
                85


<210>  749
<211>  89
<212>  PRT
<213>  Homo sapiens

<400>  749

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
```

```
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
                85


<210>  750
<211>  88
<212>  PRT
<213>  Homo sapiens

<400>  750

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 Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys
                85


<210>  751
<211>  94
<212>  PRT
<213>  Homo sapiens

<400>  751

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 Val Leu Tyr Ser
            20                  25                  30
```

```
Ser Asn Asn Lys Asn Tyr Leu Ala 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
                85                  90


<210>  752
<211>  89
<212>  PRT
<213>  Homo sapiens

<400>  752

Glu Ile Val Leu Thr Gln Ser Pro Gly 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 Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys 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
                85


<210>  753
<211>  89
<212>  PRT
<213>  Homo sapiens
```

```
<400>  753

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


Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20                  25                  30


Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
                85


<210>  754
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  754

Ala Ala Ala Leu Asp Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  755
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  755

Pro Ala Val Leu Asp Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  756
<211>  12
<212>  PRT
```

```
<213>  Middle East Respiratory Syndrome coronavirus

<400>  756

Ala Ser Ala Leu Asp Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  757
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  757

Ala Val Ala Leu Asp Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  758
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  758

Ala Ala Ala Phe Asp Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  759
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  759

Ala Ala Ala Leu Gly Thr Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  760
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  760

Ala Ala Ala Leu Asp Thr Ala Tyr Arg Pro Asn Ile
1               5                   10
```

```
<210>  761
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  761

Ala Ala Ala Leu Asp Thr Val Tyr Arg Pro Ile Ile
1               5                   10


<210>  762
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  762

Ala Ala Ala Leu Asp Thr Val Tyr Arg Ser Asn Ile
1               5                   10


<210>  763
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  763

Ala Ala Ala Leu Asp Thr Val Tyr Gly Pro Asn Ile
1               5                   10


<210>  764
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  764

Ala Ala Ala Leu Asp Thr Val Tyr Ser Pro Asn Thr
1               5                   10


<210>  765
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus
```

```
<400>  765

Ala Ala Ala Leu Asp Thr Val Tyr Thr Pro Asn Ile
1               5                   10


<210>  766
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  766

Ala Ala Ala Leu Asp Thr Val Tyr Lys Pro Asn Ile
1               5                   10


<210>  767
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  767

Ala Ala Ala Phe Asp Ala Val Tyr Arg Pro Asn Ile
1               5                   10


<210>  768
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  768

Ala Ala Ala Leu Asp Thr Val Tyr Lys Pro Asn Ile
1               5                   10


<210>  769
<211>  12
<212>  PRT
<213>  Middle East Respiratory Syndrome coronavirus

<400>  769

Ala Ala Ala Phe Asp Thr Val Cys Arg Pro Asn Ile
1               5                   10


<210>  770
<211>  12
```

<212> PRT
<213> Middle East Respiratory Syndrome coronavirus

<400> 770

Ala Ala Ala Leu Asp Thr Val His Arg Pro Asn Ile
1   5   10

<210> 771
<211> 112
<212> PRT
<213> Homo sapiens

<400> 771

Gln Val Gln Leu Val Gln 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 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 Lys Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly 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

Arg Asp Gly Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100   105   110

<210> 772
<211> 121
<212> PRT
<213> Homo sapiens

<400> 772

Glu 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 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 Asn 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 Val Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Arg Asp Leu Val Ala Ala Ala Gly Thr Ala Phe Asp Ile Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  773
<211>  120
<212>  PRT
<213>  Homo sapiens

<400>  773

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Asp Ser Val Ser Ser Asn
            20                  25                  30


Phe Val Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35                  40                  45


Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Arg Trp Tyr Asn Asp Tyr Ala
    50                  55                  60
```

```
Val Ser Val Gln Ser Arg Ile Arg Val Thr Pro Asp Thr Ser Lys Asn
65                  70                  75                  80


Gln Phe Ser Leu His Leu Asp Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95


Tyr Tyr Cys Ala Arg Gly Gln His Ser Gly Phe Asp Phe Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  774
<211>  126
<212>  PRT
<213>  Homo sapiens

<400>  774

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


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


Gln 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 Asp Thr Pro Gly Ile Ala Ala Arg Arg Tyr Tyr Tyr Tyr Gly
            100                 105                 110
```

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 775
<211> 121
<212> PRT
<213> Homo sapiens

<400> 775

Gln Val Gln Leu Val Gln 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 Ser Tyr
            20   25   30

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45

Thr Val Ile Ser Ser Asp Gly Arg Asn Lys Tyr Tyr Pro Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Gly Tyr His Asp Phe Trp Ser Gly Pro Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 776
<211> 127
<212> PRT
<213> Homo sapiens

<400> 776

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

```
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr 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 Asp Gln Val Ser Gly Ile Thr Ile Phe Gly Gly Lys Trp Arg
            100                 105                 110


Ser Pro Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  777
<211>  126
<212>  PRT
<213>  Homo sapiens

<400>  777

Gln Val Thr Leu Lys 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 Thr Asn Tyr
            20                  25                  30


Gly Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Ser His Asp Gly Thr Lys Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Glu Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Ser Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Gly Tyr Cys Ser Gly Gly Arg Cys Tyr Ser Tyr Gly
            100                 105                 110


Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  778
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  778

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Leu Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr
            20                  25                  30


Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Thr Val Thr Thr Asp Gly Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110
```

```
Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  779
<211>  89
<212>  PRT
<213>  Homo sapiens

<400>  779

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Pro Gly Gln Thr Val
1               5                   10                  15


Thr Ile Ser Cys Gly Ser Gly Val Ser Trp Tyr Gln Gln Pro Gly Ala
            20                  25                  30


Pro Lys Leu Leu Ile Tyr Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe
        35                  40                  45


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu
    50                  55                  60


Gln Ala Glu Asp Ala Glu Glu Tyr Tyr Cys Ser Trp Asp Val Phe Gly
65                  70                  75                  80


Gly Gly Thr Lys Leu Thr Val Leu Gly
                85


<210>  780
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  780

Gln Pro Val Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Thr Ile Ser Asp Val Gly Gly His
            20                  25                  30


Asn Phe Val Ser Trp Tyr Gln Gln Asn Pro Gly Lys Ala Pro Lys Leu
```

35 40 45

Ile Ile Phe Glu Val Thr Lys Arg Pro Ala Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Gly Glu Tyr Tyr Cys Ser Ser Tyr Gly Gly Ser
85 90 95

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

<210> 781
<211> 111
<212> PRT
<213> Homo sapiens

<400> 781

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1 5 10 15

Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
20 25 30

Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
35 40 45

Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
50 55 60

Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65 70 75 80

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asn Arg Leu
85 90 95

Lys Thr Tyr Val Phe Gly Thr Gly Gly Lys Val Thr Val Leu Gly
100 105 110

```
<210>  782
<211>  109
<212>  PRT
<213>  Homo sapiens

<400>  782

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Lys Phe Phe Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Ser Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Arg Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Gly Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Arg Asp Asn His
                85                  90                  95


Gln Val Phe Gly Ala Gly Thr Lys Val Thr Val Leu Ser
            100                 105


<210>  783
<211>  108
<212>  PRT
<213>  Homo sapiens

<400>  783

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 Arg Ala Ser Gln Ser Val Asn Thr Asn
            20                  25                  30
```

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Ser Ser Pro Leu
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210>  784
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  784

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Lys Ser His Asn Thr Ala Tyr Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Phe Cys Asn Ser Arg Ser Gly Ser Gln Arg Val
                85                  90                  95


Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
```

```
            100                 105


<210>  785
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  785

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80


Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Phe Asp Ser Ser Leu
                85                  90                  95


Thr Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  786
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  786

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Gly Asn
            20                  25                  30
```

```
Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Asn Leu
                85                  90                  95


Ser Gly His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100                 105                 110


<210>  787
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  787

Ser Tyr Gly Met His
1               5


<210>  788
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  788

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  789
<211>  12
<212>  PRT
<213>  Homo sapiens
```

```
<400>  789

Asp Leu Val Ala Ala Ala Gly Thr Ala Phe Asp Ile
1               5                   10


<210>  790
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  790

Thr Gly Thr Ile Ser Asp Val Gly Gly His Asn Phe Val Ser
1               5                   10


<210>  791
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  791

Glu Val Thr Lys Arg Pro Ala
1               5


<210>  792
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  792

Ser Ser Tyr Gly Gly Ser Asn Asp Val Ile
1               5                   10


<210>  793
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  793

Ser Asn Phe Val Ala Trp Asn
1               5


<210>  794
<211>  18
```

```
<212>  PRT
<213>  Homo sapiens

<400>  794

Arg Thr Tyr Tyr Arg Ser Arg Trp Tyr Asn Asp Tyr Ala Val Ser Val
1               5                   10                  15


Gln Ser




<210>  795
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  795

Gly Gln His Ser Gly Phe Asp Phe
1               5


<210>  796
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  796

Thr Gly Asn Ser Asn Asn Val Gly Asn Gln Gly Ala Ala
1               5                   10


<210>  797
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  797

Arg Asn Asn Asn Arg Pro Ser
1               5


<210>  798
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  798
```

```
Ser Ala Trp Asp Asn Arg Leu Lys Thr Tyr Val
1               5                   10


<210>  799
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  799

Ser Tyr Gly Ile Ser
1               5


<210>  800
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  800

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1               5                   10                  15


Gly



<210>  801
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  801

Asp Thr Pro Gly Ile Ala Ala Arg Arg Tyr Tyr Tyr Tyr Gly Met Asp
1               5                   10                  15


Val



<210>  802
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  802
```

```
Gln Gly Asp Ser Leu Arg Lys Phe Phe Ala Ser
1               5                   10


<210>  803
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  803

Gly Lys Asn Ser Arg Pro Ser
1               5


<210>  804
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  804

Asn Ser Arg Asp Ser Arg Asp Asn His Gln Val
1               5                   10


<210>  805
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  805

Ser Tyr Pro Met His
1               5


<210>  806
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  806

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


Gly
```

```
<210>  807
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  807

Gly Gly Tyr His Asp Phe Trp Ser Gly Pro Asp Tyr
1               5                   10


<210>  808
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  808

Arg Ala Ser Gln Ser Val Asn Thr Asn Leu Ala
1               5                   10


<210>  809
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  809

Gly Ala Ser Ser Arg Ala Thr
1               5


<210>  810
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  810

Gln His Tyr Gly Ser Ser Pro Leu Thr
1               5


<210>  811
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  811
```

```
Ser Tyr Ala Met Ser
1               5


<210>  812
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  812

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


Gly




<210>  813
<211>  18
<212>  PRT
<213>  Homo sapiens

<400>  813

Asp Gln Val Ser Gly Ile Thr Ile Phe Gly Gly Lys Trp Arg Ser Pro
1               5                   10                  15


Asp Val




<210>  814
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  814

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1               5                   10


<210>  815
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  815
```

```
Gly Lys Asn Asn Arg Pro Ser
1               5


<210>  816
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  816

Asn Ser Arg Ser Gly Ser Gln Arg Val
1               5


<210>  817
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  817

Asn Tyr Gly Leu His
1               5


<210>  818
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  818

Val Ile Ser His Asp Gly Thr Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  819
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  819

Asp Gly Gly Tyr Cys Ser Gly Gly Arg Cys Tyr Ser Tyr Gly Met Asp
1               5                   10                  15
```

Val

<210> 820
<211> 13
<212> PRT
<213> Homo sapiens

<400> 820

```
Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn Thr Val Asn
1               5                   10
```

<210> 821
<211> 7
<212> PRT
<213> Homo sapiens

<400> 821

```
Thr Asn Asn Gln Arg Pro Ser
1               5
```

<210> 822
<211> 11
<212> PRT
<213> Homo sapiens

<400> 822

```
Leu Ser Phe Asp Ser Ser Leu Thr Ser Tyr Val
1               5                   10
```

<210> 823
<211> 5
<212> PRT
<213> Homo sapiens

<400> 823

```
Arg Tyr Gly Met His
1               5
```

<210> 824
<211> 17
<212> PRT
<213> Homo sapiens

```
<400>  824

Leu Ile Ser Tyr Asp Gly Ser Lys Thr Phe Tyr Gly Glu Ser Val Lys
1               5                   10                  15


Gly




<210>  825
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  825

Ala Thr Val Thr Thr Asp Gly Tyr Tyr Tyr Met Asp Val
1               5                   10


<210>  826
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  826

Ser Gly Ser Arg Ser Asn Ile Gly Gly Asn Thr Val Asn
1               5                   10


<210>  827
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  827

Ala Asn Asn Gln Arg Pro Ser
1               5


<210>  828
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  828

Ala Ala Trp Asp Asp Asn Leu Ser Gly His Val Val
```

1   5   10

<210> 829
<211> 3
<212> PRT
<213> Homo sapiens

<400> 829

Glu Leu Arg
1

<210> 830
<211> 38
<212> PRT
<213> Homo sapiens

<400> 830

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1   5   10   15

Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
            20   25   30

Asn Ala Asn Phe Asn Lys
        35

<210> 831
<211> 38
<212> PRT
<213> Macaca mulatta

<400> 831

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1   5   10   15

Gly Ser Gly Asp Tyr Asp Ser Ile Lys Glu Pro Cys Phe Arg Glu Glu
            20   25   30

Asn Ala Asn Phe Asn Arg
        35

```
<210>  832
<211>  38
<212>  PRT
<213>  Mus musculus

<400>  832

Met Glu Pro Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu Glu Val
1               5                   10                  15


Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Asp Glu Glu
            20                  25                  30


Asn Val His Phe Asn Arg
        35


<210>  833
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  833

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys
1               5                   10


<210>  834
<211>  14
<212>  PRT
<213>  Macaca mulatta

<400>  834

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys
1               5                   10


<210>  835
<211>  14
<212>  PRT
<213>  Mus musculus

<400>  835

Asp Ala Met Ala Asp Trp Tyr Phe Lys Asn Phe Leu Cys Lys
1               5                   10
```

```
<210>  836
<211>  27
<212>  PRT
<213>  Homo sapiens

<400>  836

Asn Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro
1               5                   10                  15


Asn Asp Leu Trp Val Val Val Phe Gln Phe Gln
            20                  25


<210>  837
<211>  27
<212>  PRT
<213>  Macaca mulatta

<400>  837

Ser Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro
1               5                   10                  15


Asn Asp Leu Trp Val Val Val Phe Gln Phe Gln
            20                  25


<210>  838
<211>  30
<212>  PRT
<213>  Mus musculus

<400>  838

Asp Val Ser Gln Gly Asp Ile Ala Gln Gly Arg Tyr Ile Cys Asp Arg
1               5                   10                  15


Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln
            20                  25                  30


<210>  839
<211>  21
<212>  PRT
<213>  Homo sapiens

<400>  839
```

```
Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu Phe Glu
1               5                   10                  15


Asn Thr Val His Lys
            20


<210>  840
<211>  21
<212>  PRT
<213>  Macaca mulatta

<400>  840

Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu Phe Glu
1               5                   10                  15


Asn Thr Val His Lys
            20


<210>  841
<211>  21
<212>  PRT
<213>  Mus musculus

<400>  841

Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu
1               5                   10                  15


Ser Ile Val His Lys
            20


<210>  842
<211>  365
<212>  PRT
<213>  Homo sapiens

<400>  842

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1               5                   10                  15


Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
            20                  25                  30
```

```
Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile Ile
        35                  40                  45


Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
    50                  55                  60


Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65                  70                  75                  80


Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
                85                  90                  95


Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
            100                 105                 110


His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
        115                 120                 125


Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
    130                 135                 140


Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
145                 150                 155                 160


Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
                165                 170                 175


Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
            180                 185                 190


Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
        195                 200                 205


Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
    210                 215                 220


Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225                 230                 235                 240
```

```
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
                245                 250                 255


Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
            260                 265                 270


Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
        275                 280                 285


Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
    290                 295                 300


Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser Val
305                 310                 315                 320


Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
                325                 330                 335


His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
            340                 345                 350


Gly Thr Glu Thr Ser Gln Val Ala Pro Ala Leu Glu Ser
        355                 360                 365


<210>  843
<211>  341
<212>  PRT
<213>  Homo sapiens

<400>  843

Met Glu Pro Cys Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe
1               5                   10                  15


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


Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met
        35                  40                  45
```

```
Thr Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
    50                  55                  60


Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe
65                  70                  75                  80


Gly Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
                85                  90                  95


Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu
            100                 105                 110


Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala
        115                 120                 125


Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr
    130                 135                 140


Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr
145                 150                 155                 160


Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp Val Val Val Phe Gln
                165                 170                 175


Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu
            180                 185                 190


Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His
        195                 200                 205


Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
    210                 215                 220


Phe Ala Cys Trp Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp Ser Phe
225                 230                 235                 240


Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu Phe Glu Asn Thr Val
                245                 250                 255
```

His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys
            260   265   270

Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser
        275   280   285

Ala Gln His Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile
    290   295   300

Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser
305   310   315   320

Glu Ser Ser Ser Phe His Ser Ser Gly Thr Glu Thr Ser Gln Val Ala
                325   330   335

Pro Ala Leu Glu Ser
            340

<210> 844
<211> 334
<212> PRT
<213> Homo sapiens

<400> 844

Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile
1   5   10   15

Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met
            20   25   30

Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His
        35   40   45

Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala
    50   55   60

Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala
65   70   75   80

Val His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu

```
                85                  90                  95

Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn
            100                 105                 110

Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly
        115                 120                 125

Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala
    130                 135                 140

Asn Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro
145                 150                 155                 160

Asn Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly
                165                 170                 175

Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile
            180                 185                 190

Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys
        195                 200                 205

Thr Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
    210                 215                 220

Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys
225                 230                 235                 240

Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr
                245                 250                 255

Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala
            260                 265                 270

Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser
        275                 280                 285

Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly
```

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    290                 295                 300

Gly His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser
305                 310                 315                 320

Ser Gly Thr Glu Thr Ser Gln Val Ala Pro Ala Leu Glu Ser
                325                 330


<210>  845
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  845

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Gly Asn Tyr Arg Gly Ser Leu Ala Phe Asp Ile Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  846
<211>  113
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<212> PRT
<213> Homo sapiens

<400> 846

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Ala Trp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

Gly

<210> 847
<211> 119
<212> PRT
<213> Homo sapiens

<400> 847

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
20 25 30

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  848
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  848

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  849
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  849

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  850
<211>  119
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<212> PRT
<213> Homo sapiens

<400> 850

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Gly Thr Tyr
            20   25   30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Val Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Pro Val Leu Arg Tyr Gly Phe Asp Ile Trp Gly Gln Gly
            100   105   110

Thr Met Val Thr Val Ser Ser
        115

<210> 851
<211> 119
<212> PRT
<213> Homo sapiens

<400> 851

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20   25   30

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  852
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  852

Gln Val Gln Leu Gln Glu Ser Gly Gly 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 Ile Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr His Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Lys Phe Ser Ala Tyr Ser Gly Tyr Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  853
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  853

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  854
<211>  119
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```
<212>  PRT
<213>  Homo sapiens

<400>  854

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  855
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  855

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  856
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  856

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Arg Ala Ala Ala Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  857
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  857

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Gly Arg Tyr Ser Ser Ser Leu Gly Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  858
<211>  122
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```
<212>  PRT
<213>  Homo sapiens

<400>  858

Gln Val Gln Leu Val Gln 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 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 Asn 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 Glu Ala Pro Tyr Ser Ser Ser Leu Asp Ala Phe Asp Ile Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  859
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  859

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser His Ser Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  860
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  860

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95


Ala Arg Ser His Ser Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  861
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  861

Gln Val Thr Leu Lys Glu Ser Gly Gly Gly Val Val Gln Pro Gly Thr
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Gly Leu Ile Ser Tyr Asp Gly Ser Val Thr His Tyr Thr 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 Thr Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ser Gly Tyr Gln Glu His Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  862
<211>  118
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```
<212>  PRT
<213>  Homo sapiens

<400>  862

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Tyr Gly Asp Tyr Gly Ser Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  863
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  863

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Cys Ser Ser Thr Ser Cys Tyr Arg Gly Met Asp Val Trp
            100                 105                 110


Gly Lys Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  864
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  864

Gln Val Gln Leu Val Gln 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 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 Asn 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 Gly Arg Ala Ala Arg Pro Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  865
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  865

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  866
<211>  121
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```
<212>  PRT
<213>  Homo sapiens

<400>  866

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Pro Glu Phe Thr Phe Ser Lys Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Ser Arg Ser Gly Tyr Phe Leu Pro Leu Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  867
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  867

Glu 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 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 Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
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 Ala Val Thr Gly Gly Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  868
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  868

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Phe Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Arg
```

```
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110



<210>  869
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  869

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala His Tyr Tyr Cys Gln Ser Tyr Asp Arg Ser
                85                  90                  95


Leu Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110



<210>  870
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  870

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ile Gly Leu
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Thr
                85                  90                  95


Leu Arg Val Trp Met Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  871
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  871

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Ser Arg Ser Asn Ile Gly Ala Asp
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Gly Arg Phe
    50                  55                  60


Ser Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80
```

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110


<210>  872
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  872

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Ser Arg Ser Asn Ile Gly Ala Asp
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  873
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  873

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Asp Asn Thr Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Ala Thr Ser Ala Ser Leu Thr Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
                85                  90                  95


Leu Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Leu Leu Gly
            100                 105                 110


<210>  874
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  874

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Val Pro Gly Lys Ala Pro Lys Val
        35                  40                  45


Val Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Ala Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80
```

```
Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Lys Ser
                85                  90                  95


Leu Thr Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  875
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  875

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Arg Val
        35                  40                  45


Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Lys Ser
                85                  90                  95


Leu Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100                 105                 110


<210>  876
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  876

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
```

```
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Phe Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Arg Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Arg
            100                 105                 110


<210>  877
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  877

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


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


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80
```

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110



<210>  878
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  878

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Asp Asn Thr Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Ala Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
                85                  90                  95


Leu Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Leu Leu Arg
            100                 105                 110



<210>  879
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  879
```

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys His Ser Arg Asp Asn Asn
                85                  90                  95


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


<210>  880
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  880

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
```

```
65                  70                  75                  80


Gln Ala Glu Asp Glu Gly Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  881
<211>  112
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (83)..(83)
<223>  Xaa can be any naturally occurring amino acid

<400>  881

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Xaa Asp Glu Gly Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

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<210>  882
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  882

Leu Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
                85                  90                  95


His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  883
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  883

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45
```

```
Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110


<210>  884
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  884

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110
```

<210> 885
<211> 111
<212> PRT
<213> Homo sapiens

<400> 885

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Pro
        35   40   45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100   105   110

<210> 886
<211> 112
<212> PRT
<213> Homo sapiens

<400> 886

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu

```
        35                  40                  45


Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  887
<211>  109
<212>  PRT
<213>  Homo sapiens

<400>  887

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


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


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Thr Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp Asn Thr Asp Asn Arg
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105
```

```
<210>  888
<211>  109
<212>  PRT
<213>  Homo sapiens

<400>  888

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ile Gly Arg Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Ile Leu Val Ile Arg
        35                  40                  45


Asp Asp Arg Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Val Asn Thr Ala Thr Leu Ile Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Lys His
                85                  90                  95


Tyr Val Phe Gly Pro Gly Thr Lys Val Thr Ala Leu Gly
            100                 105


<210>  889
<211>  458
<212>  PRT
<213>  Homo sapiens

<400>  889

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1               5                   10                  15


Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
            20                  25                  30
```

```
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
        35                  40                  45


Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
    50                  55                  60


Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65                  70                  75                  80


Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
                85                  90                  95


Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
            100                 105                 110


Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
        115                 120                 125


Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
    130                 135                 140


Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
145                 150                 155                 160


Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
                165                 170                 175


Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
            180                 185                 190


Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
        195                 200                 205


Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Ala Leu Gln Leu
    210                 215                 220


His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val
225                 230                 235                 240
```

```
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr
                245                 250                 255


Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala
            260                 265                 270


Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr
        275                 280                 285


Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu
    290                 295                 300


Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe
305                 310                 315                 320


Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala
                325                 330                 335


Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala
            340                 345                 350


Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser
        355                 360                 365


Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val
    370                 375                 380


Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala
385                 390                 395                 400


Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala
                405                 410                 415


Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val
            420                 425                 430


Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr
        435                 440                 445
```

Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
    450   455

<210> 890
<211> 437
<212> PRT
<213> Mus musculus

<400> 890

Met Ala Ser Leu Gly Pro Ser Pro Trp Ala Pro Leu Ser Thr Pro Ala
1   5   10   15

Pro Thr Ala Gln Leu Leu Leu Phe Leu Leu Leu Gln Val Ser Ala Gln
            20   25   30

Pro Gln Gly Leu Ser Gly Met Gln Gly Glu Pro Ser Leu Gly Asp Ser
        35   40   45

Ser Ser Gly Glu Asp Glu Leu Gly Val Asp Val Leu Pro Ser Glu Glu
    50   55   60

Asp Ala Pro Glu Glu Ala Asp Pro Pro Asp Gly Glu Asp Pro Pro Glu
65   70   75   80

Val Asn Ser Glu Asp Arg Met Glu Glu Ser Leu Gly Leu Glu Asp Leu
                85   90   95

Ser Thr Pro Glu Ala Pro Glu His Ser Gln Gly Ser His Gly Asp Glu
            100   105   110

Lys Gly Gly Gly His Ser His Trp Ser Tyr Gly Gly Thr Leu Leu Trp
        115   120   125

Pro Gln Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
    130   135   140

Ile Arg Leu Glu Arg Thr Ala Phe Cys Arg Thr Leu Gln Pro Leu Glu
145   150   155   160

Leu Leu Gly Tyr Glu Leu Gln Pro Leu Pro Glu Leu Ser Leu Ser Asn

165 170 175

Asn Gly His Thr Val Gln Leu Thr Leu Pro Pro Gly Leu Lys Met Ala
180 185 190

Leu Gly Pro Gly Gln Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
195 200 205

Gly Thr Ser Asp His Pro Gly Ser Glu His Thr Val Asn Gly His Arg
210 215 220

Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ser Glu
225 230 235 240

Leu His Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
245 250 255

Phe Leu Gln Glu Ser Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
260 265 270

Ser His Leu Glu Glu Ile Ser Glu Glu Gly Ser Lys Ile Glu Ile Pro
275 280 285

Gly Leu Asp Val Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Tyr
290 295 300

Arg Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ser Gln Gly Val Ile
305 310 315 320

Trp Thr Val Phe Asn Glu Thr Val Lys Leu Ser Ala Lys Gln Leu His
325 330 335

Thr Leu Ser Val Ser Leu Trp Gly Pro Arg Asp Ser Arg Leu Gln Leu
340 345 350

Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Thr Ile Glu Ala Ser
355 360 365

Phe Pro Ala Ala Glu Asp Ser Ser Pro Glu Pro Val His Val Asn Ser

```
    370                 375                 380


Cys Phe Thr Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
385                 390                 395                 400


Ala Val Thr Ser Ile Ala Phe Leu Leu Gln Leu Arg Arg Gln His Arg
                405                 410                 415


His Arg Ser Gly Thr Lys Asp Arg Val Ser Tyr Ser Pro Ala Glu Met
            420                 425                 430


Thr Glu Thr Gly Ala
        435


<210>  891
<211>  38
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  891
atcgacgcgt gcctgagcga ggtgcagctg gtgcagtc                               38


<210>  892
<211>  32
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  892
caatggtcac cgtctcttca gctagcacca gg                                     32


<210>  893
<211>  35
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  893
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atcccaagct taagccagtc tgtgctgact cagcc 35

<210> 894
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 894
ggagggacca aattgaccgt cctaggtcag c 31

<210> 895
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 895
tagggcacgc gtgtgctgag cgaggtgcag ctggtgcagt c 41

<210> 896
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 896
tctagtgcta gctgaagaga cggtgaccat tg 32

<210> 897
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 897
ctagcaagct tatcccagtc tgtgctgact cagcc 35

<210> 898

```
<211>  26
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  898
atagcaccta ggacggtcag cttggt                                            26


<210>  899
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence

<400>  899

Ser Tyr Ala Met Ser
1               5


<210>  900
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa can be any naturally occurring amino acid

<400>  900

Xaa Tyr Ala Met Xaa
1               5


<210>  901
<211>  5
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```
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence


<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa can be any naturally occurring amino acid

<400>  901

Ser Tyr Xaa Met Xaa
1               5


<210>  902
<211>  17
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR2 heavy chain sequence


<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (8)..(8)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (10)..(11)
<223>  Xaa can be any naturally occurring amino acid

<400>  902

Ala Ile Ser Xaa Xaa Gly Gly Xaa Thr Xaa Xaa Ala Asp Ser Val Lys
1               5                   10                  15
```

Gly

<210> 903
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Portion of CDR2 heavy chain sequence

<400> 903

```
Ala Ile Ser Gly Ser Gly Gly Ser Thr Thr Thr Ala Asp Ser Val Lys
1               5                   10                  15
```

Gly

<210> 904
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Portion of CDR3 heavy chain sequence

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 904

```
Asn Gly Asn Tyr Arg Gly Ser Leu Xaa Ala Phe Asp Ile
1               5                   10
```

<210> 905
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Portion of CDR1 light chain sequence

<400> 905

```
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1               5                   10


<210>  906
<211>  7
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR2 light chain sequence

<400>  906

Gly Asn Asn Asn Arg Pro Ser
1               5


<210>  907
<211>  12
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR3 light chain sequence

<400>  907

Gln Ser Tyr Asp Ser Ser Leu Ser Ala Trp Val Val
1               5                   10


<210>  908
<211>  6
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Consensus sequence

<400>  908

Glu Glu Asp Leu Pro Glu
1               5


<210>  909
<211>  10
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Portion of the CDR3 heavy chain sequence

<400>  909

Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile
1               5                   10


<210>  910
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR1

<400>  910

Thr Tyr Ala Met Thr
1               5


<210>  911
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR1

<400>  911

Ile Tyr Ala Met Ser
1               5


<210>  912
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR1

<400>  912

Ser Tyr Gly Met His
1               5


<210>  913
```

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain, CDR1

<400> 913

```
Asn Tyr Ala Met Thr
1               5
```

<210> 914
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain, CDR1

<400> 914

```
Lys Tyr Ala Met Ser
1               5
```

<210> 915
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain, CDR2

<400> 915

```
Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly
```

<210> 916
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> variable heavy chain, CDR2

```
<400>  916

Ala Val Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  917
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR2

<400>  917

Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr His Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  918
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR2

<400>  918

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  919
<211>  17
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  variable heavy chain, CDR2

<400>  919

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  920
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR2

<400>  920

Leu Ile Ser Tyr Asp Gly Ser Val Thr His Tyr Thr Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  921
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR2

<400>  921

Ala Ile Ser Gly Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  922
<211>  17
<212>  PRT
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<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR2

<400>  922

Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15


Gly




<210>  923
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  923

Gly Pro Val Leu Arg Tyr Gly Phe Asp Ile
1               5                   10


<210>  924
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  924

Phe Ser Ala Tyr Ser Gly Tyr Asp Leu
1               5


<210>  925
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  925
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Ala Ala Ala Gly Phe Asp Tyr
1               5


<210>  926
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  926

Ile Gly Arg Tyr Ser Ser Ser Leu Gly Tyr
1               5                   10


<210>  927
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  927

Glu Ala Pro Tyr Ser Ser Ser Leu Asp Ala Phe Asp Ile
1               5                   10


<210>  928
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  928

Ser His Ser Ser Gly Gly Phe Asp Tyr
1               5


<210>  929
<211>  7
<212>  PRT
<213>  Artificial Sequence
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```
<220>
<223>  variable heavy chain, CDR3

<400>  929

Gly Ser Gly Tyr Gln Glu His
1               5


<210>  930
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  930

Tyr Gly Asp Tyr Gly Ser Leu Asp Tyr
1               5


<210>  931
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  931

Tyr Cys Ser Ser Thr Ser Cys Tyr Arg Gly Met Asp Val
1               5                   10


<210>  932
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  932

Gly Arg Ala Ala Arg Pro Pro Phe Asp Tyr
1               5                   10


<210>  933
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<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  933

Ser Ser Arg Ser Gly Tyr Phe Leu Pro Leu Asp Tyr
1               5                   10


<210>  934
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable heavy chain, CDR3

<400>  934

Ala Ala Val Thr Gly Gly Phe Asp Pro
1               5


<210>  935
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  935

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1               5                   10


<210>  936
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR1

<400>  936

Thr Gly Ser Arg Ser Asn Ile Gly Ala Asp Tyr Asp Val His
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1               5                   10


<210>  937
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR1

<400>  937

Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly Tyr Asn Val His
1               5                   10


<210>  938
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR1

<400>  938

Thr Gly Thr Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1               5                   10


<210>  939
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR1

<400>  939

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1               5                   10


<210>  940
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR1
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<400> 940

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Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr
1               5                   10
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<210> 941
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain, CDR1

<400> 941

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Gln Gly Asn Ser Leu Arg Tyr Tyr Tyr Pro Ser
1               5                   10
```

<210> 942
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain, CDR1

<400> 942

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Gly Gly Asp Asn Ile Gly Arg Lys Ser Val His
1               5                   10
```

<210> 943
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> variable light chain, CDR2

<400> 943

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Gly Asn Ser Asn Arg Pro Ser
1               5
```

<210> 944
<211> 7
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  944

Ala Asn Asn Asn Arg Pro Ser
1               5


<210>  945
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  945

Asp Asn Thr Asn Arg Pro Ser
1               5


<210>  946
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  946

Gly Asn Asn Asn Arg Pro Ser
1               5


<210>  947
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  947

Asp Asp Thr Asn Arg Pro Ser
1               5
```

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<210>  948
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  948

Tyr Asp Ser Asp Arg Pro Ser
1               5


<210>  949
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  949

Arg Asn Asn Gln Arg Pro Ser
1               5


<210>  950
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  950

Gly Lys Asn Asn Arg Pro Ser
1               5


<210>  951
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR2

<400>  951
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Asp Asp Arg Asp Arg Pro Ser
1               5


<210>  952
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  952

Gln Ser Tyr Asp Ser Arg Leu Ser Ala Trp Val
1               5                   10


<210>  953
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  953

Gln Ser Tyr Asp Arg Ser Leu Ser Trp Val
1               5                   10


<210>  954
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  954

Gln Ser Tyr Asp Ser Thr Leu Arg Val Trp Met
1               5                   10


<210>  955
<211>  11
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  variable light chain, CDR3

<400>  955

Gln Ser Tyr Asp Ser Ser Leu Arg Ala Trp Val
1               5                   10


<210>  956
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  956

Gln Ser Tyr Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


<210>  957
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  957

Gln Ser Tyr Asp Ser Gly Leu Arg Trp Val
1               5                   10


<210>  958
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  958

Gln Ser Tyr Asp Lys Ser Leu Thr Trp Val
1               5                   10


<210>  959
```

```
<211>  10
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<213>  Artificial Sequence

<220>
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<400>  959

Gln Ser Tyr Asp Lys Ser Leu Ser Trp Val
1               5                   10


<210>  960
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  960

Gln Ser Tyr Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


<210>  961
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  961

His Ser Arg Asp Asn Asn Gly His His Ile
1               5                   10


<210>  962
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  962

Gln Val Trp Asp Ser Ser Ser Asp His His Val Val
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```
1               5                   10


<210>  963
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  963

Ala Ala Trp Asp Asp Ser Leu Asn Gly Val Val
1               5                   10


<210>  964
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  964

Ser Ser Arg Asp Asn Thr Asp Asn Arg Val Val
1               5                   10


<210>  965
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variable light chain, CDR3

<400>  965

Gln Val Trp Asp Ser Ser Ser Lys His Tyr Val
1               5                   10


<210>  966
<211>  354
<212>  DNA
<213>  Homo sapiens

<400>  966
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60
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tcctgcaagg ccagcggcta caccttcgcc agctactaca tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc      300

tactaccggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  967
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  967

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 Ala Ser Tyr
            20                  25                  30


Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  968
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<211>  336
<212>  DNA
<213>  Homo sapiens

<400>  968
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc        60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc       120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg       180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc       240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta cctgagcagc       300

tacaccttcg gccagggcac aaagctggaa atcaag                                 336


<210>  969
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  969

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Leu Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

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<210>  970
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  970

Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  971
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  971

Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1               5                   10                  15


Gly




<210>  972
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  972

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
1               5


<210>  973
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  973

Lys Ser Ser Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
1               5                   10                  15


Ala
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<210>  974
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  974

Trp Ala Ser Thr Arg Glu Ser
1               5


<210>  975
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  975

His Gln Tyr Leu Ser Ser Tyr Thr
1               5


<210>  976
<211>  17
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (7)..(7)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  Xaa can be any naturally occurring amino acid

<400>  976

Trp Ile Asn Xaa Xaa Asn Xaa Asn Xaa Lys Tyr Asn Glu Lys Phe Lys
1               5                   10                  15


Gly
```

```
<210>  977
<211>  9
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (2)..(2)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  Xaa can be any naturally occurring amino acid

<400>  977

Ser Xaa Tyr Xaa Xaa Pro Leu Asp Xaa
1               5


<210>  978
<211>  17
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (6)..(6)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (10)..(13)
<223>  Xaa can be any naturally occurring amino acid

<400>  978

Lys Ser Ser Gln Ser Xaa Leu Tyr Ser Xaa Xaa Xaa Xaa Asn Tyr Leu
1               5                   10                  15


Ala
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<210>  979
<211>  7
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<400>  979

Trp Ala Ser Xaa Xaa Glu Ser
1               5


<210>  980
<211>  8
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (5)..(6)
<223>  Xaa can be any naturally occurring amino acid

<400>  980

His Gln Tyr Leu Xaa Xaa Tyr Thr
1               5


<210>  981
<211>  369
<212>  DNA
<213>  Homo sapiens

<400>  981
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagt gacaatgcta tcagctgggt gcgacaggcc      120

ccaggacaag ggcttgagtg gatgggggc atcattccta tctttggaaa accaaactac      180

gcacagaagt tccagggcag agtcacgatt actgcggacg aatccacgag cacagcctac      240

atggacctga ggagcctgag atctgaggac acggccgttt attactgtgc gagagattca      300
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gacgcgtatt actatggttc ggggggtatg gacgtctggg gccaaggcac cctggtcacc      360

gtctcctca                                                              369


<210>  982
<211>  123
<212>  PRT
<213>  Homo sapiens

<400>  982

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 Thr Phe Ser Asp Asn
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Lys Pro Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Asp Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Asp Ala Tyr Tyr Tyr Gly Ser Gly Gly Met Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  983
<211>  335
<212>  DNA
<213>  Homo sapiens

<400>  983
ctgcctgtgc tgactcaatc atcctctgcc tctgcttccc tgggatcctc ggtcaagctc       60
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acctgcactc tgagcagtgg gcatagtaac tacatcatcg catggcatca acagcagcca   120

gggaaggccc ctcggtactt gatgaaggtt aatagtgatg gcagccacac caagggggac   180

gggatccctg atcgcttctc aggctccagc tctggggctg accgctacct caccatctcc   240

aacctccagt ctgaggatga ggctagttat ttctgtgaga cctgggacac taagattcat   300

gtcttcggaa ctgggaccaa ggtctccgtc ctcag   335

<210> 984
<211> 111
<212> PRT
<213> Homo sapiens

<400> 984

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Leu Pro Val Leu Thr Gln Ser Ser Ser Ala Ser Ala Ser Leu Gly Ser
1               5                   10                  15


Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gly His Ser Asn Tyr Ile
            20                  25                  30


Ile Ala Trp His Gln Gln Gln Pro Gly Lys Ala Pro Arg Tyr Leu Met
        35                  40                  45


Lys Val Asn Ser Asp Gly Ser His Thr Lys Gly Asp Gly Ile Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Thr Ile Ser
65                  70                  75                  80


Asn Leu Gln Ser Glu Asp Glu Ala Ser Tyr Phe Cys Glu Thr Trp Asp
                85                  90                  95


Thr Lys Ile His Val Phe Gly Thr Gly Thr Lys Val Ser Val Leu
            100                 105                 110
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<210> 985
<211> 363
<212> DNA
<213> Homo sapiens

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<400>  985
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg ctcctggagg tatcttcaac accaatgctt tcagctgggt ccgacaggcc      120

cctggacaag gtcttgagtg ggtgggaggg gtcatccctt tgtttcgaac agcaagctac      180

gcacagaacg tccagggcag agtcaccatt accgcggacg aatccacgaa cacagcctac      240

atggagctta ccagcctgag atctgcggac acggccgtgt attactgtgc gagaagtagt      300

ggttaccatt ttaggagtca ctttgactcc tggggcctgg gaaccctggt caccgtctcc      360

tca                                                                    363


<210>  986
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  986

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 Pro Gly Gly Ile Phe Asn Thr Asn
            20                  25                  30


Ala Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45


Gly Gly Val Ile Pro Leu Phe Arg Thr Ala Ser Tyr Ala Gln Asn Val
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Thr Ser Leu Arg Ser Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Ser Gly Tyr His Phe Arg Ser His Phe Asp Ser Trp Gly
            100                 105                 110


Leu Gly Thr Leu Val Thr Val Ser Ser
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        115                 120


<210>  987
<211>  363
<212>  DNA
<213>  Homo sapiens

<400>  987
caggtgcagc tggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg ctcctggagg tatcttcaac accaatgctt tcagctgggt ccgacaggcc      120

cctggacaag gtcttgagtg ggtgggaggg gtcatccctt tgtttcgaac agcaagctac      180

gcacagaacg tccagggcag agtcaccatt accgcggacg aatccacgaa cacagcctac      240

atggagctta ccagcctgag atctgcggac acggccgtgt attactgtgc gagaagtagt      300

ggttaccatt ttaggagtca ctttgactcc tggggcctgg gaaccctggt caccgtctcc      360

tca                                                                    363


<210>  988
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  988

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Ala Ser Pro Gly Lys
1               5                   10                  15


Thr Val Thr Ile Ser Cys Thr Gly Ser Ser Gly Asn Ile Ala Ala Asn
            20                  25                  30


Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45


Ile Tyr Glu Asp Asp Arg Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Ile Asp Arg Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Thr Tyr Asp Thr
```

```
                85                  90                  95


Asn Asn His Ala Val Phe Gly Gly Gly Thr His Leu Thr Val Leu
            100                 105                 110


<210>  989
<211>  333
<212>  DNA
<213>  Homo sapiens

<400>  989
aattttatgc tgactcagcc ccactctgtg tcggcgtctc cggggaagac ggtgaccatc       60

tcctgcaccg gcagcagtgg caacattgcc gccaactatg tgcagtggta ccaacaacgt      120

ccgggcagtg cccccactac tgtgatctat gaggatgacc gaagaccctc tggggtccct      180

gatcggttct ctggctccat cgacaggtcc tccaactctg cctccctcac catctcagga      240

ctgaagactg aggacgaggc tgactactac tgtcagactt atgataccaa caatcatgct      300

gtgttcggag gaggcaccca cctgaccgtc ctc                                   333


<210>  990
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  990

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Lys His Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Gly Thr Ser Asn Ile Gly Arg Asn
            20                  25                  30


His Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Glu Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Val Ser Gly Leu Gln
65                  70                  75                  80
```

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Asn Leu
                85   90   95

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 991
<211> 330
<212> DNA
<213> Homo sapiens

<400> 991
tcctatgagc tgactcagcc accctcagcg tctgggaaac acgggcagag ggtcaccatc   60

tcttgttctg gaggcacctc caacatcgga cgtaatcatg ttaactggta ccagcaactc   120

ccaggaacgg cccccaaact cctcatctat agtaatgaac agcggccctc aggggtccct   180

gaccgattct ctggctccaa atctggcacc tccgcctccc tggccgtgag tgggctccag   240

tctgaggatg aggctgatta ttactgtgca tcatgggatg acaacttgag tggttgggtg   300

ttcggcggag ggaccaagct gaccgtccta   330

<210> 992
<211> 120
<212> PRT
<213> Homo sapiens

<400> 992

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 Thr Phe Ser Ala Tyr
            20   25   30

Ala Phe Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Thr Gly Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Leu Thr Ser Thr Ala Tyr

65   70   75   80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Arg Gly Leu Tyr Tyr Tyr Glu Ser Ser Leu Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 993
<211> 361
<212> DNA
<213> Homo sapiens

<400> 993
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttctggagg caccttcagc gcttatgctt tcacctgggt gcggcaggcc   120

cctggacaag ggcttgagtg gatgggaggc atcaccggaa tgtttggcac agcaaactac   180

gcacagaagt tccagggcag agtcacgatt accgcggacg aactcacgag cacagcctac   240

atggagttga gctccctgac atctgaagac acggcccttt attattgtgc gagaggattg   300

tattactatg agagtagtct tgactattgg ggccagggaa ccctggtcac cgtctcctca   360

g   361

<210> 994
<211> 110
<212> PRT
<213> Homo sapiens

<400> 994

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1   5   10   15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20   25   30

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu

```
        35                  40                  45


Met Ile Tyr Glu Val Thr Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Ala Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Phe Cys Cys Ser Tyr Ala Gly His
                85                  90                  95


Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  995
<211>  361
<212>  DNA
<213>  Homo sapiens

<400>  995
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaggg cttctggagg caccttcagc gcttatgctt tcacctgggt gcggcaggcc      120

cctggacaag ggcttgagtg gatgggaggc atcaccggaa tgtttggcac agcaaactac      180

gcacagaagt tccagggcag agtcacgatt accgcggacg aactcacgag cacagcctac      240

atggagttga gctccctgac atctgaagac acggcccttt attattgtgc gagaggattg      300

tattactatg agagtagtct tgactattgg ggccagggaa ccctggtcac cgtctcctca      360

g                                                                      361


<210>  996
<211>  108
<212>  PRT
<213>  Homo sapiens

<400>  996

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Lys
```

```
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys 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 Ser Cys Gln Gln Tyr Asp Gly Val Pro
                85                  90                  95


Arg Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys
            100                 105


<210>  997
<211>  330
<212>  DNA
<213>  Homo sapiens

<400>  997
cagtctgtgc tgactcagcc accctccgcg tccgggtctc ctggacagtc agtcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact ctgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatgatt tatgaggtca ctaagcggcc ctcaggggtc      180

cctgatcgct tctctgcctc caagtctggc aacacggcct ccctgaccgt ctctgggctc      240

caggctgagg atgaggctga ttatttctgc tgctcatatg caggccacag tgcttatgtc      300

ttcggaactg ggaccaaggt caccgtcctg                                       330


<210>  998
<211>  124
<212>  PRT
<213>  Homo sapiens

<400>  998

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 Thr Ser Ser Glu Val Thr Phe Ser Ser Phe
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
        35                  40                  45


Gly Gly Ile Ser Pro Met Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Arg Thr Ala Tyr
65                  70                  75                  80


Met Asp Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Pro Ser Tyr Ile Cys Ser Gly Gly Thr Cys Val Phe Asp
            100                 105                 110


His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  999
<211>  324
<212>  DNA
<213>  Homo sapiens

<400>  999
gaaattgtgc tgactcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca gggccagtca gagtcttagc agcaagtact tagcctggta tcagcagaaa      120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180

gacaggttca gtggcagtgg gtctgggaca gacttcaccc tcaccatcag tagactggag      240

cctgaagatt ttgcagtgta ttcctgtcag cagtatgatg gcgtacctcg gacgttcggc      300

caagggacca cggtggaaat caaa                                             324


<210>  1000
<211>  110
<212>  PRT
<213>  Homo sapiens
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<400> 1000

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1   5   10   15

Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asn Gln
            20   25   30

Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35   40   45

Ser Tyr Arg Asn Asn Asp Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
    50   55   60

Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
65   70   75   80

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Thr Trp Asp Ser Ser Leu
                85   90   95

Ser Ala Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1001
<211> 372
<212> DNA
<213> Homo sapiens

<400> 1001
caggtgcagc tggtgcagtc aggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcacgt cctctgaagt caccttcagt agttttgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gctgggaggg atcagcccta tgtttggaac acctaattac 180

gcgcagaagt tccaaggcag agtcaccatt accgcggacc agtccacgag gacagcctac 240

atggacctga ggagcctgag atctgaggac acggccgtgt attattgtgc gagatctcct 300

tcttacattt gttctggtgg aacctgcgtc tttgaccatt ggggccaggg aaccctggtc 360

accgtctcct ca 372

<210> 1002
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1002

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Ser Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 1003
<211> 372
<212> DNA
<213> Homo sapiens

<400> 1003

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caggtacagc tgcagcagtc aggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcacgt cctctgaagt caccttcagt agttttgcta tcagctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gctgggaggg atcagcccta tgtttggaac acctaattac      180

gcgcagaagt tccaaggcag agtcaccatt accgcggacc agtccacgag gacagcctac      240

atggacctga ggagcctgag atctgaggac acggccgtgt attattgtgc gagatctcct      300

tcttacattt gttctggtgg aacctgcgtc tttgaccatt ggggccaggg aaccctggtc      360
```

```
accgtctcct ca                                                         372


<210>  1004
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  1004

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 Thr Ser Gly Val Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Gly Val Phe Gly Val Pro Lys Tyr Ala Gln Asn Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Pro Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Pro Gly Tyr Tyr Val Gly Lys Asn Gly Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1005
<211>  330
<212>  DNA
<213>  Homo sapiens

<400>  1005
cagcctgggc tgactcagcc accctcggtg tccaagggct tgagacagac cgccacactc      60

acctgcactg ggaacagcaa caatgttggc aaccaaggag cagcttggct gcagcagcac     120
```

```
cagggccacc ctcccaaact cctatcctac aggaataatg accggccctc agggatctca      180

gagagattct ctgcatccag gtcaggaaac acagcctccc tgaccattac tggactccag      240

cctgaggacg aggctgacta ttactgctca acatgggaca gcagcctcag tgctgtggta      300

ttcggcggag ggaccaagct gaccgtccta                                       330


<210>  1006
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1006

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                   10                  15


Thr Ala Ile Leu Thr Cys Thr Gly Asp Ser Asn Asn Val Gly His Gln
            20                  25                  30


Gly Thr Ala Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
        35                  40                  45


Ser Tyr Arg Asn Gly Asn Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
    50                  55                  60


Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Ile Gly Leu Gln
65                  70                  75                  80


Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Val Trp Asp Ser Ser Leu
                85                  90                  95


Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1007
<211>  321
<212>  DNA
<213>  Homo sapiens

<400>  1007
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60
```

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagagg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagac ttcactctca ccattagcag cctgcagcct 240

gaagattttg cagtgtatta ctgtcagcag tatgatagtt caccgtacac ttttggccag 300

gggaccaagg tagagatcaa a 321

<210> 1008
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1008

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Met Thr Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Val Trp Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


Met Glu Val Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ala Ser Val Leu Arg Tyr Phe Asp Trp Gln Pro Glu Ala
            100                 105                 110


Leu Asp Ile Trp Gly Leu Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 1009

<211> 366
<212> DNA
<213> Homo sapiens

<400> 1009
caggtgcagc tggtgcaatc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaaga cttctggagt caccttcagc agctatgcta tcagttgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcggtg tctttggtgt accaaagtac 180

gcgcagaact tccagggcag agtcacaatt accgcggaca aaccgacgag tacagtctac 240

atggagctga acagcctgag agctgaggac acggccgtgt attactgtgc gagagagccc 300

gggtactacg taggaaagaa tggttttgat gtctggggcc aagggacaat ggtcaccgtc 360

tcttca 366

<210> 1010
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1010

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Pro Cys Gly Gly Asn Asn Ile Gly Gly Tyr Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Leu Leu Val Ile Tyr
35 40 45

Asp Asp Lys Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ala
50 55 60

Asn Ser Gly Ser Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Gly Asp Tyr Tyr Cys Gln Val Trp Asp Ser Gly Asn Asp Arg
85 90 95

Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

            100   105

<210> 1011
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1011
tcctatgagc tgactcagcc accctcggtg tccaagggct tgagacagac cgccatactc   60

acctgcactg gagacagcaa caatgttggc caccaaggta cagcttggct gcaacaacac   120

cagggccacc ctcccaaact cctatcctac aggaatggca accggccctc agggatctca   180

gagagattct ctgcatccag gtcaggaaat acagcctccc tgaccattat tggactccag   240

cctgaggacg aggctgacta ctactgctca gtatgggaca gcagcctcag tgcctgggtg   300

ttcggcggag ggaccaagct gaccgtccta   330

<210> 1012
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1012

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 Pro Phe Ser Met Thr
            20   25   30

Ala Phe Thr Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ser Pro Ile Phe Arg Thr Pro Lys Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Asn
65   70   75   80

Met Glu Leu Thr Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Arg Thr Leu Ser Ser Tyr Gln Pro Asn Asn Asp Ala Phe Ala Ile
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1013
<211>  378
<212>  DNA
<213>  Homo sapiens

<400>  1013
caggtgcagc tggtgcagtc tggggctgag gtgaggaagc ctggggcctc agtgaaggtc       60

tcatgtaagg cttctggata caccttcacc ggttattata ttcactgggt gcgacaggcc      120

cctggacaag gacttgagtg gatgggttgg atcaacccta tgactggtgg cacaaactat      180

gcacagaagt ttcaggtctg ggtcaccatg acccgggaca cgtccatcaa cacagcctac      240

atggaggtga gcaggctgac atctgacgac acggccgtgt attactgtgc gagggggggct      300

tccgtattac gatattttga ctggcagccc gaggctcttg atatctgggg cctcgggacc      360

acggtcaccg tctcctca                                                     378


<210>  1014
<211>  106
<212>  PRT
<213>  Homo sapiens

<400>  1014

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 Arg Leu Glu Pro
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro Gln
                85                  90                  95


Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210>  1015
<211>  324
<212>  DNA
<213>  Homo sapiens

<400>  1015
cagcctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccagcatt       60

ccctgtgggg ggaacaacat tggaggctac agtgtacact ggtaccaaca aaagccgggc      120

caggcccccc tcttggtcat ttatgacgat aaagaccggc cctcagggat ccctgagcga      180

ttctctggcg ccaactctgg gagcacggcc accctgacaa tcagcagggt cgaagccggg      240

gatgagggcg actactactg tcaggtgtgg gatagtggta atgatcgtcc gctgttcggc      300

ggagggacca agctgaccgt ccta                                             324


<210>  1016
<211>  123
<212>  PRT
<213>  Homo sapiens

<400>  1016

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 Pro Phe Ser Met Thr
            20                  25                  30


Ala Phe Thr Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ser Pro Ile Phe Arg Thr Pro Lys Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Asn
65                  70                  75                  80


Met Glu Leu Thr Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Thr Leu Ser Ser Tyr Gln Pro Asn Asn Asp Ala Phe Ala Ile
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1017
<211>  369
<212>  DNA
<213>  Homo sapiens

<400>  1017
caggtgcagc tggtgcagtc tggggctgaa gtgaagaagc ctggctcctc ggtgaaggtt       60

tcctgcaagg cttctggagg ccccttcagc atgactgctt tcacctggct gcgacaggcc      120

cctggacaag ggcttgagtg gatgggtggg atcagcccta tctttcgtac accgaagtac      180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgaa cacagccaac      240

atggagctga ccagcctgaa atctgaggac acggccgtgt attactgtgc gagaaccctt      300

tcctcctacc aaccgaataa tgatgctttt gctatctggg gccaagggac aatggtcacc      360

gtctcttca                                                              369


<210>  1018
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1018

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
```

20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ile Gly Leu Arg
65 70 75 80

Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Arg Leu
85 90 95

Ser Ala Ser Leu Phe Gly Thr Gly Thr Thr Val Thr Val Leu
100 105 110

<210> 1019
<211> 318
<212> DNA
<213> Homo sapiens

<400> 1019
gaaattgtgt tgacgcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240

gaagattttg cagtctattt ctgtcagcag tatggtagct cacctcaatt cggccaaggg 300

acacgactgg agattaaa 318

<210> 1020
<211> 369
<212> DNA
<213> Homo sapiens

<400> 1020
caggtgcagc tggtgcagtc tggggctgaa gtgaagaagc ctggctcctc ggtgaaggtt 60

tcctgcaagg cttctggagg ccccttcagc atgactgctt tcacctggct gcgacaggcc 120 cctggacaag ggcttgagtg gatgggtggg atcagcccta tctttcgtac accgaagtac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgaa cacagccaac 240

atggagctga ccagcctgaa atctgaggac acggccgtgt attactgtgc gagaaccctt 300

tcctcctacc aaccgaataa tgatgctttt gctatctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 1021

<400> 1021
000

<210> 1022
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1022
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccag gtcaggcacc tcagcctccc tggccatcat tggactccgg 240

cctgaggatg aagctgatta ttactgtcag tcgtatgaca gcaggctcag tgcttctctc 300

ttcggaactg ggaccacggt caccgtcctc 330

<210> 1023
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<400> 1023

Ser Tyr Ala Phe Ser
1 5

<210> 1024
<211> 5
<212> PRT

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<213>  Homo sapiens

<400>  1024

Thr Asn Ala Phe Ser
1               5


<210>  1025
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1025

Ala Tyr Ala Phe Thr
1               5


<210>  1026
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1026

Ser Phe Ala Ile Ser
1               5


<210>  1027
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1027

Ser Tyr Ala Ile Ser
1               5


<210>  1028
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1028

Gly Tyr Tyr Ile His
1               5
```

```
<210>  1029
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1029

Met Thr Ala Phe Thr
1               5


<210>  1030
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1030

Asp Asn Ala Ile Ser
1               5


<210>  1031
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Consensus Sequence

<400>  1031

Gly Ile Ile Pro Met Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1               5                   10                  15


Gly



<210>  1032
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1032

Gly Val Ile Pro Leu Phe Arg Thr Ala Ser Tyr Ala Gln Asn Val Gln
1               5                   10                  15


Gly
```

```
<210>  1033
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1033

Gly Ile Ile Gly Met Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1               5                   10                  15


Gly




<210>  1034
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1034

Gly Ile Ser Pro Met Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1               5                   10                  15


Gly




<210>  1035
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1035

Gly Ile Ile Gly Val Phe Gly Val Pro Lys Tyr Ala Gln Lys Phe Gln
1               5                   10                  15


Gly




<210>  1036
<211>  17
<212>  PRT
<213>  Homo sapiens
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<400> 1036

Trp Ile Asn Pro Met Thr Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1   5   10   15

Val

<210> 1037
<211> 17
<212> PRT
<213> Homo sapiens

<400> 1037

Gly Ile Ser Pro Ile Phe Arg Thr Pro Lys Tyr Ala Gln Lys Phe Gln
1   5   10   15

Gly

<210> 1038
<211> 17
<212> PRT
<213> Homo sapiens

<400> 1038

Gly Ile Ile Pro Ile Phe Gly Lys Pro Asn Tyr Ala Gln Lys Phe Gln
1   5   10   15

Gly

<210> 1039
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<400> 1039

Ser Ser Gly Tyr Tyr Tyr Gly Gly Gly Phe Asp Val

```
1               5                   10


<210>  1040
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  1040

Ser Ser Gly Tyr His Phe Gly Arg Ser His Phe Asp Ser
1               5                   10


<210>  1041
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1041

Gly Leu Tyr Tyr Tyr Glu Ser Ser Leu Asp Tyr
1               5                   10


<210>  1042
<211>  15
<212>  PRT
<213>  Homo sapiens

<400>  1042

Ser Pro Ser Tyr Ile Cys Ser Gly Gly Thr Cys Val Phe Asp His
1               5                   10                  15


<210>  1043
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  1043

Glu Pro Gly Tyr Tyr Val Gly Lys Asn Gly Phe Asp Val
1               5                   10


<210>  1044
<211>  17
<212>  PRT
<213>  Homo sapiens
```

```
<400>  1044

Gly Ala Ser Val Leu Arg Tyr Phe Asp Trp Gln Pro Glu Ala Leu Asp
1               5                   10                  15


Ile




<210>  1045
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  1045

Thr Leu Ser Ser Tyr Gln Pro Asn Asn Asp Ala Phe Ala Ile
1               5                   10


<210>  1046
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  1046

Asp Ser Asp Ala Tyr Tyr Tyr Gly Ser Gly Gly Met Asp Val
1               5                   10


<210>  1047
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  1047

Thr Gly Ser Ser Ser Asn Ile Gly Asn Tyr Val Ala
1               5                   10


<210>  1048
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  1048

Thr Gly Ser Ser Ser Asn Ile Ala Ala Asn Tyr Val Gln
1               5                   10
```

<210> 1049
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<400> 1049

```
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Ser Val Ser
1               5                   10
```

<210> 1050
<211> 13
<212> PRT
<213> Homo sapiens

<400> 1050

```
Thr Gly Asn Ser Asn Asn Val Gly Asn Gln Gly Ala Ala
1               5                   10
```

<210> 1051
<211> 13
<212> PRT
<213> Homo sapiens

<400> 1051

```
Thr Gly Asp Ser Asn Asn Val Gly His Gln Gly Thr Ala
1               5                   10
```

<210> 1052
<211> 11
<212> PRT
<213> Homo sapiens

<400> 1052

```
Gly Gly Asn Asn Ile Gly Gly Tyr Ser Val His
1               5                   10
```

<210> 1053
<211> 11
<212> PRT

```
<213>  Homo sapiens

<400>  1053

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10


<210>  1054
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  1054

Arg Ala Ser Gln Ser Leu Ser Ser Lys Tyr Leu Ala
1               5                   10


<210>  1055
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  1055

Thr Gly Ser Ser Ser Asn Ile Gly Asn Tyr Val Ala
1               5                   10


<210>  1056
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  1056

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
1               5                   10


<210>  1057
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1057

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1               5                   10
```

```
<210>  1058
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  1058

Thr Leu Ser Ser Gly His Ser Asn Tyr Ile Ile Ala
1               5                   10


<210>  1059
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Consensus Sequence

<400>  1059

Ser Asn Ser Asp Arg Pro Ser
1               5


<210>  1060
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1060

Glu Asp Asp Arg Arg Pro Ser
1               5


<210>  1061
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1061

Glu Val Thr Lys Arg Pro Ser
1               5


<210>  1062
<211>  7
<212>  PRT
<213>  Homo sapiens
```

```
<400>  1062

Arg Asn Asn Asp Arg Pro Ser
1               5


<210>  1063
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1063

Arg Asn Gly Asn Arg Pro Ser
1               5


<210>  1064
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1064

Asp Asp Lys Asp Arg Pro Ser
1               5


<210>  1065
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1065

Asp Ala Ser Asn Arg Ala Thr
1               5


<210>  1066
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1066

Gly Ala Ser Ser Arg Ala Thr
1               5


<210>  1067
<211>  7
```

```
<212>  PRT
<213>  Homo sapiens

<400>  1067

Ser Asn Asn Gln Arg Pro Ser
1               5


<210>  1068
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1068

Ala Ala Ser Ser Leu Gln Arg
1               5


<210>  1069
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1069

Ser Asn Glu Gln Arg Pro Ser
1               5


<210>  1070
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1070

Val Asn Ser Asp Gly Ser His Thr Lys Gly Asp
1               5                   10


<210>  1071
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Consensus Sequence

<400>  1071
```

```
Gln Ser Tyr Asp Ser Leu Ser Ala Tyr Val
1               5                   10


<210>  1072
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1072

Gln Ser Tyr Asp Thr Asn Asn His Ala Val
1               5                   10


<210>  1073
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1073

Cys Ser Tyr Ala Gly His Ser Ala Tyr Val
1               5                   10


<210>  1074
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1074

Ser Thr Trp Asp Ser Ser Leu Ser Ala Val Val
1               5                   10


<210>  1075
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1075

Ser Val Trp Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


<210>  1076
<211>  11
<212>  PRT
<213>  Homo sapiens
```

<400> 1076

```
Gln Val Trp Asp Ser Gly Asn Asp Arg Pro Leu
1               5                   10
```

<210> 1077
<211> 9
<212> PRT
<213> Homo sapiens

<400> 1077

```
Gln Gln Tyr Gly Ser Ser Pro Gln Val
1               5
```

<210> 1078
<211> 9
<212> PRT
<213> Homo sapiens

<400> 1078

```
Gln Gln Tyr Asp Gly Val Pro Arg Thr
1               5
```

<210> 1079
<211> 11
<212> PRT
<213> Homo sapiens

<400> 1079

```
Gln Ser Tyr Asp Ser Arg Leu Ser Ala Ser Leu
1               5                   10
```

<210> 1080
<211> 9
<212> PRT
<213> Homo sapiens

<400> 1080

```
Gln Gln Tyr Asp Ser Ser Pro Tyr Thr
1               5
```

<210> 1081

```
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1081

Ala Ser Trp Asp Asp Asn Leu Ser Gly Trp Val
1               5                   10


<210>  1082
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1082

Glu Thr Trp Asp Thr Lys Ile His Val
1               5


<210>  1083
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic peptide

<400>  1083

Gly Thr Glu Thr Ser Gln Val Ala Pro Ala
1               5                   10


<210>  1084
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic 6xHis tag

<400>  1084

His His His His His His
1               5


<210>  1085
<211>  4
<212>  PRT
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<213> Influenza A virus

<400> 1085

Ile Asn Gly Trp
1

<210> 1086
<211> 4
<212> PRT
<213> Influenza A virus

<400> 1086

Ile Asp Gly Trp
1

<210> 1087
<211> 4
<212> PRT
<213> Influenza A virus

<400> 1087

Val Ala Gly Trp
1

<210> 1088
<211> 4
<212> PRT
<213> Influenza A virus

<400> 1088

Val Asp Gly Trp
1

<210> 1089
<211> 4
<212> PRT
<213> Influenza A virus

<400> 1089

Ile Ala Gly Trp
1

```
<210>  1090
<211>  87
<212>  PRT
<213>  Homo sapiens

<400>  1090

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
1               5                   10                  15


Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Met Phe Gly Thr Pro Asn
        35                  40                  45


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


Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg
                85


<210>  1091
<211>  87
<212>  PRT
<213>  Homo sapiens

<400>  1091

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
1               5                   10                  15


Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn
        35                  40                  45


Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
    50                  55                  60
```

```
Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg
                85



<210>  1092
<211>  108
<212>  PRT
<213>  Homo sapiens

<400>  1092

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Thr Ser Ser Glu Val
1               5                   10                  15


Thr Phe Ser Ser Phe Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Leu Gly Gly Ile Ser Pro Met Phe Gly Thr Pro Asn
        35                  40                  45


Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Gln Ser
    50                  55                  60


Thr Arg Thr Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Glu Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg Ser Pro Ser Tyr Ile Cys Ser Gly Gly
                85                  90                  95


Thr Cys Val Phe Asp His Trp Gly Gln Gly Thr Leu
            100                 105



<210>  1093
<211>  104
<212>  PRT
<213>  Homo sapiens

<400>  1093
```

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
1   5   10   15

Thr Phe Ser Ala Tyr Ala Phe Thr Trp Val Arg Gln Ala Pro Gly Gln
            20   25   30

Gly Leu Glu Trp Met Gly Gly Ile Ile Gly Met Phe Gly Thr Ala Asn
        35   40   45

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

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr
65   70   75   80

Ala Leu Tyr Tyr Cys Ala Arg Gly Leu Tyr Tyr Tyr Glu Ser Ser Phe
                85   90   95

Asp Tyr Trp Gly Gln Gly Thr Leu
            100

<210> 1094
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1094

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
1   5   10   15

Pro Phe Ser Met Thr Ala Phe Thr Trp Leu Arg Gln Ala Pro Gly Gln
            20   25   30

Gly Leu Glu Trp Met Gly Gly Ile Ser Pro Ile Phe Arg Thr Pro Lys
        35   40   45

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

Thr Asn Thr Ala Asn Met Glu Leu Thr Ser Leu Lys Ser Glu Asp Thr

```
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg Thr Leu Ser Ser Tyr Gln Pro Asn Asn
                85                  90                  95


Asp Ala Phe Ala Ile Trp Gly Gln Gly Thr Met
            100                 105


<210>  1095
<211>  106
<212>  PRT
<213>  Homo sapiens

<400>  1095

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Val
1               5                   10                  15


Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Met Gly Gly Ile Ile Gly Val Phe Gly Val Pro Lys
        35                  40                  45


Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Pro
    50                  55                  60


Thr Ser Thr Val Tyr Met Glu Leu Asn Ser Leu Arg Ala Glu Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg Glu Pro Gly Tyr Tyr Val Gly Lys Asn
                85                  90                  95


Gly Phe Asp Val Trp Gly Gln Gly Thr Met
            100                 105


<210>  1096
<211>  105
<212>  PRT
<213>  Homo sapiens

<400>  1096
```

```
Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Pro Gly Gly
1               5                   10                  15


Ile Phe Asn Thr Asn Ala Phe Ser Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Val Gly Gly Val Ile Pro Leu Phe Arg Thr Ala Ser
        35                  40                  45


Tyr Ala Gln Asn Val Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
    50                  55                  60


Thr Asn Thr Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Ala Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg Ser Ser Gly Tyr His Phe Arg Ser His
                85                  90                  95


Phe Asp Ser Trp Gly Leu Gly Thr Leu
            100                 105


<210>  1097
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1097

Arg Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
1               5                   10                  15


Thr Phe Thr Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln
            20                  25                  30


Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Met Thr Gly Gly Thr Asn
        35                  40                  45


Tyr Ala Gln Lys Phe Gln Val Trp Val Thr Met Thr Arg Asp Thr Ser
    50                  55                  60
```

```
Ile Asn Thr Ala Tyr Met Glu Val Thr Arg Leu Thr Ser Asp Asp Thr
65                  70                  75                  80


Ala Val Tyr Tyr Cys Ala Arg Gly Ala Ser Val Leu Arg Tyr Phe Asp
                85                  90                  95


Trp Gln Pro Glu Ala Leu Asp Ile Trp Gly Leu Gly Thr Thr
            100                 105                 110


<210>  1098
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1098

Gly Gly Thr Phe Ser Ser Tyr Ala
1               5


<210>  1099
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1099

Gly Gly Thr Phe Ser Ser Tyr Ala
1               5


<210>  1100
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1100

Glu Val Thr Phe Ser Ser Phe Ala
1               5


<210>  1101
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1101
```

```
Gly Gly Thr Phe Ser Ala Tyr Ala
1               5


<210>  1102
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1102

Gly Gly Pro Phe Ser Met Thr Ala
1               5


<210>  1103
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1103

Gly Val Thr Phe Ser Ser Tyr Ala
1               5


<210>  1104
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1104

Gly Gly Ile Phe Asn Thr Asn Ala
1               5


<210>  1105
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1105

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210>  1106
<211>  8
<212>  PRT
<213>  Homo sapiens
```

```
<400>  1106

Ile Ile Pro Met Phe Gly Thr Pro
1               5


<210>  1107
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1107

Ile Ile Pro Ile Phe Gly Thr Pro
1               5


<210>  1108
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1108

Ile Ser Pro Met Phe Gly Thr Pro
1               5


<210>  1109
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1109

Ile Ile Gly Met Phe Gly Thr Ala
1               5


<210>  1110
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1110

Ile Ser Pro Ile Phe Arg Thr Pro
1               5


<210>  1111
```

```
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1111

Ile Ile Gly Val Phe Gly Val Pro
1               5


<210>  1112
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1112

Val Ile Pro Leu Phe Arg Thr Ala
1               5


<210>  1113
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1113

Ile Asn Pro Met Thr Gly Gly Thr
1               5


<210>  1114
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1114

Ala Arg Ser Pro Ser Tyr Ile Cys Ser Gly Gly Thr Cys Val Phe Asp
1               5                   10                  15


His



<210>  1115
<211>  13
<212>  PRT
<213>  Homo sapiens
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<400> 1115

Ala Arg Gly Leu Tyr Tyr Tyr Glu Ser Ser Phe Asp Tyr
1   5   10

<210> 1116
<211> 16
<212> PRT
<213> Homo sapiens

<400> 1116

Ala Arg Thr Leu Ser Ser Tyr Gln Pro Asn Asn Asp Ala Phe Ala Ile
1   5   10   15

<210> 1117
<211> 15
<212> PRT
<213> Homo sapiens

<400> 1117

Ala Arg Glu Pro Gly Tyr Tyr Val Gly Lys Asn Gly Phe Asp Val
1   5   10   15

<210> 1118
<211> 14
<212> PRT
<213> Homo sapiens

<400> 1118

Ala Arg Ser Ser Gly Tyr His Phe Arg Ser His Phe Asp Ser
1   5   10

<210> 1119
<211> 19
<212> PRT
<213> Homo sapiens

<400> 1119

Ala Arg Gly Ala Ser Val Leu Arg Tyr Phe Asp Trp Gln Pro Glu Ala
1   5   10   15

Leu Asp Ile

```
<210>  1120
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1120

Ser Gly Asn Ile Ala Ala Asn Tyr
1               5


<210>  1121
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1121

Ser Ser Asp Val Gly Gly Tyr Asn Ser
1               5


<210>  1122
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1122

Ser Asn Asn Val Gly Asn Gln Gly
1               5


<210>  1123
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1123

Ser Asn Asn Val Gly His Gln Gly
1               5


<210>  1124
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1124
```

```
Asn Ile Gly Gly Tyr Ser
1               5


<210>  1125
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1125

Gln Ser Ser Val Ser Ser Tyr
1               5


<210>  1126
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  1126

Gln Ser Leu Ser Ser Lys Tyr
1               5


<210>  1127
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1127

Ser Ser Asn Ile Gly Ser Asn Thr
1               5


<210>  1128
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1128

Gln Ser Ile Ser Ser Tyr
1               5


<210>  1129
<211>  8
<212>  PRT
```

```
<213>  Homo sapiens

<400>  1129

Thr Ser Asn Ile Gly Arg Asn His
1               5


<210>  1130
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1130

Glu Asp Asp
1


<210>  1131
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1131

Glu Val Thr
1


<210>  1132
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1132

Arg Asn Asn
1


<210>  1133
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1133

Arg Asn Gly
1
```

```
<210>  1134
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1134

Asp Asp Lys
1


<210>  1135
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1135

Asp Ala Ser
1


<210>  1136
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1136

Gly Ala Ser
1


<210>  1137
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1137

Ser Asn Asn
1


<210>  1138
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1138

Ala Ala Ser
```

1

<210> 1139
<211> 3
<212> PRT
<213> Homo sapiens

<400> 1139

```
Ser Asn Glu
1
```

<210> 1140
<211> 10
<212> PRT
<213> Homo sapiens

<400> 1140

```
Gln Thr Tyr Asp Thr Asn Asn His Ala Val
1               5                   10
```

<210> 1141
<211> 10
<212> PRT
<213> Homo sapiens

<400> 1141

```
Cys Ser Tyr Ala Gly His Ser Ala Tyr Val
1               5                   10
```

<210> 1142
<211> 11
<212> PRT
<213> Homo sapiens

<400> 1142

```
Ser Thr Trp Asp Ser Ser Leu Ser Ala Val Val
1               5                   10
```

<210> 1143
<211> 11
<212> PRT
<213> Homo sapiens

```
<400>  1143

Ser Val Trp Asp Ser Ser Leu Ser Ala Trp Val
1               5                   10


<210>  1144
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1144

Gln Val Trp Asp Ser Gly Asn Asp Arg Pro Leu
1               5                   10


<210>  1145
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1145

Gln Gln Tyr Gly Ser Ser Pro Gln
1               5


<210>  1146
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1146

Gln Gln Tyr Asp Gly Val Pro Arg Thr
1               5


<210>  1147
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1147

Gln Ser Tyr Asp Ser Arg Leu Ser Ala Ser Leu
1               5                   10


<210>  1148
<211>  9
```

```
<212>  PRT
<213>  Homo sapiens

<400>  1148

Gln Gln Tyr Asp Ser Ser Pro Tyr Thr
1               5


<210>  1149
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1149

Ala Ser Trp Asp Asp Asn Leu Ser Gly Trp Val
1               5                   10


<210>  1150
<211>  2
<212>  PRT
<213>  Homo sapiens

<400>  1150

Ala Arg
1


<210>  1151
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1151

Gln Val Gln Leu Val Gln Gly Ala Glu Val
1               5                   10


<210>  1152
<211>  5
<212>  PRT
<213>  Homo sapiens

<400>  1152

Val Thr Val Ser Ser
1               5
```

<210> 1153
<211> 354
<212> DNA
<213> Homo sapiens

<400> 1153
caggtccagc tcgtccagtc cggcgctgaa gtggtgaaac ccggggcatc cgtcaaagtc 60

tcttgtaagg ctagtggcta caccttcaca tcctactgga tgcattgggt gaaacaggca 120

cctggccagg gactcgaatg gatcggagcc gtgtctcctg gaaattccga cacctcctac 180

aacgaaaaat tcaagggcaa ggcaaccctc actgtggata ctagtgcttc taccgcctac 240

atggaactct catctctccg ctctgaggac actgccgtct actactgtac tcggtcacga 300

tacgggaaca acgctctcga ttactgggga cagggcacac tggtcactgt ctct 354

<210> 1154
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1154

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

Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr 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

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly

```
        100                 105                 110


Thr Leu Val Thr Val Ser
        115



<210>  1155
<211>  321
<212>  DNA
<213>  Homo sapiens

<400>  1155
gatattcagc tcacacagag cccatcttct ctgtctgctt ctgtgggcga tcgagtgaca       60

atcacttgtc gggctagtca gggcatttct agcaacattg tgtggctcca gcagaaacct      120

ggcaaagccc caaaaggcct catctaccac ggaaccaacc tggaatctgg cgtgccatct      180

cggtttagtg gatctggatc cgggaccgat tacacactca ccatctcttc actggaacct      240

gaggatttcg ccacctacta ctgtgtccag tactcccagt ttccacccac ttttggacag      300

ggaaccaaac tcgagatcaa a                                                321



<210>  1156
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1156

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
            20                  25                  30


Ile Val Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Gly Leu Ile
        35                  40                  45


Tyr His Gly Thr Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  1157
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1157

Gly Tyr Thr Phe Thr Ser Tyr Trp
1               5


<210>  1158
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1158

Val Ser Pro Gly Asn Ser Asp Thr
1               5


<210>  1159
<211>  12
<212>  PRT
<213>  Homo sapiens

<400>  1159

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr
1               5                   10


<210>  1160
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1160

Gln Gly Ile Ser Ser Asn Ile Val Trp
1               5
```

```
<210>  1161
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1161

His Gly Thr
1


<210>  1162
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1162

Val Gln Tyr Ser Gln Phe Pro Pro Thr
1               5


<210>  1163
<211>  354
<212>  DNA
<213>  Homo sapiens

<400>  1163
caggtccagc tcgtccagtc cggcgctgaa gtggtgaaac ccggggcatc cgtcaaagtc       60

tcttgtaagg ctagtggcta caccttcaca tcctactgga tgcattgggt gaaacaggca      120

cctggccagg gactcgaatg gatcggagcc gtgtctcctg gaaattccga cacctcctac      180

aacgaaaaat tcaagggcaa ggcaaccctc actgtggaca aatctgcctc taccgcctac      240

atggaactct catctctccg ctctgaggat actgctgtgt actactgtac ccggtcacga      300

tacggcaata acgccctcga ttactggggg cagggaactc tggtcactgt gtct            354


<210>  1164
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1164

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


Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu 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


Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser
        115


<210>  1165
<211>  357
<212>  DNA
<213>  Mus musculus

<400>  1165
caggtccagc tgcagcagtc tgggactgtg ctcgcaaggc ctggggcttc agtgaagatg       60

tcctgcaagg cttctggcta cacctttacc agttactgga tgcactgggt aaaacagagg      120

cctggacagg gtctggaatg gattggcgct gtttctcctg gaaatagtga tactagctac      180

aaccagaagt tcaagggcaa ggccacactg actgcagtca catccaccag cactgcctac      240

atggagttca gcagcctgac aaatgaggac tctgcggtct attactgtac aagaagtcga      300

tatggtaaca atgctttgga ctactggggc caagggacca cggtcaccgt ctcctca         357


<210>  1166
<211>  119
<212>  PRT
<213>  Mus musculus
```

<400> 1166

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

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

Lys Gly Lys Ala Thr Leu Thr Ala Val Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 1167
<211> 330
<212> DNA
<213> Mus musculus

<400> 1167
gacatcgagc tcacccagtc tcctgcttcc ttagctgtat ctctggggca gagggccacc 60

atctcataca gggccagcaa aagtgtcagt acatctggct atagttatat gcactggaac 120

caacagaaac caggacagcc acccagactc ctcatctatc ttgtatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc acattaaggg agcttacacg 300

ttcggagggg ggaccaagct ggaaataaaa 330

```
<210>  1168
<211>  330
<212>  DNA
<213>  Mus musculus

<400>  1168
gacatcgagc tcactcagtc tccagcttct ttggctgtgt ctctagggca gagggccacc       60

atctcctgca gagccagcgc aagtgttgat aattatggca ttagttttat gaactggttc      120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa ccaaggatcc      180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat      240

cctatggagg aggatgatac tgcaacctat tactgtcagc acattaaggg agcttacacg      300

ttcggagggg ggaccaagct ggagctgaaa                                       330


<210>  1169
<211>  321
<212>  DNA
<213>  Mus musculus

<400>  1169
gacatcgagc tcactcagtc tccatcctcc atgtctgtat ctctgggaga cacagtcaac       60

atcacttgcc gtgcaagtca gggcattagc agtaatatag tgtggttgca gcagaaacca      120

gggaagtcat ttaagggcct gatctatcat gggaccaatt tggaagatgg agttccatca      180

aggttcagtg gcagtggatc tggagccgat tattctctca ccatcagcag cctggaatct      240

gaggattttg cagactatta ctgtgtacag tattctcagt ttcctcccac gttcggctcg      300

gggaccaagc tggagctgaa a                                                321


<210>  1170
<211>  107
<212>  PRT
<213>  Mus musculus

<400>  1170

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


Asp Thr Val Asn Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
```

```
            20                  25                  30

Ile Val Trp Leu Gln Gln Lys Pro Gly Lys Ser Phe Lys Gly Leu Ile
        35                  40                  45

Tyr His Gly Thr Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ala Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65                  70                  75                  80

Glu Asp Phe Ala Asp Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
            100                 105


<210>  1171
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1171

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

Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu 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
```

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser
        115

<210> 1172
<211> 118
<212> PRT
<213> Mus musculus

<400> 1172

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

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

Lys Gly Lys Ala Thr Leu Thr Ala Val Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser
        115

<210> 1173
<211> 107
<212> PRT

```
<213>  Homo sapiens

<400>  1173

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
            20                  25                  30


Ile Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Gly Leu Ile
        35                  40                  45


Tyr His Gly Thr Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  1174
<211>  98
<212>  PRT
<213>  Homo sapiens

<400>  1174

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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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



<210>  1175
<211>  294
<212>  DNA
<213>  Homo sapiens

<400>  1175
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga            294


<210>  1176
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chemically synthesized peptide

<400>  1176

Ile Ser Pro Met Phe Gly Thr Pro
1               5


<210>  1177
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
```

```
<223>  Chemically synthesized peptide

<400>  1177

Ile Ile Pro Ile Phe Gly Thr Ala
1               5


<210>  1178
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chemically synthesized peptide

<400>  1178

Ile Ser Pro Ile Phe Gly Thr Ala
1               5


<210>  1179
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chemically synthesized peptide


<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  wherein said Xaa is an Isoleucine or a Serine

<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  wherein said Xaa is an Isoleucine or a Methionine

<400>  1179

Ile Xaa Pro Xaa Phe Gly Thr Ala
1               5


<210>  1180
<211>  8
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Chemically synthesized peptide


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  wherein said Xaa is a Glycine or a Glutamic acid

<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  wherein said Xaa is a Glycine or a Valine

<400>  1180

Xaa Xaa Thr Phe Ser Ser Tyr Ala
1               5


<210>  1181
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chemically synthesized peptide


<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  wherein said Xaa is an Isoleucine or a Serine

<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  wherein said Xaa is an Isoleucine or a Methionine

<400>  1181

Ile Xaa Pro Xaa Phe Gly Thr Ala
1               5


<210>  1182
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain
```

```
<400>  1182
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60

tcctgcaagg ccagcggcta caccttcgcc agccaatgga tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc      300

tggtaccggc cgctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1183
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain

<400>  1183

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 Ala Ser Gln
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

Leu Val Thr Val Ser Ser
        115

<210> 1184
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain

<400> 1184
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc   60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc   120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg   180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc   240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta catcagcagc   300

tacaccttcg gccagggcac aaagctggaa atcaag   336

<210> 1185
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain

<400> 1185

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 Ile Leu Tyr Ser
            20   25   30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 His Gln
                85                  90                  95


Tyr Ile Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 1186
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1186

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caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg        60

tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca       120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac       180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac       240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacg       300

tggtatcggc cgaatgacta ctggggccag ggcaccctgg tgaccgtgag cagc             354
```

<210> 1187
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1187

```
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 Ala Ser Ser
            20                  25                  30
```

```
Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Asn Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1188
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain

<400>  1188
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc        60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc       120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg       180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc       240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta caaaagcagc       300

tacaccttcg gccagggcac aaagctggaa atcaag                                 336


<210>  1189
<211>  112
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Variable light chain

<400> 1189

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 Ile Leu Tyr Ser
            20   25   30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 His Gln
                85   90   95

Tyr Lys Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 1190
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1190
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg   60

tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca   120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac   180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac   240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaaccacc   300

```
cgttatcggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc           354


<210>  1191
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain

<400>  1191

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 Ala Ser Ser
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Thr Arg Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1192
<211>  336
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain
```

<400> 1192

Gly Ala Cys Ala Thr Cys Gly Thr Gly Ala Thr Gly Ala Cys Cys Cys
1   5   10   15

Ala Gly Ala Gly Cys Cys Cys Cys Gly Ala Cys Ala Gly Cys Cys Thr
            20   25   30

Gly Gly Cys Cys Gly Thr Gly Ala Gly Cys Cys Thr Gly Gly Gly Cys
        35   40   45

Gly Ala Gly Cys Gly Gly Gly Cys Cys Ala Cys Cys Ala Thr Cys Ala
    50   55   60

Ala Cys Thr Gly Cys Ala Ala Gly Ala Gly Cys Ala Gly Cys Cys Ala
65   70   75   80

Gly Ala Gly Cys Ala Thr Cys Cys Thr Gly Thr Ala Cys Ala Gly Cys
                85   90   95

Ala Gly Cys Ala Ala Cys Cys Ala Gly Ala Ala Gly Ala Ala Cys Thr
            100   105   110

Ala Cys Cys Thr Gly Gly Cys Cys Thr Gly Gly Thr Ala Thr Cys Ala
        115   120   125

Gly Cys Ala Gly Ala Ala Gly Cys Cys Cys Gly Gly Cys Cys Ala Gly
    130   135   140

Ala Gly Cys Cys Cys Cys Ala Ala Gly Cys Thr Gly Cys Thr Gly Ala
145   150   155   160

Thr Cys Thr Ala Cys Thr Gly Gly Gly Cys Cys Ala Gly Cys Ala Cys
                165   170   175

Cys Cys Gly Gly Gly Ala Gly Ala Gly Cys Gly Gly Cys Gly Thr Gly
            180   185   190

Cys Cys Cys Gly Ala Cys Cys Gly Gly Thr Thr Thr Ala Gly Cys Gly

195 200 205

Gly Cys Ala Gly Cys Gly Gly Cys Thr Cys Cys Gly Gly Cys Ala Cys
210 215 220

Cys Gly Ala Cys Thr Thr Cys Ala Cys Cys Cys Thr Gly Ala Cys Cys
225 230 235 240

Ala Thr Cys Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala Gly Gly
245 250 255

Cys Cys Gly Ala Gly Gly Ala Cys Gly Thr Gly Gly Cys Cys Gly Thr
260 265 270

Gly Thr Ala Cys Thr Ala Cys Thr Gly Cys Cys Ala Cys Cys Ala Gly
275 280 285

Thr Ala Cys Cys Gly Thr Ala Gly Cys Ala Gly Cys Thr Ala Cys Ala
290 295 300

Cys Cys Thr Thr Cys Gly Gly Cys Cys Ala Gly Gly Gly Cys Ala Cys
305 310 315 320

Ala Ala Ala Gly Cys Thr Gly Gly Ala Ala Ala Thr Cys Ala Ala Gly
325 330 335

<210> 1193
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain

<400> 1193

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 Ile Leu Tyr Ser
20 25 30

```
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Arg Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 1194
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1194

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caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg        60

tcctgcaagg ccagcggcta caccttcgcc agccaatata tgcactggat gcggcaggca       120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac       180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac       240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagactgacc       300

tattatcggc cgccggacta ctggggccag ggcaccctgg tgaccgtgag cagc             354
```

<210> 1195
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1195

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 Ala Ser Gln
            20   25   30

Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 1196
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain

<400> 1196
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc   60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc   120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg   180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc   240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta ctatagcagc   300 tacaccttcg gccagggcac aaagctggaa atcaag   336

<210> 1197
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain

<400> 1197

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Tyr Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 1198
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain

<400> 1198
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg   60

```
tcctgcaagg ccagcggcta caccttcgcc agcgcgtgga tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacg      300

tattaccggc cgctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1199
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain

<400>  1199

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 Ala Ser Ala
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

```
<210>  1200
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain

<400>  1200
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc       60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg      180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc      240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta catgagcagc      300

tacaccttcg gccagggcac aaagctggaa atcaag                                336


<210>  1201
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain

<400>  1201

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Met Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1202
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR1

<400>  1202

Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  1203
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR1

<400>  1203

Gly Tyr Thr Phe Ala Ser Gln Trp
1               5


<210>  1204
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR1

<400>  1204

Gly Tyr Thr Phe Ala Ser Ser Trp
1               5


<210>  1205
```

```
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR1

<400>  1205

Gly Tyr Thr Phe Ala Ser Gln Tyr
1               5


<210>  1206
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR1

<400>  1206

Gly Tyr Thr Phe Ala Ser Ala Trp
1               5


<210>  1207
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR1

<400>  1207

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1208
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR2

<400>  1208

Ile Asn Pro Gly Asn Val Asn Thr
```

```
1               5


<210>  1209
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR2

<400>  1209

Trp Ala Ser Thr Arg Glu
1               5


<210>  1210
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR3

<400>  1210

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1211
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR3

<400>  1211

Ser Thr Trp Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1212
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain, CDR3
```

<400> 1212

Ser Thr Trp Tyr Arg Pro Asn Asp Tyr
1   5

<210> 1213
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain, CDR3

<400> 1213

Thr Thr Arg Tyr Arg Pro Leu Asp Tyr
1   5

<210> 1214
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain, CDR3

<400> 1214

Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr
1   5

<210> 1215
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain, CDR3

<400> 1215

His Gln Tyr Leu Ser Ser Tyr Thr
1   5

<210> 1216
<211> 8
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR3

<400>  1216

His Gln Tyr Ile Ser Ser Tyr Thr
1               5


<210>  1217
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR3

<400>  1217

His Gln Tyr Lys Ser Ser Tyr Thr
1               5


<210>  1218
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR3

<400>  1218

His Gln Tyr Arg Ser Ser Tyr Thr
1               5


<210>  1219
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain, CDR3

<400>  1219

His Gln Tyr Tyr Ser Ser Tyr Thr
1               5
```

<210> 1220
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain, CDR3

<400> 1220

```
His Gln Tyr Met Ser Ser Tyr Thr
1               5
```

<210> 1221
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized primer

<400> 1221

```
tctgagtagg tgtcattcta ttctggg                                          27
```

<210> 1222
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized primer

<400> 1222

```
cactaggggt tcctagatct ctccc                                            25
```

<210> 1223
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically synthesized probe

<400> 1223

```
Thr Cys Thr Thr Cys Cys Cys Ala Ala Thr Cys Cys Thr Cys Cys Cys
1               5                   10                  15
```

```
Cys Cys Thr Thr Gly Cys Thr Gly Thr Cys
            20                  25


<210>  1224
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1224

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


Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
            20                  25                  30


Thr Phe Ser Gly Tyr Ser Thr His Trp Leu Arg Gln Val Pro Gly Gln
        35                  40                  45


Gly Leu Glu Trp Ile Gly Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr
    50                  55                  60


Tyr Ala Glu Asn Phe Arg Gly Arg Val Thr Leu Thr Arg Asp Thr Ser
65                  70                  75                  80


Ile Thr Thr Asp Tyr Leu Glu Val Arg Gly Leu Arg Ser Asp Asp Thr
                85                  90                  95


Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asp Asp Tyr Ser Phe Asp His
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1225
<211>  354
<212>  DNA
<213>  Artificial Sequence
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<220>
<223>  Synthetic Oligonucleotide


<220>
<221>  misc_feature
<222>  (62)..(62)
<223>  n is a, c, g, or t

<220>
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<222>  (90)..(90)
<223>  n is a, c, g, or t

<220>
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<222>  (120)..(120)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (182)..(182)
<223>  n is a, c, g, or t

<220>
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<222>  (190)..(192)
<223>  n is a, c, g, or t

<220>
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<222>  (208)..(208)
<223>  n is a, c, g, or t

<220>
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<222>  (256)..(256)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (279)..(279)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (288)..(288)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (297)..(297)
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<223>  n is a, c, g, or t

<400>  1225
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaagtc        60

tnctgcaagg cttctggata caccttcagn ggctactcta cacactggct gcgacaggtn       120

cctggacagg gacttgagtg gattggatgg gacaacccta gtagtggtga cacgacctat       180

gnagagaatn nncggggcag ggtcaccntg accagggaca cgtccatcac cacagattac       240

ttggaagtga ggggtntaag atctgacgac acggccgtnt attattgngc cagaggngga       300

gatgactaca gctttgacca ttggggtcag ggcaccctgg tcaccgtctc ctca             354


<210>  1226
<211>  105
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1226

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


Thr Val Arg Ile Thr Cys Arg Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Glu Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Asp His Leu
                85                  90                  95


Leu Leu Phe Gly Gln Gly Thr Lys Leu
            100                 105
```

```
<210>  1227
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  1227
tcttctgagc tgactcagga cccagctgtg tctgtggcct tgggacagac agtcaggatc       60

acatgccgag gagacagcct cagaagttat tatgcaagct ggtaccaaca gaagccagga      120

caggcccctg tacttgtcat ctatggtgaa aacaaccgac cctcagggat cccagaccga      180

ttctctggct ccagctcagg agacacagct tccttgacca tcactggggc tcaggcggaa      240

gatgaggctg actattactg taactcccgg gacagcagtg atcaccttct cctattcggt      300

ggagggacca agttgaccgt cctaggt                                          327


<210>  1228
<211>  330
<212>  PRT
<213>  Homo sapiens

<400>  1228

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


Lys Ala 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> 1229
<211> 992
<212> DNA
<213> Homo sapiens

<400> 1229
ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc acctctgggg   60

gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt   120

ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag   180

gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct   240

acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa gcagagccca   300

aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc ctggggggac   360

cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg   420

aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt   480

acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca   540

gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg   600

agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca   660

aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc cgggatgagc   720

tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg   780

ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc   840

tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc   900

agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc   960

agaagagcct ctccctgtct ccgggtaaat ga   992

```
<210>  1230
<211>  330
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1230

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


Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110


Pro Ala Pro Glu Ala Ala 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>  1231
<211>  992
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  1231
ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc acctctgggg       60
```

gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt 120

ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag 180

gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct 240

acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa gcagagccca 300

aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaagcc gccgggggac 360

cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg 420

aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt 480

acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca 540

gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg 600

agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca 660

aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc cgggatgagc 720

tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg 780

ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc 840

tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc 900

agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc 960

agaagagcct ctccctgtct ccgggtaaat ga 992

<210> 1232
<211> 97
<212> PRT
<213> Homo sapiens

<400> 1232

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


Lys



<210>  1233
<211>  290
<212>  DNA
<213>  Homo sapiens

<400>  1233
ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc acctctgggg       60

gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt      120

ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag      180

gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct      240

acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa                 290


<210>  1234
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1234

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1               5                   10                  15


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
```

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60


Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110
```

<210> 1235
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1235

```
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc       60

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac      120

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag      180

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac      240

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc      300

cccatcgaga aaaccatctc caaagccaaa                                       330
```

<210> 1236
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1236

```
Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1               5                   10                  15


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
```

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60


Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110


<210>  1237
<211>  330
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  1237
gcacctgaag ccgccggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc       60

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac      120

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag      180

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac      240

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc      300

cccatcgaga aaaccatctc caaagccaaa                                       330


<210>  1238
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1238

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
```

```
1               5                   10                  15


Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30


Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45


Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60


Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80


Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95


Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105


<210>  1239
<211>  324
<212>  DNA
<213>  Homo sapiens

<400>  1239
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag       60

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      120

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      180

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      240

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc      300

ctctccctgt ctccgggtaa atga                                             324


<210>  1240
<211>  16
<212>  PRT
<213>  Homo sapiens

<400>  1240
```

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 1241
<211> 48
<212> DNA
<213> Homo sapiens

<400> 1241
gcagagccca aatcttgtga caaaactcac acatgcccac cgtgccca   48

<210> 1242
<211> 453
<212> PRT
<213> Homo sapiens

<400> 1242

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

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
            20   25   30

Thr Phe Ser Gly Tyr Ser Thr His Trp Leu Arg Gln Val Pro Gly Gln
        35   40   45

Gly Leu Glu Trp Ile Gly Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr
    50   55   60

Tyr Ala Glu Asn Phe Arg Gly Arg Val Thr Leu Thr Arg Asp Thr Ser
65   70   75   80

Ile Thr Thr Asp Tyr Leu Glu Val Arg Gly Leu Arg Ser Asp Asp Thr
                85   90   95

Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asp Asp Tyr Ser Phe Asp His
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115   120   125

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190


Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys
    210                 215                 220


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270


Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly Lys
    450


<210>  1243
<211>  453
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1243

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


Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
            20                  25                  30


Thr Phe Ser Gly Tyr Ser Thr His Trp Leu Arg Gln Val Pro Gly Gln
```

```
        35                  40                  45

Gly Leu Glu Trp Ile Gly Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr
    50                  55                  60

Tyr Ala Glu Asn Phe Arg Gly Arg Val Thr Leu Thr Arg Asp Thr Ser
65                  70                  75                  80

Ile Thr Thr Asp Tyr Leu Glu Val Arg Gly Leu Arg Ser Asp Asp Thr
                85                  90                  95

Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asp Asp Tyr Ser Phe Asp His
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
```

```
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys
```

450

<210> 1244
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1244

```
Gly Tyr Ser Thr His
1               5
```

<210> 1245
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Polypeptide

<400> 1245

```
Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr Tyr Ala Glu Asn Phe Arg
1               5                   10                  15


Gly
```

<210> 1246
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1246

```
Gly Gly Asp Asp Tyr Ser Phe Asp His
1               5
```

<210> 1247
<211> 11
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1247

Arg Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1               5                   10


<210>  1248
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1248

Gly Glu Asn Asn Arg Pro Ser
1               5


<210>  1249
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1249

Asn Ser Arg Asp Ser Ser Asp His Leu Leu Leu
1               5                   10


<210>  1250
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  1250

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asn Gly Asn Tyr Arg Gly Ser Leu Ala Phe Asp Ile Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1251
<211>  113
<212>  PRT
<213>  Homo sapiens

<400>  1251

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80
```

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


Gly




<210>  1252
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1252

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115
```

```
<210>  1253
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1253

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  1254
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1254

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  1255
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1255

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Gly Thr Tyr
            20                  25                  30


Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Val Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Pro Val Leu Arg Tyr Gly Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  1256
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1256

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115
```

```
<210>  1257
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1257

Gln Val Gln Leu Gln Glu Ser Gly Gly 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 Ile Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr His Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Phe Ser Ala Tyr Ser Gly Tyr Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1258
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1258

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  1259
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1259

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  1260
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1260

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115
```

```
<210>  1261
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  1261

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Ala Ala Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  1262
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1262

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Gly Arg Tyr Ser Ser Ser Leu Gly Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  1263
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  1263

Gln Val Gln Leu Val Gln 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 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 Asn 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 Glu Ala Pro Tyr Ser Ser Ser Leu Asp Ala Phe Asp Ile Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1264
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1264

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser His Ser Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

```
<210>  1265
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1265

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser His Ser Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1266
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  1266

Gln Val Thr Leu Lys Glu Ser Gly Gly Gly Val Val Gln Pro Gly Thr
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
```

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Gly Leu Ile Ser Tyr Asp Gly Ser Val Thr His Tyr Thr 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 Thr Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Ser Gly Tyr Gln Glu His Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1267
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1267

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Tyr Gly Asp Tyr Gly Ser Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1268
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  1268

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Tyr Cys Ser Ser Thr Ser Cys Tyr Arg Gly Met Asp Val Trp
            100                 105                 110


Gly Lys Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

```
<210>  1269
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1269

Gln Val Gln Leu Val Gln 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 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 Asn 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 Gly Arg Ala Ala Arg Pro Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  1270
<211>  119
<212>  PRT
<213>  Homo sapiens

<400>  1270

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
            20                  25                  30
```

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Ala Asn Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Asn Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100   105   110

Thr Met Val Thr Val Ser Ser
        115

<210> 1271
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1271

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Pro Glu Phe Thr Phe Ser Lys Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ser Ser Arg Ser Gly Tyr Phe Leu Pro Leu Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1272
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1272

Glu 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 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 Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
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 Ala Val Thr Gly Gly Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

<210> 1273
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1273

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Phe Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Thr Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Arg
85 90 95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 1274
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1274

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

```
Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala His Tyr Tyr Cys Gln Ser Tyr Asp Arg Ser
                85                  90                  95


Leu Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1275
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1275

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ile Gly Leu
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Thr
                85                  90                  95


Leu Arg Val Trp Met Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
```

```
<210>  1276
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1276

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Ser Arg Ser Asn Ile Gly Ala Asp
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Gly Arg Phe
    50                  55                  60


Ser Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110


<210>  1277
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1277

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Ile Thr Ile Ser Cys Thr Gly Ser Arg Ser Asn Ile Gly Ala Asp
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
```

        35   40   45

Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100   105   110

<210> 1278
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1278

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20   25   30

Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Asp Asn Thr Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Ala Thr Ser Ala Ser Leu Thr Ile Thr Gly Leu
65   70   75   80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
                85   90   95

Leu Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Leu Leu Gly
            100   105   110

<210> 1279
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1279

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Ile Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Val Pro Gly Lys Ala Pro Lys Val
        35   40   45

Val Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Ala Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Lys Ser
                85   90   95

Leu Thr Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100   105   110

<210> 1280
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1280

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asn Ile Gly Ala Gly
            20   25   30

```
Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Arg Val
        35                  40                  45


Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Lys Ser
                85                  90                  95


Leu Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100                 105                 110


<210>  1281
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1281

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Phe Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Arg Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Arg
```

```
            100                 105                 110


<210>  1282
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1282

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


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


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110


<210>  1283
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1283

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30
```

```
Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Asp Asn Thr Asn Arg Pro Ser Gly Val Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Ala Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
                85                  90                  95


Leu Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Leu Leu Arg
            100                 105                 110


<210>  1284
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1284

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys His Ser Arg Asp Asn Asn
                85                  90                  95
```

```
Gly His His Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
            100                 105                 110


<210>  1285
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1285

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Gly Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1286
<211>  112
<212>  PRT
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (83)..(83)
<223>  Xaa can be any naturally occurring amino acid

<400>  1286
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```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Arg Gly
            20                  25                  30


Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Xaa Asp Glu Gly Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1287
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1287

Leu Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
```

```
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
                85                  90                  95


His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1288
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1288

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100                 105                 110


<210>  1289
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1289
```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Ala Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Arg Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
            100   105   110

<210> 1290
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1290

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Pro
        35   40   45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

```
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100                 105                 110


<210>  1291
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1291

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Thr Asp Tyr Phe Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  1292
<211>  109
<212>  PRT
<213>  Homo sapiens
```

```
<400>  1292

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


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


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Thr Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp Asn Thr Asp Asn Arg
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>  1293
<211>  109
<212>  PRT
<213>  Homo sapiens

<400>  1293

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ile Gly Arg Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Ile Leu Val Ile Arg
        35                  40                  45


Asp Asp Arg Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
```

```
Ser Ser Val Asn Thr Ala Thr Leu Ile Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Lys His
                85                  90                  95


Tyr Val Phe Gly Pro Gly Thr Lys Val Thr Ala Leu Gly
            100                 105


<210>  1294
<211>  458
<212>  PRT
<213>  Homo sapiens

<400>  1294

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1               5                   10                  15


Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
            20                  25                  30


Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
        35                  40                  45


Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
    50                  55                  60


Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65                  70                  75                  80


Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
                85                  90                  95


Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
            100                 105                 110


Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
        115                 120                 125
```

```
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
    130                 135                 140

Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
145                 150                 155                 160

Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
                165                 170                 175

Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
            180                 185                 190

Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
        195                 200                 205

Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Ala Leu Gln Leu
    210                 215                 220

His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val
225                 230                 235                 240

Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr
                245                 250                 255

Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala
            260                 265                 270

Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr
        275                 280                 285

Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu
    290                 295                 300

Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe
305                 310                 315                 320

Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala
                325                 330                 335
```

```
Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala
            340                 345                 350


Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser
        355                 360                 365


Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val
    370                 375                 380


Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala
385                 390                 395                 400


Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala
                405                 410                 415


Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val
            420                 425                 430


Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr
        435                 440                 445


Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
    450                 455


<210>  1295
<211>  437
<212>  PRT
<213>  Mus musculus

<400>  1295

Met Ala Ser Leu Gly Pro Ser Pro Trp Ala Pro Leu Ser Thr Pro Ala
1               5                   10                  15


Pro Thr Ala Gln Leu Leu Leu Phe Leu Leu Leu Gln Val Ser Ala Gln
            20                  25                  30


Pro Gln Gly Leu Ser Gly Met Gln Gly Glu Pro Ser Leu Gly Asp Ser
        35                  40                  45


Ser Ser Gly Glu Asp Glu Leu Gly Val Asp Val Leu Pro Ser Glu Glu
```

```
    50                  55                  60


Asp Ala Pro Glu Glu Ala Asp Pro Pro Asp Gly Glu Asp Pro Pro Glu
65                  70                  75                  80


Val Asn Ser Glu Asp Arg Met Glu Glu Ser Leu Gly Leu Glu Asp Leu
                85                  90                  95


Ser Thr Pro Glu Ala Pro Glu His Ser Gln Gly Ser His Gly Asp Glu
            100                 105                 110


Lys Gly Gly Gly His Ser His Trp Ser Tyr Gly Gly Thr Leu Leu Trp
        115                 120                 125


Pro Gln Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
    130                 135                 140


Ile Arg Leu Glu Arg Thr Ala Phe Cys Arg Thr Leu Gln Pro Leu Glu
145                 150                 155                 160


Leu Leu Gly Tyr Glu Leu Gln Pro Leu Pro Glu Leu Ser Leu Ser Asn
                165                 170                 175


Asn Gly His Thr Val Gln Leu Thr Leu Pro Pro Gly Leu Lys Met Ala
            180                 185                 190


Leu Gly Pro Gly Gln Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
        195                 200                 205


Gly Thr Ser Asp His Pro Gly Ser Glu His Thr Val Asn Gly His Arg
    210                 215                 220


Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ser Glu
225                 230                 235                 240


Leu His Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
                245                 250                 255


Phe Leu Gln Glu Ser Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
```

```
            260                 265                 270

Ser His Leu Glu Glu Ile Ser Glu Glu Gly Ser Lys Ile Glu Ile Pro
        275                 280                 285

Gly Leu Asp Val Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Tyr
    290                 295                 300

Arg Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ser Gln Gly Val Ile
305                 310                 315                 320

Trp Thr Val Phe Asn Glu Thr Val Lys Leu Ser Ala Lys Gln Leu His
                325                 330                 335

Thr Leu Ser Val Ser Leu Trp Gly Pro Arg Asp Ser Arg Leu Gln Leu
            340                 345                 350

Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Thr Ile Glu Ala Ser
        355                 360                 365

Phe Pro Ala Ala Glu Asp Ser Ser Pro Glu Pro Val His Val Asn Ser
    370                 375                 380

Cys Phe Thr Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
385                 390                 395                 400

Ala Val Thr Ser Ile Ala Phe Leu Leu Gln Leu Arg Arg Gln His Arg
                405                 410                 415

His Arg Ser Gly Thr Lys Asp Arg Val Ser Tyr Ser Pro Ala Glu Met
            420                 425                 430

Thr Glu Thr Gly Ala
        435


<210>  1296
<211>  38
<212>  DNA
<213>  Artificial sequence
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<220>
<223> Chemically synthesized primer

<400> 1296
atcgacgcgt gcctgagcga ggtgcagctg gtgcagtc   38

<210> 1297
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 1297
caatggtcac cgtctcttca gctagcacca gg   32

<210> 1298
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 1298
atcccaagct taagccagtc tgtgctgact cagcc   35

<210> 1299
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 1299
ggagggacca aattgaccgt cctaggtcag c   31

<210> 1300
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> Chemically synthesized primer

<400> 1300

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tagggcacgc gtgtgctgag cgaggtgcag ctggtgcagt c                           41


<210>  1301
<211>  32
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  1301
tctagtgcta gctgaagaga cggtgaccat tg                                     32


<210>  1302
<211>  35
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  1302
ctagcaagct tatcccagtc tgtgctgact cagcc                                  35


<210>  1303
<211>  26
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Chemically synthesized primer

<400>  1303
atagcaccta ggacggtcag cttggt                                            26


<210>  1304
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence

<400>  1304

Ser Tyr Ala Met Ser
1               5
```

```
<210>  1305
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa can be any naturally occurring amino acid

<400>  1305

Xaa Tyr Ala Met Xaa
1               5


<210>  1306
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 heavy chain sequence


<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa can be any naturally occurring amino acid

<400>  1306

Ser Tyr Xaa Met Xaa
1               5


<210>  1307
```

```
<211>  17
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR2 heavy chain sequence


<220>
<221>  misc_feature
<222>  (4)..(5)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (8)..(8)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (10)..(11)
<223>  Xaa can be any naturally occurring amino acid

<400>  1307

Ala Ile Ser Xaa Xaa Gly Gly Xaa Thr Xaa Xaa Ala Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  1308
<211>  17
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR2 heavy chain sequence

<400>  1308

Ala Ile Ser Gly Ser Gly Gly Ser Thr Thr Thr Ala Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  1309
```

```
<211>  13
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR3 heavy chain sequence


<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  Xaa can be any naturally occurring amino acid

<400>  1309

Asn Gly Asn Tyr Arg Gly Ser Leu Xaa Ala Phe Asp Ile
1               5                   10


<210>  1310
<211>  14
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR1 light chain sequence

<400>  1310

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1               5                   10


<210>  1311
<211>  7
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Portion of CDR2 light chain sequence

<400>  1311

Gly Asn Asn Asn Arg Pro Ser
1               5


<210>  1312
<211>  12
<212>  PRT
<213>  Artificial sequence
```

<220>
<223> Portion of CDR3 light chain sequence

<400> 1312

Gln Ser Tyr Asp Ser Ser Leu Ser Ala Trp Val Val
1   5   10

<210> 1313
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus sequence

<400> 1313

Glu Glu Asp Leu Pro Glu
1   5

<210> 1314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Portion of the CDR3 heavy chain sequence

<400> 1314

Asn Gly Asn Tyr Arg Gly Ala Phe Asp Ile
1   5   10

<210> 1315
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1315
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg   60

agctgcaaag cgagcggcta tacctttgcg agcgcgtgga tgcattggat gcgccaggcg   120

ccgggccagg gcctggaatg gattggctgg attaacccgg gcaacgtgaa caccaaatat   180

```
aacgaaaaat ttaaaggccg cgcgaccctg accgtggata ccagcaccaa caccgcgtat      240

atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcagcacc      300

tattatcgcc cgctggatta ttggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1316
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1316

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 Ala Ser Ala
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1317
<211>  336
<212>  DNA
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```
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1317
gatattgtga tgacccagag cccggatagc ctggcggtga gcctgggcga acgcgcgacc        60

attaactgca aaagcagcca gagcattctg tatagcagca accagaaaaa ctatctggcg       120

tggtatcagc agaaaccggg ccagagcccg aaactgctga tttattgggc gagcacccgc       180

gaaagcggcg tgccggatcg ctttagcggc agcggcagcg gcaccgattt taccctgacc       240

attagcagcc tgcaggcgga agatgtggcg gtgtattatt gccatcagta tatgagcagc       300

tatacctttg gccagggcac caaactggaa attaaa                                 336


<210>  1318
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1318

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95
```

```
Tyr Met Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1319
<211>  981
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1319
gcgagcacca aaggcccgag cgtgtttccg ctggcgccgt gcagccgcag caccagcgaa        60

agcaccgcgg cgctgggctg cctggtgaaa gattattttc cggaaccggt gaccgtgagc       120

tggaacagcg gcgcgctgac cagcggcgtg catacctttc cggcggtgct gcagagcagc       180

ggcctgtata gcctgagcag cgtggtgacc gtgccgagca gcagcctggg caccaaaacc       240

tatacctgca acgtggatca taaaccgagc aacaccaaag tggataaacg cgtggaaagc       300

aaatatggcc cgccgtgccc gagctgcccg gcgccggaat ttctgggcgg cccgagcgtg       360

tttctgtttc cgccgaaacc gaaagatacc ctgatgatta gccgcacccc ggaagtgacc       420

tgcgtggtgg tggatgtgag ccaggaagat ccggaagtgc agtttaactg gtatgtggat       480

ggcgtggaag tgcataacgc gaaaaccaaa ccgcgcgaag aacagtttaa cagcacctat       540

cgcgtggtga gcgtgctgac cgtgctgcat caggattggc tgaacggcaa agaatataaa       600

tgcaaagtga gcaacaaagg cctgccgagc agcattgaaa aaaccattag caaagcgaaa       660

ggccagccgc gcgaaccgca ggtgtatacc ctgccgccga gcccggaaga aatgaccaaa       720

aaccaggtga gcctgacctg cctggtgaaa ggcttttatc cgagcgatat tgcggtggaa       780

tgggaaagca acggccagcc ggaaaacaac tataaaacca ccccgccggt gctggatagc       840

gatggcagct ttttctgta tagccgcctg accgtggata aaagccgctg gcaggaaggc        900

aacgtgttta gctgcagcgt gatgcatgaa gcgctgcata accattatac ccagaaaagc       960

ctgagcctga gcctgggcaa a                                                 981


<210>  1320
<211>  327
<212>  PRT
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```
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1320

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15


Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80


Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95


Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110


Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125


Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140


Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160


Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175


Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
```

```
            180                 185                 190


Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205


Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220


Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Pro Glu Glu Met Thr Lys
225                 230                 235                 240


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270


Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285


Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320


Leu Ser Leu Ser Leu Gly Lys
                325


<210>  1321
<211>  975
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1321
accaaaggcc cgagcgtgtt tccgctggcg ccgtgcagcc gcagcaccag cgaaagcacc        60

gcggcgctgg gctgcctggt gaaagattat tttccggaac cggtgaccgt gagctggaac       120
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agcggcgcgc tgaccagcgg cgtgcatacc tttccggcgg tgctgcagag cagcggcctg 180

tatagcctga gcagcgtggt gaccgtgccg agcagcagcc tgggcaccaa aacctatacc 240

tgcaacgtgg atcataaacc gagcaacacc aaagtggata aacgcgtgga aagcaaatat 300

ggcccgccgt gcccgccgtg cccggcgccg gaatttctgg gcggcccgag cgtgtttctg 360

tttccgccga aaccgaaaga taccctgatg attagccgca ccccggaagt gacctgcgtg 420

gtggtggatg tgagccagga agatccggaa gtgcagttta actggtatgt ggatggcgtg 480

gaagtgcata acgcgaaaac caaaccgcgc gaagaacagt ttaacagcac ctatcgcgtg 540

gtgagcgtgc tgaccgtgct gcatcaggat tggctgaacg gcaaagaata taaatgcaaa 600

gtgagcaaca aaggcctgcc gagcagcatt gaaaaaacca ttagcaaagc gaaaggccag 660

ccgcgcgaac cgcaggtgta taccctgccg ccgagcccgg aagaaatgac caaaaaccag 720

gtgagcctga cctgcctggt gaaaggcttt tatccgagcg atattgcggt ggaatgggaa 780

agcaacggcc agccggaaaa caactataaa accaccccgc cggtgctgga tagcgatggc 840

agcttttttc tgtatagcaa actgaccgtg gataaaagcc gctggcagga aggcaacgtg 900

tttagctgca gcgtgatgca tgaagcgctg cataaccatt atacccagaa aagcctgagc 960

ctgagcctgg gcaaa 975

<210> 1322
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1322

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
1 5 10 15

Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
20 25 30

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
35 40 45

```
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
    50                  55                  60


Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr
65                  70                  75                  80


Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
                85                  90                  95


Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
            100                 105                 110


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        115                 120                 125


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    130                 135                 140


Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
145                 150                 155                 160


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
                165                 170                 175


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            180                 185                 190


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
        195                 200                 205


Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    210                 215                 220


Gln Val Tyr Thr Leu Pro Pro Ser Pro Glu Glu Met Thr Lys Asn Gln
225                 230                 235                 240


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                245                 250                 255
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            260                 265                 270


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        275                 280                 285


Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
    290                 295                 300


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
305                 310                 315                 320


Leu Ser Leu Gly Lys
                325


<210>  1323
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1323

Gly Tyr Thr Phe Ala Ser Ala Trp
1               5


<210>  1324
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1324

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1325
<211>  8
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1325

Ile Asn Pro Gly Asn Val Asn Thr
1   5

<210> 1326
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1326

Trp Ala Ser Thr Arg Glu
1   5

<210> 1327
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1327

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
1   5

<210> 1328
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1328

His Gln Tyr Met Ser Ser Tyr Thr
1   5

<210> 1329
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1329
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg 60

tcctgcaagg ccagcggcta caccttcgcc agccaatgga tgcactggat gcggcaggca 120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac 180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc 300

tggtaccggc cgctggacta ctggggccag ggcaccctgg tgaccgtgag cagc 354

<210> 1330
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1330

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 Ala Ser Gln
            20   25   30

Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1331
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1331
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc       60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg      180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc      240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta catcagcagc      300

tacaccttcg gccagggcac aaagctggaa atcaag                                336


<210>  1332
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1332

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 Ile Leu Tyr Ser
            20                  25                  30
```

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 His Gln
                85   90   95

Tyr Ile Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 1333
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1333
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg   60

tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca   120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac   180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac   240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacg   300

tggtatcggc cgaatgacta ctggggccag ggcaccctgg tgaccgtgag cagc   354

<210> 1334
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1334

```
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 Ala Ser Ser
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Asn Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1335
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1335
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc        60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc       120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg       180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc       240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta caaaagcagc       300
```

```
tacaccttcg gccagggcac aaagctggaa atcaag                               336


<210>  1336
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1336

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Lys Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1337
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1337
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60
```

```
tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaaccacc      300

cgttatcggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1338
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1338

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 Ala Ser Ser
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Thr Arg Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

<210> 1339
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1339
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc 60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg 180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc 240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta ccgtagcagc 300

tacaccttcg gccagggcac aaagctggaa atcaag 336

<210> 1340
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1340

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Arg Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1341
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1341
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60

tcctgcaagg ccagcggcta caccttcgcc agccaatata tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagactgacc      300

tattatcggc cgccggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1342
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1342

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 Ala Ser Gln
            20                  25                  30


Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1343
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1343
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc       60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg      180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc      240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta ctatagcagc      300

tacaccttcg gccagggcac aaagctggaa atcaag                                336


<210>  1344
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1344
```

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Tyr Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1345
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1345

Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  1346
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1346
```

```
Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  1347
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1347

Gly Tyr Thr Phe Ala Ser Ser Trp
1               5


<210>  1348
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1348

Ser Thr Trp Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1349
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1349

Ser Thr Trp Tyr Arg Pro Asn Asp Tyr
1               5


<210>  1350
<211>  9
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Synthetic Oligopeptide

<400>  1350

Thr Thr Arg Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1351
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1351

Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr
1               5


<210>  1352
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1352

His Gln Tyr Leu Ser Ser Tyr Thr
1               5


<210>  1353
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1353

His Gln Tyr Ile Ser Ser Tyr Thr
1               5


<210>  1354
```

```
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1354

His Gln Tyr Lys Ser Ser Tyr Thr
1               5


<210>  1355
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1355

His Gln Tyr Arg Ser Ser Tyr Thr
1               5


<210>  1356
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1356

His Gln Tyr Tyr Ser Ser Tyr Thr
1               5


<210>  1357
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1357
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60
```

```
tcctgcaagg ccagcggcta caccttcgcc agctactaca tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc      300

tactaccggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354
```

<210> 1358
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1358

```
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 Ala Ser Tyr
            20                  25                  30


Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

<210> 1359
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1359

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gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc       60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg      180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc      240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta cctgagcagc      300

tacaccttcg gccagggcac aaagctggaa atcaag                                336
```

<210> 1360
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1360

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85   90   95

Tyr Leu Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 1361
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1361
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc   60

tcctgcaaga cttctggata caccttcacc gaccactata tccactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggatgg atcaacccta gcagtggtgg cacagagtat   180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgcccattag cacggcctac   240

atggatctga gcgggctgag atctgacgac acggccgttt attactgtgc gagagagact   300

atcggtggct ggaacgcttt ggacgtctgg ggccaaggaa ccctggtcac cgtctcctca   360

<210> 1362
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Polypeptide

<400> 1362

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

```
Gly Trp Ile Asn Pro Ser Ser Gly Gly Thr Glu Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Pro Ile Ser Thr Ala Tyr
65                  70                  75                  80


Met Asp Leu Ser Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1363
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Polynucleotide

<400>  1363
cagcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga attaatactg taaactggta ccagcagctc      120

ccaagaacgc ccccaaact cctcatctat actaataatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctgacacc tcagcctccc tggccatcag tggcctccag      240

tctgaggatg aggctgatta ttactgtgca gcttgggatg acaccctgaa tggtccacta      300

ttcggcggag ggaccaaggt gaccgtccta ggt                                   333


<210>  1364
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1364
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```
Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Arg Thr Pro Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Asp Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Thr Leu
                85                  90                  95


Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110
```

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<210>  1365
<211>  357
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1365
gaggtgcagc tggtgcagtc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat      180

gcacagaagt ttcagggcag ggtcaccgtg accacagaca cgtccacgag cacagcctac      240

atggagctga ggagcctgag atctgacgac acggccgtct attactgtgc gagagagggt      300

gttcactcgg atgcttttga tgtgtggggc caagggacca cggtcaccgt ctcctca         357


<210>  1366
```

```
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1366

Glu Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Val 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 Glu Gly Val His Ser Asp Ala Phe Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  1367
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1367
gaaacgacac tcacgcagtc tccagccacc ctgtctgtgt ctccagggga aagggccacc       60
```

```
ctctcctgca gggccagtca gagtgtttac accaacttag cctggtacca acagaaacct      120

ggccaggctc ccagtctcct catctatggt gcatccagcc gggccaccgg catcccagac      180

agattcagtg gcagcgggtc tgggacagac ttcactctca ccatcagcag actggagcct      240

gaagattttg cagtgtatta ctgtcagcag tatggtagct cacatttcac tttcggccct      300

gggaccaaag tggatatcaa a                                                321


<210>  1368
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1368

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


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Thr Asn
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ser Leu Leu Ile
        35                  40                  45


Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser His Phe
                85                  90                  95


Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  1369
<211>  360
<212>  DNA
```

<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1369
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc   60

tcctgcaaga cttctggata caccttcacc gaccactata tccactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggatgg atcaacccta gcagtggtgg cacagagtat   180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgcccattag cacggcctac   240

atggatctga gcgggctgag atctgacgac acggccgttt attactgtgc gagagagact   300

atcggtggct ggaacgcttt ggacgtctgg ggccaaggga ccacggtcac cgtctcctca   360

<210> 1370
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1370

Glu 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 Thr Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asn Pro Ser Ser Gly Gly Thr Glu Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Pro Ile Ser Thr Ala Tyr
65   70   75   80

Met Asp Leu Ser Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  1371
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1371
cagtctgtgc tgactcagcc accctcagcg tctgggtccc ccgggcagag ggtcaccatg       60

tcttgctctg gaagcagctc caccatcggg aggcattctg taaactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat gctaacaatc agcggccctc aggggtccct      180

ggccgattct ctgcctccaa gtctgacacc tcagcctccc tggccatcag tgggctccgg      240

tccgaggatg aggctaatta ttactgtgca gcgtgggatg acagtctcag tggcgtgctc      300

tttggcggtg ggaccaaggt gaccgtccta ggt                                   333


<210>  1372
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1372

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Arg Val Thr Met Ser Cys Ser Gly Ser Ser Ser Thr Ile Gly Arg His
            20                  25                  30


Ser Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45
```

```
Ile Tyr Ala Asn Asn Gln Arg Pro Ser Gly Val Pro Gly Arg Phe Ser
    50                  55                  60


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


Ser Glu Asp Glu Ala Asn Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Ser Gly Val Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  1373
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1373
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaaga cttctggata caccttcacc gaccactata tccactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcaacccta gcagtggtgg cacagagtat      180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgcccattag cacggcctac      240

atggatctga gcgggctgag atctgacgac acggccgttt attactgtgc gagagagact      300

atcggtggct ggaacgcttt ggacgtctgg ggccaaggca ccctggtcac cgtctcctca      360


<210>  1374
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1374

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Ser Ser Gly Gly Thr Glu Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Pro Ile Ser Thr Ala Tyr
65                  70                  75                  80


Met Asp Leu Ser Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1375
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1375
ctgcctgtgc tgactcagcc accctcagtg tcagtggccc caggacagac ggccaggata       60

acctgtgggg gacacaagat tggaactaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tactggtcgt ctatgatgat cgcgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gggcacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg gatagtaata gtgatcatgt ggtgttcggc      300

ggagggacca agctgaccgt cctaagt                                          327


<210>  1376
```

```
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1376

Met Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly His Lys Ile Gly Thr Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45


Asp Asp Arg Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Gly Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Asn Ser Asp His
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
            100                 105


<210>  1377
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1377
gaggtgcagc tggtgcagtc tggggctgat gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggata caccttcacc ggctactata tacactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat      180
```

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtct atttttgtgt gagagaggtg 300

aaagattact attattacat ggacgtctgg ggcagaggga ccacggtcac cgtctcctca 360

<210> 1378
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1378

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln 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 Phe Cys
85 90 95

Val Arg Glu Val Lys Asp Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1379
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1379
aattttatgc tgactcagcc ccactctgtg tcggaatctc cggggaagac ggttaccatc   60

tcgtgcaccc gcagcagcgg cagcattgcc agcaactccg tgcagtggta cctgcagcgc   120

ccgggcagtg cccccaccac tctgatcttt gacaataaac aaagaccgtc tggggtccct   180

gatcgcttct ctggctccat cgacagctcc tccaactctg cctccctcag catctctggg   240

ctgacgactg aggacgaggc tgactatttc tgtcagtctt atgatgacag tgagcaagtg   300

gtgttcggcg gagggaccaa gctgaccgtc ctaagt   336

<210> 1380
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1380

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
            20   25   30

Ser Val Gln Trp Tyr Leu Gln Arg Pro Gly Ser Ala Pro Thr Thr Leu
        35   40   45

Ile Phe Asp Asn Lys Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Ser Ile Ser Gly
65   70   75   80

Leu Thr Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr Asp Asp
                85   90   95

```
Ser Glu Gln Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
            100                 105                 110


<210>  1381
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1381
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc        60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc       120

cctggacaag ggcttgagtg gttggggtgg gtcaaccctc acagtggtgg cacaaactat       180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac       240

atggagctga gcagactgag atctgacgac acggccgtat attactgtgc gagagagact       300

gatatctctg ctaattatca ctttgactac tggggccagg gcaccctggt caccgtctcc       360

tca                                                                     363


<210>  1382
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1382

Glu Val Gln 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 Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
        35                  40                  45


Gly Trp Val Asn Pro His Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
```

```
    50                  55                  60


Gln 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 Glu Thr Asp Ile Ser Ala Asn Tyr His Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1383
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1383
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgatgttggg agttataacg ctgtctcctg gtaccaacac      120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaagcggcc ctcaggggtt      180

tctaatcggt tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc      240

cgggctgagg acgaggctga ttattattgt gcaacatggg atgacagcct gaaaggtccg      300

gtgttcggcg gagggaccaa gctgaccgtc ctgggt                                336


<210>  1384
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1384

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
```

```
1               5                   10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
            20                  25                  30


Asn Ala Val Ser Trp Tyr Gln His His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Arg Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser
                85                  90                  95


Leu Lys Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


Glu



<210>  1385
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1385
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc        60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc       120

cctggacaag ggcttgaatg gatgggatgg atcaacccta aaactggtga cacaaactat       180

gcacagaagt ttcagggcag ggtcgccttg agcagggaca cgtccttcaa cacagcctac       240

atggacctga gcagcctcag atctgacgac acggccgtct attactgtgc gagagagggc       300

ctgtcgacca gcagtcccct tgactactgg ggccagggaa ccctggtcac cgtctcctca       360
```

<210> 1386
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1386

```
Glu 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 Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Lys Thr Gly Asp Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Ala Leu Ser Arg Asp Thr Ser Phe Asn Thr Ala Tyr
65                  70                  75                  80


Met Asp Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Gly Leu Ser Thr Ser Ser Pro Leu Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 1387
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1387

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cagcctgggc tgactcagcc accctcagtg tcagtggccc caggacagtc ggccaagatt       60

acctgtggag aaaacgaact tgcaacaaat attgtacact ggtaccagca gaagccaggc      120

caggcccctg tgctggtcat ctatcatgat aacgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaacgctgg gaacacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg acttttactg tcagctgtgg gatagtgcta gtgatcaagt ggtcttcggc      300

ggagggacca cgttgaccgt cctaggt                                          327


<210>  1388
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1388

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Ser Ala Lys Ile Thr Cys Gly Glu Asn Glu Leu Ala Thr Asn Ile Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


His Asp Asn Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ala Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Phe Tyr Cys Gln Leu Trp Asp Ser Ala Ser Asp Gln
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Thr Leu Thr Val Leu Gly
            100                 105


<210>  1389
```

<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1389
gaggtgcagc tggtgcagtc aggggctgag gtgaagaggc ctggggcctc attgaaggtt 60

tcctgcaagg catctggata caccttcacc agccactata tacactgggt gcgacaggcc 120

cccggacaag ggcttgagtg gatgggatgg atcaacactg gcaatggtga cacaagatat 180

tcacagaggt tccagggcag agtcaccgtt accagggaca catccgcgag cacagtctac 240

atggaactga gcagcctgag atctgaagac acggccgtgt attactgtgc gagagagtct 300

agcagcagct ggtttgttgc ttttgatgtc tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 1390
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1390

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

Ser Leu Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser His
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asn Thr Gly Asn Gly Asp Thr Arg Tyr Ser Gln Arg Phe
    50   55   60

Gln Gly Arg Val Thr Val Thr Arg Asp Thr Ser Ala 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 Ser Ser Ser Ser Trp Phe Val Ala Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1391
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1391
cagcctgtgc tgactcagcc accctcggtg tcattggccc caggacagac ggccaggatt 60

acctgttcgg aaaagaacat tcgaagtaaa agagtgcact ggtaccagca gaagccaggc 120

caggcccctg tcctggtcat gtattctgat aacggccggc gctcagggat ccctgaccga 180

ttttctggct ccaactctgg gaacacggcc accctgacca tcaccagggt cgaagccggt 240

gatgagggcg acttttactg tcaggtgtgg gatccgatta ctgatcaggt ggttttcggc 300

ggagggacca agctgaccgt cctaggt 327

<210> 1392
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1392

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Leu Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Ser Glu Lys Asn Ile Arg Ser Lys Arg Val
20 25 30

```
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Met Tyr
        35                  40                  45


Ser Asp Asn Gly Arg Arg Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Gly Asp Phe Tyr Cys Gln Val Trp Asp Pro Ile Thr Asp Gln
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>  1393
<211>  372
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1393
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tcctgtaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc       120

cctggagaag ggcttgagtg gctgggatgg atcaaccctc acagtggtgg cacaaactat       180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac       240

atggagctga gcagcctgag atctgaggac acggctgtgt attactgtgc gagggagatt       300

gtggtggtga ctgctccggc tgctgcggct atggacgtct ggggccaagg caccctggtc       360

accgtctcct ca                                                           372


<210>  1394
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
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<400> 1394

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Gln Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Leu
        35   40   45

Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln 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 Glu Ile Val Val Val Thr Ala Pro Ala Ala Ala Ala Met Asp
            100   105   110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1395
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1395
cagtctgtgc tgactcagcc accctccgcg tccgggtctc ctggacagtc agtcaccatc   60

tcctgcactg gaagcagcag tgacgttgct atttatgacc gtgtctcctg gtaccagcag   120

cccccaggca cagcccccaa actcattctt tatgatgtcc atgatcggcc ctcaggggtc   180

cctgatcgct tctctgggtc caagtctggc aacacggcct ccctgaccat ctctgggctc   240

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caggctgagg acgaggctga ttattactgc agttcataca caaccagcgg cacttttgtc      300

ttcggaagtg ggaccaaggt caccgtccta ggt                                   333


<210>  1396
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1396

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asp Val Ala Ile Tyr
            20                  25                  30


Asp Arg Val Ser Trp Tyr Gln Gln Pro Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45


Ile Leu Tyr Asp Val His Asp Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Ser
                85                  90                  95


Gly Thr Phe Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  1397
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1397
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gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaacgtc        60

tcctgtaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggatgg atcaacccca acagtggtgg cacaaactat       180

gcacagaagt ttcagggcag ggtcaccgtg accacagaca cgtccaacag cacagcctac       240

atggagctga acaggctgaa atctgacgac acggccgtgt attattgtgc gagagagggg       300

tccggggacc ttgattcctt atacatggac gtctggggca aagggacaat ggtcaccgtc       360

tcttca                                                                  366


<210>  1398
<211>  324
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1398
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acctgtgggg caaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc       120

caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga       180

ttctctggct ccaactctgg gaacacggcc accctgacca tcaccagggt cgaagccggg       240

gatgaggccg actattactg tcagctatgg gatggtggga gtgatgtggt tttcggcgga       300

gggaccaagc tgaccgtcct aggt                                              324


<210>  1399
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1399

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Asn Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
```

```
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Val Thr Thr Asp Thr Ser Asn Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Asn Arg Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Gly Ser Gly Asp Leu Asp Ser Leu Tyr Met Asp Val Trp
            100                 105                 110


Gly Lys Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1400
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1400

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Ala Asn Asn Ile Gly Ser Lys Ser Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45


Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
```

```
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Leu Trp Asp Gly Gly Ser Asp Val
                85                  90                  95


Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>  1401
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1401
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaaga cttctggata caccttcacc gaccactata tccactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcaacccta gcagtggtgg cacagagtat      180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgcccattag cacggcctac      240

atggatctga gcgggctgag atctgacgac acggccgttt attactgtgc gagagagact      300

atcggtggct ggaacgcttt ggacgtctgg ggccaaggaa ccctggtcac cgtctcctca      360


<210>  1402
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1402

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30
```

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asn Pro Ser Ser Gly Gly Thr Glu Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Pro Ile Ser Thr Ala Tyr
65   70   75   80

Met Asp Leu Ser Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1403
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1403
cagcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc   60

tcttgttctg gaagcagctc caacatcgga attaatactg taaactggta ccagcagctc   120

ccaagaacgc ccccaaact cctcatctat actaataatc agcggccctc aggggtccct   180

gaccgattct ctggctccaa gtctgacacc tcagcctccc tggccatcag tggcctccag   240

tctgaggatg aggctgatta ttactgtgca gcttgggatg acaccctgaa tggtccacta   300

ttcggcggag ggaccaaggt gaccgtccta ggt   333

<210> 1404
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1404

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Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Arg Thr Pro Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Asp Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Thr Leu
                85                  90                  95


Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110
```

<210> 1405
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1405

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Gly Tyr Thr Phe Thr Asp His Tyr
1               5
```

<210> 1406
<211> 8
<212> PRT
<213> Artificial Sequence

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<220>
<223>  Synthetic Oligopeptide

<400>  1406

Ile Asn Pro Ser Ser Gly Gly Thr
1               5


<210>  1407
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1407

Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val
1               5                   10


<210>  1408
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1408

Ser Ser Asn Ile Gly Ile Asn Thr
1               5


<210>  1409
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1409

Thr Asn Asn
1


<210>  1410
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```
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1410

Ala Ala Trp Asp Asp Thr Leu Asn Gly Pro Leu
1               5                   10


<210>  1411
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1411

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210>  1412
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1412

Ile Asn Pro Asn Ser Gly Gly Thr
1               5


<210>  1413
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1413

Ala Arg Glu Gly Val His Ser Asp Ala Phe Asp Val
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```
1               5                   10


<210>  1414
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1414

Gln Ser Val Tyr Thr Asn
1               5


<210>  1415
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1415

Gly Ala Ser
1


<210>  1416
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  57

<400>  1416

Gln Gln Tyr Gly Ser Ser His Phe Thr
1               5


<210>  1417
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide
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<400>  1417

Gly Tyr Thr Phe Thr Asp His Tyr
1               5


<210>  1418
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1418

Ile Asn Pro Ser Ser Gly Gly Thr
1               5


<210>  1419
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1419

Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val
1               5                   10


<210>  1420
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1420

Ser Ser Thr Ile Gly Arg His Ser
1               5


<210>  1421
<211>  3
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1421

Ala Asn Asn
1

<210> 1422
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1422

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Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Leu
1               5                   10
```

<210> 1423
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1423

```
Gly Tyr Thr Phe Thr Asp His Tyr
1               5
```

<210> 1424
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1424

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Ile Asn Pro Ser Ser Gly Gly
1               5
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```
<210>  1425
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1425

Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val
1               5                   10


<210>  1426
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1426

Lys Ile Gly Thr Lys Ser
1               5


<210>  1427
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1427

Asp Asp Arg
1


<210>  1428
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1428
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```
Gln Val Trp Asp Ser Asn Ser Asp His Val Val
1               5                   10


<210>  1429
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1429

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210>  1430
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1430

Ile Asn Pro Asn Ser Gly Gly Thr
1               5


<210>  1431
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1431

Val Arg Glu Val Lys Asp Tyr Tyr Tyr Tyr Met Asp Val
1               5                   10


<210>  1432
<211>  8
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> Synthetic Oligopeptide

<400> 1432

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Ser Gly Ser Ile Ala Ser Asn Ser
1               5
```

<210> 1433
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1433

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Asp Asn Lys
1
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<210> 1434
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1434

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Gln Ser Tyr Asp Asp Ser Glu Gln Val Val
1               5                   10
```

<210> 1435
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1435

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Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5
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<210> 1436

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<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1436

Val Asn Pro His Ser Gly Gly Thr
1               5


<210>  1437
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1437

Ala Arg Glu Thr Asp Ile Ser Ala Asn Tyr His Phe Asp Tyr
1               5                   10


<210>  1438
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1438

Ser Ser Asp Val Gly Ser Tyr Asn Ala
1               5


<210>  1439
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1439

Glu Val Ser
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1


<210>  1440
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1440

Ala Thr Trp Asp Asp Ser Leu Lys Gly Pro Val
1               5                   10


<210>  1441
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1441

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210>  1442
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1442

Ile Asn Pro Lys Thr Gly Asp Thr
1               5


<210>  1443
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide
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<400> 1443

Ala Arg Glu Gly Leu Ser Thr Ser Ser Pro Leu Asp Tyr
1   5   10

<210> 1444
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1444

Glu Leu Ala Thr Asn Ile
1   5

<210> 1445
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1445

His Asp Asn
1

<210> 1446
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1446

Gln Leu Trp Asp Ser Ala Ser Asp Gln Val Val
1   5   10

<210> 1447
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1447

Gly Tyr Thr Phe Thr Ser His Tyr
1   5

<210> 1448
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1448

Ile Asn Thr Gly Asn Gly Asp Thr
1   5

<210> 1449
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1449

Ala Arg Glu Ser Ser Ser Ser Trp Phe Val Ala Phe Asp Val
1   5   10

<210> 1450
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1450

Asn Ile Arg Ser Lys Arg
1   5

```
<210>  1451
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1451

Ser Asp Asn
1


<210>  1452
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1452

Gln Val Trp Asp Pro Ile Thr Asp Gln Val Val
1               5                   10


<210>  1453
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1453

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210>  1454
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligopeptide

<400>  1454
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Ile Asn Pro His Ser Gly Gly Thr
1   5

<210> 1455
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1455

Ala Arg Glu Ile Val Val Val Thr Ala Pro Ala Ala Ala Ala Met Asp
1   5   10   15

Val

<210> 1456
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1456

Ser Ser Asp Val Ala Ile Tyr Asp Arg
1   5

<210> 1457
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1457

Asp Val His
1

<210> 1458

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1458

Ser Ser Tyr Thr Thr Ser Gly Thr Phe Val
1   5   10

<210> 1459
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1459

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1   5

<210> 1460
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1460

Ile Asn Pro Asn Ser Gly Gly Thr
1   5

<210> 1461
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1461

Ala Arg Glu Gly Ser Gly Asp Leu Asp Ser Leu Tyr Met Asp Val

1   5   10   15

<210> 1462
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1462

Asn Ile Gly Ser Lys Ser
1   5

<210> 1463
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1463

Asp Asp Ser
1

<210> 1464
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1464

Gln Leu Trp Asp Gly Gly Ser Asp Val Val
1   5   10

<210> 1465
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1465

Gly Tyr Thr Phe Thr Asp His Tyr
1   5

<210> 1466
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1466

Ile Asn Pro Ser Ser Gly Gly Thr
1   5

<210> 1467
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1467

Ala Arg Glu Thr Ile Gly Gly Trp Asn Ala Leu Asp Val
1   5   10

<210> 1468
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1468

Ser Ser Asn Ile Gly Ile Asn Thr
1   5

<210> 1469
<211> 3
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1469

Thr Asn Asn
1

<210> 1470
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1470

Ala Ala Trp Asp Asp Thr Leu Asn Gly Pro Leu
1   5   10

<210> 1471
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1471
caggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcaatt atatcatttg atggaagtaa aaaatattat   180

gcaaactccg tgaagggccg atccaccatc tccagagaca attccaagaa cacgctgtct   240

ctgcaaatga acagcctggg acctgaggac acggctctat attactgtgc gaaactgccc   300

tccccgtatt actttgatag tcggttcgtg tgggtcgccg ccagcgcatt tcacttctgg   360

ggccagggaa tcctggtcac cgtctcttca   390

<210> 1472
<211> 130
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 1472

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

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser
65 70 75 80

Leu Gln Met Asn Ser Leu Gly Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Ser Pro Tyr Tyr Phe Asp Ser Arg Phe Val Trp Val
100 105 110

Ala Ala Ser Ala Phe His Phe Trp Gly Gln Gly Ile Leu Val Thr Val
115 120 125

Ser Ser
130

<210> 1473
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic polypeptide

<400> 1473

```
Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
            20                  25                  30


Thr Val His Trp Phe Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Ser Leu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Gln Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1474
<211>  330
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  1474
aattttatgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgctctg gaagcagctc caacatcgga ggtaatactg tacactggtt ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat actaatagtc tgcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggata acagcctaaa tggtcaggtg      300

ttcggcggag ggaccaagct gaccgtccta                                       330


<210>  1475
```

```
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  1475

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
            20                  25                  30


Thr Val His Trp Phe Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Ser Leu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asn Ser Leu
                85                  90                  95


Asn Gly Gln Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1476
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  1476

Gly Phe Thr Phe Ser Asn Tyr Gly
1               5


<210>  1477
```

```
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic oligopeptide

<400>  1477

Ile Ser Phe Asp Gly Ser Lys Lys
1               5


<210>  1478
<211>  25
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide

<400>  1478

Cys Ala Lys Leu Pro Ser Pro Tyr Tyr Phe Asp Ser Arg Phe Val Trp
1               5                   10                  15


Val Ala Ala Ser Ala Phe His Phe Trp
            20                  25


<210>  1479
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic oligopeptide

<400>  1479

Ser Ser Asn Ile Gly Gly Asn Thr
1               5


<210>  1480
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic oligopeptide
```

<400> 1480

Thr Asn Ser
1

<210> 1481
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<400> 1481

```
Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Gln Val Phe
1               5                   10
```

<210> 1482
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 1453

<400> 1482

```
Cys Ala Ala Trp Asp Asn Ser Leu Asn Gly Gln Val Phe
1               5                   10
```

<210> 1483
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligopeptide

<400> 1483

```
Gly Asn Thr Asn Arg Pro Ser
1               5
```

<210> 1484
<211> 5
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  1484

Gly Gly Gly Gly Ser
1               5


<210>  1485
<211>  372
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-14

<400>  1485
caggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc        60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat       180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac       240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagctcta       300

cctagtggga ctatactggt cggaggttgg ttcgacccct ggggccaggg aaccctggtc       360

accgtctcct ca                                                           372


<210>  1486
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-14

<400>  1486

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
```

```
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


Gln 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 Ala Leu Pro Ser Gly Thr Ile Leu Val Gly Gly Trp Phe Asp
            100                 105                 110


Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1487
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-14

<400>  1487
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc       60

tcctgcaccc gcagcagtgg caacattgcc agcaattatg tgcagtggta ccaacagcgc      120

ccgggcagtg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct      180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga      240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgatagcag caatctttgg      300

gtgttcggcg gagggaccaa gctgaccgtc cta                                   333


<210>  1488
<211>  111
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  Variable light chain of Ab-14

<400>  1488

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15


Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Asn Ile Ala Ser Asn
            20                  25                  30


Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45


Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85                  90                  95


Ser Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1489
<211>  372
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-16

<400>  1489
gaggtgcagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc        60

tcctgtgcag cctctggatt cacctttagc agctatgccc tgagctgggt ccgccaggct       120

ccagggaagg ggctggagtg ggtctcagct attagtggtg gtggtggtag cacatactac       180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagacgtg       300
```

```
tttccagaga ctttttcgat gaactacggt atggacgtct ggggccaagg aaccctggtc      360

accgtctcct ca                                                          372


<210>  1490
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain Ab-16

<400>  1490

Glu Val Gln Leu Val Gln 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 Ser Tyr
            20                  25                  30


Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Val Phe Pro Glu Thr Phe Ser Met Asn Tyr Gly Met Asp
            100                 105                 110


Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1491
<211>  324
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  Variable light chain of Ab-16

<400>  1491
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc       60

acatgccaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga      120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga      180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa      240

gatgaggctg actattactg taactcccgg gacagcagtg gtaaccatta tgtcttcgga      300

actgggacca aggtcaccgt ccta                                             324


<210>  1492
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-16

<400>  1492

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
                85                  90                  95


Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
```

            100   105

<210> 1493
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-22

<400> 1493
```
caggtgcagc tggtgcagtc tgggggaggc gtggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgtcaagct      120

ccagggaagg gtctggagtg ggtctctctt attagtgggg atggtggtag cacatactat      180

gcagactctg tgaagggccg attcaccatc tccagagaca acagcaaaaa ctccctgtat      240

ctgcaaatga acagtctgag aactgaggac accgccttgt attactgtgc aaaagtgctc      300

ctcccctgta gtagtaccag ctgctatgga agcgtcggtg cttttgatat ctggggccaa      360

gggaccacgg tcaccgtctc ctca                                             384
```

<210> 1494
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-22

<400> 1494

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Ser Gly Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Leu Leu Pro Cys Ser Ser Thr Ser Cys Tyr Gly Ser Val
            100   105   110

Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 1495
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain Ab-22

<400> 1495
taggacgatg agctcggtcc cagctccgaa gacataatga tcactattat tatcccacac   60

ctgacagtaa taatcggcct catcaccggc ttcgaccctg ctgatggtca gggtggccgt   120

gttcccagag ttggagccag agaatcgctc agagatccct gagggccggt ccctatcaga   180

gtagatgacc aacgcagggg cctggcctgg cttctgctgg taccagtgca cactcttcct   240

tccaatgtcg cttcccccac aggtaatcct ggccgtcttt cctggggcca ctgacactga   300

gggtgcctga gtcagcacag gcag   324

<210> 1496
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-22

<400> 1496

Leu Pro Val Leu Thr Gln Ala Pro Ser Val Ser Val Ala Pro Gly Lys
1   5   10   15

Thr Ala Arg Ile Thr Cys Gly Gly Ser Asp Ile Gly Arg Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ala Leu Val Ile Tyr
35 40 45

Ser Asp Arg Asp Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Asn Ser Asp His
85 90 95

Tyr Val Phe Gly Ala Gly Thr Glu Leu Ile Val Leu
100 105

<210> 1497
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-30

<400> 1497
caggtgcagc tggtgcagtc tgggggaagt gtggtacggc ctggggaatc cctcagactc 60

tcctgtgtag cctctggatt catctttgat aattatgaca tgagttgggt ccgccaagtt 120

ccagggaagg ggctggagtg ggtctctcgt gttaattgga atggtggtag cacaacttat 180

gcagacgctg tgaagggccg attcaccatc tccagagaca acaccaagaa ctccctgtat 240

ctacaaatga acaacctgag agccgaagac acggccgtgt attactgtgt gcgcgagttt 300

gtcggtgctt atgatctctg gggccagggg accacggtca ccgtctcctc a 351

<210> 1498
<211> 117
<212> PRT
<213> Artificial Sequence

```
<220>
<223>  Variable heavy chain of Ab-30

<400>  1498

Gln Val Gln Leu Val Gln Ser Gly Gly Ser Val Val Arg Pro Gly Glu
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Asp Asn Tyr
            20                  25                  30


Asp Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Arg Glu Phe Val Gly Ala Tyr Asp Leu Trp Gly Gln Gly Thr Thr
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  1499
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-30

<400>  1499
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa      120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcaggggtt      180
```

```
tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcac tctgccgttc      300

ggcggaggga ccaagctgac cgtccta                                          327


<210>  1500
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-30

<400>  1500

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95


Thr Leu Pro Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1501
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-31
```

```
<400>  1501
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc caggggccac agtgaaggtc       60

tcctgcaagg tttttggaga caccttccgc ggcctctata tacactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag agtcacgatt accacggacg aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagcggacta      300

cgttggggga tctggggctg gttcgacccc tggggccagg gcaccctggt caccgtctcc      360

tca                                                                    363


<210>  1502
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-31

<400>  1502

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Thr Val Lys Val Ser Cys Lys Val Phe Gly Asp Thr Phe Arg Gly Leu
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Thr Asp Glu 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 Ser Gly Leu Arg Trp Gly Ile Trp Gly Trp Phe Asp Pro Trp Gly
```

```
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1503
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-31

<400>  1503
gaaattgtgt tgacgcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca gggccagtca gagtattggc aacagcttag cctggtacca gcagaaacct      120

ggccaggctc ccaggctcct catgtatggt gcatccagca gggccactgg catcccagac      180

aggttcagtg gcagtggggc tgggacagac ttcactctca ccatcagcag cctagagcct      240

gaagattttg caacgtatta ctgtcagcag catactatcc caacattctc tttcggccct      300

gggaccaaag tggaagtcaa a                                                321


<210>  1504
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-31

<400>  1504

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 Ile Gly Asn Ser
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met
        35                  40                  45


Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
```

    50   55   60

Ser Gly Ala Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Thr Ile Pro Thr Phe
                85   90   95

Ser Phe Gly Pro Gly Thr Lys Val Glu Val Lys
            100   105

<210> 1505
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-32

<400> 1505
gaggtgcagc tggtgcagtc tggggctgag ctgaagaagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttttggagg caccttcagt gacaatgcta tcagctgggt gcgacaggcc   120

cctggacaag ggcctgagtg gatggggggc atcattccta tctttggaaa accaaactac   180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cactgcctac   240

atggtcctga gcagcctgag atctgaggac acggccgtat attactgtgc gagaactatg   300

gttcggggct ttcttggggt tatggacgtc tggggccaag ggaccacggt caccgtctcc   360

tca   363

<210> 1506
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-32

<400> 1506

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Ser
1   5   10   15

```
Ser Val Lys Val Ser Cys Lys Ala Phe Gly Gly Thr Phe Ser Asp Asn
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Pro Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Lys Pro Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Val Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Thr Met Val Arg Gly Phe Leu Gly Val Met Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 1507
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-32

<400> 1507

```
gatattgtga tgacccagac tccatccttc ctgtccgcat ccataggaga cagagtcacc        60

atcacttgcc gggccagtca gggcattggc agttatttag cctggtatca gcaaagacca       120

ggggaagccc ctaagctcct gatctatgct gcatcgactt tgcaaagtgg agtcccatca       180

aggttcagcg gcagtggatc tgggacggac ttcactctca caatcagcaa cctgcagcct       240

gaagattttg caacttatta ctgtcaacag cttaataatt acccgatcac cttcggccaa       300

gggacacgac tggagattaa a                                                 321
```

<210> 1508

```
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-32

<400>  1508

Asp Ile Val Met Thr Gln Thr Pro Ser Phe Leu Ser Ala Ser Ile Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Ser Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Lys Leu Leu Ile
        35                  40                  45


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


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Asn Tyr Pro Ile
                85                  90                  95


Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210>  1509
<211>  375
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-38

<400>  1509
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
```

```
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcag      300

ttcgttacga tttttggagt gccaagatac ggtatggacg tctggggcca agggaccacg      360

gtcaccgtct cctca                                                       375
```

```
<210>  1510
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-38

<400>  1510

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Gln Phe Val Thr Ile Phe Gly Val Pro Arg Tyr Gly Met
            100                 105                 110


Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  1511
```

```
<211>  315
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-38

<400>  1511
cagtctgccc tgactcagcc accctcagtg tccgtgtccc caggacagac agccaacatc       60

ccctgctctg gagataaatt ggggaataaa tatgcttact ggtatcagca gaagccaggc      120

cagtcccctg tactgctcat ctatcaagat atcaagcggc cctcaaggat ccctgagcga      180

ttctctggct ccaactctgc ggacacagcc actctgacca tcagcgggac ccaggctatg      240

gatgaggctg actattactg tcagacgtgg gacaacagcg tggtcttcgg cggcgggacc      300

aagctgaccg tcctc                                                       315


<210>  1512
<211>  105
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-38

<400>  1512

Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15


Thr Ala Asn Ile Pro Cys Ser Gly Asp Lys Leu Gly Asn Lys Tyr Ala
            20                  25                  30


Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Leu Ile Tyr
        35                  40                  45


Gln Asp Ile Lys Arg Pro Ser Arg Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Ala Asp Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Thr Trp Asp Asn Ser Val Val Phe
```

85 90 95

Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1513
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-42

<400> 1513
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtct attactgtgc gagagggcgt 300

caaatgttcg gtgcgggaat tgatttctgg ggcccgggca ccctggtcac cgtctcctca 360

<210> 1514
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-42

<400> 1514

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 Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

```
    50                  55                  60


Gln 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 Arg Gln Met Phe Gly Ala Gly Ile Asp Phe Trp Gly Pro
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1515
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-42

<400>  1515
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc       60

tcctgcaccc gcagcagtgg cagcattgac agcaactatg tgcagtggta ccagcagcgc      120

ccgggcagcg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct      180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga      240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgatagcaa caatcgtcat      300

gtgatattcg gcggagggac caagctgacc gtccta                                336


<210>  1516
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-42

<400>  1516

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
```

1   5   10   15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Asp Ser Asn
            20   25   30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35   40   45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85   90   95

Asn Asn Arg His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1517
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-46

<400> 1517
gaggtgcagc tggtggagtc tggggctgaa gtaaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagg tttcaggagg cacattcggc acctatgctc tcaactgggt gcgccaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcgtccctc tcattggtct agtaaactac 180

gcacataact ttgagggcag aatctcgatt accgcggaca agtccacggg cacagcctac 240

atggaactga gcaacctgag atctgacgac acggccgtgt attactgtgc gagagaggtc 300

tacggtggta actccgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 1518
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-46

<400> 1518

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Gly Thr Tyr
            20   25   30

Ala Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Arg Ile Val Pro Leu Ile Gly Leu Val Asn Tyr Ala His Asn Phe
    50   55   60

Glu Gly Arg Ile Ser Ile Thr Ala Asp Lys Ser Thr Gly Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Asn Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Val Tyr Gly Gly Asn Ser Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 1519
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-46

<400> 1519
aattttatgc tgactcagcc ccactcagtg tcggagtctc cggggaagac ggtaaccatc   60

tcctgcactc gcagtagtgg caacattggc accaactatg tgcagtggta ccagcagcgc   120 ccgggcagtg cccccgtcgc tttgatctac gaggattatc gaagaccctc tggggtccct 180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcat catctctgga 240

ctgaagcctg aggacgaggc tgactactac tgtcagtctt atcatagcag cggttgggaa 300

ttcggcggag ggaccaagct gaccgtcctc 330

<210> 1520
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-46

<400> 1520

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Asn Ile Gly Thr Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Val Ala Leu
35 40 45

Ile Tyr Glu Asp Tyr Arg Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Ile Ile Ser Gly
65 70 75 80

Leu Lys Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr His Ser
85 90 95

Ser Gly Trp Glu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1521
<211> 360
<212> DNA
<213> Artificial Sequence

```
<220>
<223>  Variable heavy chain of Ab-50

<400>  1521
caggtgcagc tggtgcagtc tggaggtgag gtgaagaagc cgggggcctc agtgaaggtc       60

tcctgcaagg cttctggtta caccttgagc agtcatggta taacctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcagcgctc acaatggtca cgctagcaat      180

gcacagaagg tggaggacag agtcactatg actactgaca catccacgaa cacagcctac      240

atggaactga ggagcctgac agctgacgac acggccgtgt attactgtgc gagagtacat      300

gctgccctct actatggtat ggacgtctgg ggccaaggaa ccctggtcac cgtctcctca      360


<210>  1522
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-50

<400>  1522

Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu Ser Ser His
            20                  25                  30


Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Ala His Asn Gly His Ala Ser Asn Ala Gln Lys Val
    50                  55                  60


Glu Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Thr Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val His Ala Ala Leu Tyr Tyr Gly Met Asp Val Trp Gly Gln
```

```
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120



<210>  1523
<211>  324
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-50

<400>  1523
cagtctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa ggtgtgcact ggtatcagca gaagccaggc      120

caggcccctg tactggtcgt ctatgatgat agtgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcattg ggtgttcggc      300

ggagggacca agctgaccgt ccta                                             324


<210>  1524
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-50

<400>  1524

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Gly Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45


Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
```

```
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
                85                  90                  95


Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1525
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-52

<400>  1525
caggtgcagc tgcaggagtc gggggaggc gtggtgcagc ctgggaggtc cctgagactc       60

tcctgttcag cctctggatt caccttcagc agacatggca tgcactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtg atatcacatg atggaagtgt aaaatactat      180

gcagactcca tgaagggccg attcagcatc tccagagaca attccaacaa cacactgtat      240

ctccaaatgg acagcctgag agctgacgac acggccgttt attactgtgc gagaggactg      300

tcgtaccagg tgtcggggtg gttcgacccc tggggccagg gcaccctggt caccgtctcc      360

tca                                                                    363


<210>  1526
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable heavy chain of Ab-52

<400>  1526

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg His
            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 Asp Gly Ser Val Lys Tyr Tyr Ala Asp Ser Met
    50                  55                  60


Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Leu Ser Tyr Gln Val Ser Gly Trp Phe Asp Pro Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1527
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-52

<400>  1527
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc       60

tcctgcaccc gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc      120

ccgggcagtg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct      180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga      240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgatagcac caccccttcg      300

gtgttcggcg gcgggaccaa gctgaccgtc cta                                   333


<210>  1528
```

<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-52

<400> 1528

```
Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15


Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
            20                  25                  30


Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35                  40                  45


Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65                  70                  75                  80


Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85                  90                  95


Thr Thr Pro Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 1529
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-55

<400> 1529

```
caggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc        60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggatgg accagccctc ataatggtct cacagcattt       180
```

gcacagatcc tagagggccg agtcaccatg accacagaca catccacgaa cacagcctac 240

atggaattga ggaacctgac atttgatgac acggccgttt atttctgtgc gaaagtacat 300

cctgtcttct cttatgcgtt ggacgtctgg ggccaaggca ccctggtcac cgtctcctca 360

<210> 1530
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-55

<400> 1530

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

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Thr Ser Pro His Asn Gly Leu Thr Ala Phe Ala Gln Ile Leu
    50   55   60

Glu Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Asn Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Asn Leu Thr Phe Asp Asp Thr Ala Val Tyr Phe Cys
                85   90   95

Ala Lys Val His Pro Val Phe Ser Tyr Ala Leu Asp Val Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1531
<211> 330
<212> DNA

<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-55

<400> 1531
aattttatgc tgactcagcc ccactctgtg tcggagtccc cggggaagac ggtaaccatc   60

tcctgcaccc gcagcagtgg cagcattgcc agcaactatg tacagtggta ccagcagcgc   120

ccgggcagtt cccccaccac tgtgatctat gaagataacc aaagaccctc tggggtccct   180

gatcggttct ctggctccat cgacacctcc tccaactctg cctccctcac catctctgga   240

ctgaagacta aggacgaggc ggactactac tgtcagtctt atgatggcat cactgtgatt   300

ttcggcggag ggaccaagtt gaccgtccta   330

<210> 1532
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-55

<400> 1532

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
            20   25   30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
        35   40   45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Ile Asp Thr Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

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

Ile Thr Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1533
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-56

<400> 1533
gaggtgcagc tggtggagtc tggagctgag gtgatgaacc ctgggtcctc ggtgagggtc 60

tcctgcaggg gttctggagg cgacttcagt acctatgctt tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180

gcacagaagt tccagggcag ggtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgacgat acggccgtgt attactgtgc gagagatggc 300

tatggttcgg acccggtgct atggggccag ggcaccctgg tcaccgtctc ctca 354

<210> 1534
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-56

<400> 1534

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

Ser Val Arg Val Ser Cys Arg Gly Ser Gly Gly Asp Phe Ser Thr Tyr
20 25 30

Ala Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln 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 Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Ser Asp Pro Val Leu Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1535
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-56

<400>  1535
aattttatgc tgactcagcc ccactctgtg tcggggtctc cggggaagac ggtaaccctc        60

ccctgcaccc gcagcagtgg cagcattgcc agccactatg tccagtggta ccagcagcgc       120

ccgggcagtg cccccaccac tgtgatctat gaggataaca agagaccctc tggggtccct       180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcag catctctgga       240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgatagcag caatcgttgg       300

gtgttcggcg gagggaccaa gctgaccgtc cta                                    333


<210>  1536
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-56

<400>  1536

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Gly Ser Pro Gly Lys
1               5                   10                  15
```

Thr Val Thr Leu Pro Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser His
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Ser Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
85 90 95

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1537
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-65

<400> 1537
gaggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc aactatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat 180

gcacagaagg tccagggcag agtcaccatg accacagaca catccacgag cacaggctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaggagat 300

tttcggaaac cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 1538
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain of Ab-65

<400> 1538

Glu 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 Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val
    50   55   60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Gly 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 Asp Phe Arg Lys Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 1539
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable light chain of Ab-65

<400> 1539
ctgcctgtgc tgactcagcc ggcttccctc tctgcatccc ccggagcatc agccagtctc   60

acctgcacct tacgcagtgg cctcaatgtt ggttcctaca ggatatactg gtaccagcag   120

aagccaggga gtcgtcccca gtatctcctg aactacaaat cagactcaaa taaacagcag   180

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gcctctggag tccccagccg cttctctgga tccaaggatg cttcggccaa tgcagggatt      240

ttactcatct ccgggctcca gtctgaggat gaggctgact attactgtat gatttggtac      300

agcagcgctg tggtattcgg cggagggacc aagctgaccg tccta                      345


<210>  1540
<211>  115
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Variable light chain of Ab-65

<400>  1540

Leu Pro Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala
1               5                   10                  15


Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Leu Asn Val Gly Ser
            20                  25                  30


Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Arg Pro Gln Tyr
        35                  40                  45


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


Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65                  70                  75                  80


Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
                85                  90                  95


Met Ile Trp Tyr Ser Ser Ala Val Val Phe Gly Gly Gly Thr Lys Leu
            100                 105                 110


Thr Val Leu
        115


<210>  1541
<211>  5
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Heavy chain CDR1 consensus, Ab-42

<400> 1541

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Ser Tyr Ala Ile Ser
1               5
```

<210> 1542
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR1 of Ab-14, Ab-55

<400> 1542

```
Ser Tyr Gly Ile Ser
1               5
```

<210> 1543
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR1 of Ab-16

<400> 1543

```
Ser Tyr Ala Leu Ser
1               5
```

<210> 1544
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR1 of Ab-22

<400> 1544

```
Asp Tyr Ala Met His
1               5
```

```
<210>  1545
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-30

<400>  1545

Asn Tyr Asp Met Ser
1               5


<210>  1546
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-31

<400>  1546

Gly Leu Tyr Ile His
1               5


<210>  1547
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-32

<400>  1547

Asp Asn Ala Ile Ser
1               5


<210>  1548
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-38

<400>  1548
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```
Ser Tyr Ala Met Ser
1               5


<210>  1549
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-46

<400>  1549

Thr Tyr Ala Leu Asn
1               5


<210>  1550
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-50

<400>  1550

Ser His Gly Ile Thr
1               5


<210>  1551
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 Ab-52

<400>  1551

Arg His Gly Met His
1               5


<210>  1552
<211>  5
<212>  PRT
<213>  Artificial Sequence
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```
<220>
<223>  Heavy chain CDR1 of Ab-56

<400>  1552

Thr Tyr Ala Phe Ser
1               5


<210>  1553
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR1 of Ab-65

<400>  1553

Asn Tyr Gly Ile Ser
1               5


<210>  1554
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR2 consensus

<400>  1554

Trp Ile Ser Pro Ile Gly Gly Ser Thr Asn Tyr Ala Gln Lys Val Gln
1               5                   10                  15


Gly



<210>  1555
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR2 of Ab-14

<400>  1555

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Glu
```

1   5   10   15

Asp

<210> 1556
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-16

<400> 1556

Ala Ile Ser Gly Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Asp

<210> 1557
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-22

<400> 1557

Leu Ile Ser Gly Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Asp

<210> 1558
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-30

<400> 1558

Arg Val Asn Trp Asn Gly Gly Ser Thr Thr Tyr Ala Asp Ala Val Lys
1   5   10   15

Asp

<210> 1559
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-31

<400> 1559

Trp Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Glu
1   5   10   15

Asp

<210> 1560
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-32

<400> 1560

Trp Ile Ile Pro Ile Phe Gly Lys Pro Asn Tyr Ala Gln Lys Phe Glu
1   5   10   15

Asp

<210> 1561
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-38

<400> 1561

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Asp

<210> 1562
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-42

<400> 1562

Trp Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Glu
1   5   10   15

Asp

<210> 1563
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-46

<400> 1563

Arg Ile Val Pro Leu Ile Gly Leu Val Asn Tyr Ala His Asn Phe Glu
1   5   10   15

Asp

<210> 1564
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-50

<400> 1564

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

Asp

<210> 1565
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-52

<400> 1565

Val Ile Ser His Asp Gly Ser Val Lys Tyr Tyr Ala Asp Ser Met Lys
1   5   10   15

Asp

<210> 1566
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR2 of Ab-55

<400> 1566

Trp Thr Ser Pro His Asn Gly Leu Thr Ala Phe Ala Gln Ile Leu Glu
1   5   10   15

Asp

<210> 1567
<211> 17
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR2 of Ab-56

<400>  1567

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


Asp




<210>  1568
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR2 of Ab-65

<400>  1568

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val Glu
1               5                   10                  15


Asp




<210>  1569
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 consensus


<220>
<221>  misc_feature
<222>  (3)..(17)
<223>  Xaa can be any naturally occurring amino acid

<400>  1569

Gly Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
```

Xaa Asp Val

<210> 1570
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-14

<400> 1570

```
Ala Leu Pro Ser Gly Thr Ile Leu Val Gly Gly Trp Phe Asp Pro
1               5                   10                  15
```

<210> 1571
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-16

<400> 1571

```
Asp Val Phe Pro Glu Thr Phe Ser Met Asn Tyr Gly Met Asp Val
1               5                   10                  15
```

<210> 1572
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-22

<400> 1572

```
Val Leu Leu Pro Cys Ser Ser Thr Ser Cys Tyr Gly Ser Val Gly Ala
1               5                   10                  15
```

Phe Asp Ile

<210> 1573

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<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-30

<400>  1573

Glu Phe Val Gly Ala Tyr Asp Leu
1               5


<210>  1574
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-31

<400>  1574

Gly Leu Arg Trp Gly Ile Trp Gly Trp Phe Asp Pro
1               5                   10


<210>  1575
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-32

<400>  1575

Thr Met Val Arg Gly Phe Leu Gly Val Met Asp Val
1               5                   10


<210>  1576
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-38

<400>  1576

Asp Gln Phe Val Thr Ile Phe Gly Val Pro Arg Tyr Gly Met Asp Val
```

1   5   10   15

<210> 1577
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-42

<400> 1577

Gly Arg Gln Met Phe Gly Ala Gly Ile Asp Phe
1   5   10

<210> 1578
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-46

<400> 1578

Glu Val Tyr Gly Gly Asn Ser Asp Tyr
1   5

<210> 1579
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-50

<400> 1579

Val His Ala Ala Leu Tyr Tyr Gly Met Asp Val
1   5   10

<210> 1580
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain CDR3 of Ab-52

```
<400>  1580

Gly Leu Ser Tyr Gln Val Ser Gly Trp Phe Asp Pro
1               5                   10


<210>  1581
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-55

<400>  1581

Val His Pro Val Phe Ser Tyr Ala Leu Asp Val
1               5                   10


<210>  1582
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-56

<400>  1582

Asp Gly Tyr Gly Ser Asp Pro Val Leu
1               5


<210>  1583
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy chain CDR3 of Ab-65

<400>  1583

Gly Asp Phe Arg Lys Pro Phe Asp Tyr
1               5


<210>  1584
<211>  13
<212>  PRT
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```
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 consensus

<400>  1584

Thr Arg Ser Ser Gly Ser Ile Gly Ser Asn Tyr Val Gln
1               5                   10


<210>  1585
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-14

<400>  1585

Thr Arg Ser Ser Gly Asn Ile Ala Ser Asn Tyr Val Gln
1               5                   10


<210>  1586
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-16

<400>  1586

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1               5                   10


<210>  1587
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-22

<400>  1587

Gly Gly Ser Asp Ile Gly Arg Lys Ser Val His
1               5                   10
```

```
<210>  1588
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-30

<400>  1588

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1               5                   10


<210>  1589
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-31

<400>  1589

Arg Ala Ser Gln Ser Ile Gly Asn Ser Leu Ala
1               5                   10


<210>  1590
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-32

<400>  1590

Arg Ala Ser Gln Gly Ile Gly Ser Tyr Leu Ala
1               5                   10


<210>  1591
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR1 of Ab-38

<400>  1591
```

Ser Gly Asp Lys Leu Gly Asn Lys Tyr Ala Tyr
1   5   10

<210> 1592
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-42

<400> 1592

Thr Arg Ser Ser Gly Ser Ile Asp Ser Asn Tyr Val Gln
1   5   10

<210> 1593
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-46

<400> 1593

Thr Arg Ser Ser Gly Asn Ile Gly Thr Asn Tyr Val Gln
1   5   10

<210> 1594
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-50

<400> 1594

Gly Gly Asn Asn Ile Gly Ser Lys Gly Val His
1   5   10

<210> 1595
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-52

<400> 1595

Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn Tyr Val Gln
1   5   10

<210> 1596
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-55

<400> 1596

Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn Tyr Val Gln
1   5   10

<210> 1597
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-56

<400> 1597

Thr Arg Ser Ser Gly Ser Ile Ala Ser His Tyr Val Gln
1   5   10

<210> 1598
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 of Ab-65

<400> 1598

Thr Leu Arg Ser Gly Leu Asn Val Gly Ser Tyr Arg Ile Tyr
1   5   10

<210> 1599

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

<220>
<223>  Light chain CDR2 of consensus, Ab-14, Ab-42, Ab-52, Ab-55

<400>  1599

Glu Asp Asn Gln Arg Pro Ser
1               5


<210>  1600
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-16

<400>  1600

Gly Lys Asn Asn Arg Pro Ser
1               5


<210>  1601
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-22

<400>  1601

Ser Asp Arg Asp Arg Pro Ser
1               5


<210>  1602
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-30

<400>  1602

Asp Val Ser Asn Arg Pro Ser
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1   5

<210> 1603
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR2 of Ab-31

<400> 1603

Gly Ala Ser Ser Arg Ala Thr
1   5

<210> 1604
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR2 of Ab-32

<400> 1604

Ala Ala Ser Thr Leu Gln Ser
1   5

<210> 1605
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR2 of Ab-38

<400> 1605

Gln Asp Ile Lys Arg Pro Ser
1   5

<210> 1606
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR2 of Ab-46

```
<400>  1606

Glu Asp Tyr Arg Arg Pro Ser
1               5


<210>  1607
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-50

<400>  1607

Asp Asp Ser Asp Arg Pro Ser
1               5


<210>  1608
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-56

<400>  1608

Glu Asp Asn Lys Arg Pro Ser
1               5


<210>  1609
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR2 of Ab-65

<400>  1609

Tyr Lys Ser Asp Ser Asn Lys Gln Gln Ala Ser
1               5                   10


<210>  1610
<211>  9
<212>  PRT
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```
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 consensus

<400>  1610

Gln Ser Tyr Asp Ser Ser Thr Trp Val
1               5


<210>  1611
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-14

<400>  1611

Gln Ser Tyr Asp Ser Ser Asn Leu Trp Val
1               5                   10


<210>  1612
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-16

<400>  1612

Asn Ser Arg Asp Ser Ser Gly Asn His Tyr Val
1               5                   10


<210>  1613
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-22

<400>  1613

Gln Val Trp Asp Asn Asn Ser Asp His Tyr Val
1               5                   10
```

<210> 1614
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-30

<400> 1614

Ser Ser Tyr Thr Ser Ser Thr Leu Pro
1 5

<210> 1615
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-31

<400> 1615

Gln Gln His Thr Ile Pro Thr Phe Ser
1 5

<210> 1616
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-32

<400> 1616

Gln Gln Leu Asn Asn Tyr Pro Ile Thr
1 5

<210> 1617
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-38

<400> 1617

Gln Thr Trp Asp Asn Ser Val Val
1   5

<210> 1618
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-42

<400> 1618

Gln Ser Tyr Asp Ser Asn Asn Arg His Val Ile
1   5   10

<210> 1619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-46

<400> 1619

Gln Ser Tyr His Ser Ser Gly Trp Glu
1   5

<210> 1620
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR3 of Ab-50

<400> 1620

Gln Val Trp Asp Ser Ser Ser Asp His Trp Val
1   5   10

<210> 1621
<211> 10
<212> PRT
<213> Artificial Sequence

```
<220>
<223>  Light chain CDR3 of Ab-52

<400>  1621

Gln Ser Tyr Asp Ser Thr Thr Pro Ser Val
1               5                   10


<210>  1622
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-55

<400>  1622

Gln Ser Tyr Asp Gly Ile Thr Val Ile
1               5


<210>  1623
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-56

<400>  1623

Gln Ser Tyr Asp Ser Ser Asn Arg Trp Val
1               5                   10


<210>  1624
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light chain CDR3 of Ab-65

<400>  1624

Met Ile Trp Tyr Ser Ser Ala Val Val
1               5


<210>  1625
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<211> 717
<212> DNA
<213> Homo sapiens

<400> 1625
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tcctgtgcag cctctggatt cgccttcagt agttatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagggacagg   300

agctactacc ttgactactg gggccaggga accctggtca ccgtctcctc aggtggcggc   360

ggttccggag gtggtggttc tggcggtggt ggcagcgaaa cgacactcac gcagtctcca   420

gccaccctgt ctttgtctcc aggggaaagg gccaccctct cctgcagggc cagtcagagt   480

gttaggagca acttagcctg gtaccagcag aaacctggcc aggctcccag gcccctcatc   540

tatgatgcat ccaccagggc cactggcatc ccagacaggt tcagtggcag tgggtctggg   600

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt ttattactgt   660

cagcagcgta gcaactggcc tccgacgttc ggccaaggga ccaaggtgga agtcaaa   717

<210> 1626
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1626
gaggtgcagc tggtgcagtc tgggggaggc gtggtccagc ctgggaagtc cctgagactc   60

tcctgtgcag cctctggatt cgccttcagt agttatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagggacagg   300

agctactacc ttgactactg gggccaggga accctggtca ccgtctcctc a   351

<210> 1627
<211> 987
<212> DNA

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<213>  Homo sapiens

<400>  1627
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg        60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg       120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca       180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc       240

tacatctgca acgtgaatca caagcccagc accaaggtgg acaagaaagc agagcccaaa       300

tcttgtgaca aaactcacac atccccaccg tgcccagcac ctgaactcct ggggggaccg       360

tcagtcttcc tcttcccccc aaaacccaag gacaccctca ggatctcccg gacccctgag       420

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac       480

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacagcacg       540

taccgggtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac       600

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc       660

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc       720

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg       780

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac       840

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag       900

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag       960

agcctctccc tgtctccggg taaatga                                           987


<210>  1628
<211>  318
<212>  DNA
<213>  Homo sapiens

<400>  1628
acgacactca cgcagtctcc agccaccctg tctttgtctc caggggaaag ggccaccctc        60

tcctgcaggg ccagtcagag tgttaggagc aacttagcct ggtaccagca gaaacctggc       120

caggctccca ggcccctcat ctatgatgca tccaccaggg ccactggcat cccagacagg       180

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa       240
```

```
gattttgcag tttattactg tcagcagcgt agcaactggc ctccgacgtt cggccaaggg      300

accaaggtgg aagtcaaa                                                    318


<210>  1629
<211>  348
<212>  DNA
<213>  Homo sapiens

<400>  1629
gatggtacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg       60

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      120

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      180

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      240

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      300

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttga                   348


<210>  1630
<211>  102
<212>  PRT
<213>  Homo sapiens

<400>  1630

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Pro Gly Ser Leu Arg
1               5                   10                  15


Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Met Ser Trp
            20                  25                  30


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


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


Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
65                  70                  75                  80


Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asp Tyr Trp Gly Gln Gly Thr
```

```
                85                  90                  95


Leu Val Thr Val Ser Ser
            100



<210>  1631
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  1631

Gln Val Gln Leu Val Gln 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 Val Ser Ser Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly 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 Glu Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115



<210>  1632
<211>  117
<212>  PRT
<213>  Homo sapiens

<400>  1632
```

```
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys 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


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala 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 Gly Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Trp Gly Tyr Ser Phe Gly Asp Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  1633
<211>  127
<212>  PRT
<213>  Homo sapiens

<400>  1633

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 Thr Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


Gln 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 Val Gly Tyr Tyr Gly Asp Tyr Ala Trp Gly Tyr Tyr Tyr Tyr
            100                 105                 110


Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  1634
<211>  122
<212>  PRT
<213>  Homo sapiens

<400>  1634

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys 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


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala 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 Arg Trp Leu Gln Ile Gly Glu Asp Ala Phe Asp Ile Trp
```

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1635
<211> 116
<212> PRT
<213> Homo sapiens

<400> 1635

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly 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

Arg Asn Phe Gly Glu Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 1636
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1636

```
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Lys
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
            20                  25                  30


Ala 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 Asn 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 Arg Ser Tyr Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  1637
<211>  124
<212>  PRT
<213>  Homo sapiens

<400>  1637

Gln Val Gln Leu Val Gln Ser Gly Gly 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 Ser
            20                  25                  30


Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ala Tyr Ile Lys Gln Asp Gly Ser Glu Lys Tyr 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 Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gln Gly Trp Gly Trp Asp Gly Thr Glu Tyr Tyr Ser Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1638
<211>  123
<212>  PRT
<213>  Homo sapiens

<400>  1638

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


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


Gln 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 Asp Asp Leu Ser Asp Tyr Gly Glu Trp Leu Gly Pro Asp Tyr
```

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1639
<211> 81
<212> PRT
<213> Homo sapiens

<400> 1639

Gln Leu Thr Gln Pro Ser Ser Gly Ser Pro Gly Gln Arg Thr Ile Ser
1 5 10 15

Cys Gly Ser Ser Gly Asn Val Ser Trp Tyr Gln Gln Pro Gly Ala Pro
20 25 30

Lys Leu Leu Ile Tyr Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly
35 40 45

Ser Lys Ser Gly Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Glu Asp
50 55 60

Glu Ala Asp Tyr Tyr Cys Val Phe Gly Gly Thr Lys Leu Thr Val Leu
65 70 75 80

Gly

<210> 1640
<211> 106
<212> PRT
<213> homo sapiens

<400> 1640

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 Arg Ala Thr Gln Ser Ile Ser Thr His Leu
20 25 30

```
Asn Trp Tyr Gln Gln Arg Gly Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45


Gly Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60


Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65                  70                  75                  80


Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Arg Ser Tyr Pro Trp Thr
                85                  90                  95


Phe Gly Gln Gly Thr Asn Val Glu Ile Lys
            100                 105


<210>  1641
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1641

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Ser Ile Gly Ser Glu
            20                  25                  30


Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Thr Ala Trp Asp Asp Thr Leu
                85                  90                  95
```

```
Asn Gly Arg Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1642
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1642

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Ile Thr Leu Thr Cys Asp Leu Asn Ser Gly Leu Val Ser Ser Ser
            20                  25                  30


His Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr
        35                  40                  45


Leu Ile Tyr Asn Thr Asn Ile Arg Ser Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ala Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Met Gly Ser
                85                  90                  95


Gly Ile Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1643
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1643

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Leu Gly Gly His
            20                  25                  30
```

```
Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Tyr Asp Val Phe Asn Arg Pro Ser Gly Val Ser Ser Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Phe Cys Ser Ser Tyr Thr Ile Thr
                85                  90                  95


Asn Ile Val Val Phe Gly Arg Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  1644
<211>  106
<212>  PRT
<213>  Homo sapiens

<400>  1644

Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
1               5                   10                  15


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn Leu
            20                  25                  30


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
        35                  40                  45


Asp Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65                  70                  75                  80


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Thr
                85                  90                  95
```

```
Phe Gly Gln Gly Thr Lys Val Glu Val Lys
            100                 105


<210>  1645
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1645

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Phe Cys Ser Ser Tyr Thr Ile Thr
                85                  90                  95


Asp Ile Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
            100                 105                 110


<210>  1646
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1646

Gln Pro Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Gly Asn
```

```
            20                  25                  30


Thr Val Asn Trp Tyr Gln His Val Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80


Ser Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Thr Trp Glu Asp Ser Leu
                85                  90                  95


Ser Gly Tyr Val Phe Gly Pro Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


<210>  1647
<211>  15
<212>  PRT
<213>  Homo sapiens

<400>  1647

Arg Thr Met His Pro Ser Asp Glu Phe Leu Pro Leu Gly Met Pro
1               5                   10                  15


<210>  1648
<211>  15
<212>  PRT
<213>  Homo sapiens

<400>  1648

Val Val Pro Leu Gly Arg Cys Val Ser His Pro Ala Ile Cys Ala
1               5                   10                  15


<210>  1649
<211>  15
<212>  PRT
<213>  Homo sapiens

<400>  1649
```

Ser Val Asp Asp Cys Arg Trp Asn Leu Asn Cys Glu Pro Pro Pro
1   5   10   15

<210> 1650
<211> 13
<212> PRT
<213> Homo sapiens

<400> 1650

Cys Leu Ser Ala Thr Cys Asp Cys Thr Leu Cys Gly Pro
1   5   10

<210> 1651
<211> 15
<212> PRT
<213> Homo sapiens

<400> 1651

Gly Thr Gly Leu Val Pro Leu Phe Asp Pro Arg Tyr Arg Phe Leu
1   5   10   15

<210> 1652
<211> 15
<212> PRT
<213> Homo sapiens

<400> 1652

Pro Asn Cys Trp Val Gly Leu Thr Gly Ala His Ser Cys Phe Leu
1   5   10   15

<210> 1653
<211> 14
<212> PRT
<213> Homo sapiens

<400> 1653

Tyr Gln Ala Asp Cys Leu Met Asn Arg Cys Pro Thr Ala Glu
1   5   10

<210> 1654
<211> 669
<212> PRT
<213> Homo sapiens

```
<400>  1654

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1               5                   10                  15


Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20                  25                  30


His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35                  40                  45


Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50                  55                  60


Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65                  70                  75                  80


Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
                85                  90                  95


Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100                 105                 110


Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
        115                 120                 125


Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
    130                 135                 140


Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145                 150                 155                 160


Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
                165                 170                 175


Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180                 185                 190


Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
```

        195   200   205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
    210   215   220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225   230   235   240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
                245   250   255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
            260   265   270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
        275   280   285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
    290   295   300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305   310   315   320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Pro Ser Val Tyr Ala Trp
                325   330   335

Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr
            340   345   350

Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Ala Thr
        355   360   365

Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala Asp Ser Phe Val
    370   375   380

Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Val
385   390   395   400

Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Met Gly Cys Val

```
                405                 410                 415

Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser Thr Gly Asn Tyr
            420                 425                 430

Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu
        435                 440                 445

Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr
    450                 455                 460

Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr
465                 470                 475                 480

Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser
                485                 490                 495

Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser
            500                 505                 510

Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu
        515                 520                 525

Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe
    530                 535                 540

Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp
545                 550                 555                 560

Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys Ala Phe Gly Gly
                565                 570                 575

Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val
            580                 585                 590

Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala
        595                 600                 605

Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val
```

```
    610                 615                 620


Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr
625                 630                 635                 640


Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr
                645                 650                 655


His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys Ser
            660                 665


<210>  1655
<211>  20
<212>  PRT
<213>  Homo sapiens

<400>  1655

Arg Val Val Val Leu Ser Phe Glu Leu Gly Pro Pro Gly Gly Pro Phe
1               5                   10                  15


Gly Glu Val Phe
            20


<210>  1656
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  1656

Val Val Val Ser Phe Glu Leu Asn Leu Cys Pro Phe Gly Glu
1               5                   10


<210>  1657
<211>  11
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<222>  (5)..(7)
<223>  Wherein Xaa is any amino acid.
```

<400> 1657

```
Ser Phe Glu Leu Xaa Xaa Xaa Pro Phe Gly Glu
1               5                   10
```

<210> 1658
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (5)..(9)
<223> Wherein Xaa is any amino acid.

<400> 1658

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Ser Phe Glu Leu Xaa Xaa Xaa Xaa Xaa Pro Phe Gly Glu
1               5                   10
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<210> 1659
<211> 5
<212> PRT
<213> Homo sapiens

<400> 1659

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Val Tyr Asp Asn Lys
1               5
```

<210> 1660
<211> 5
<212> PRT
<213> Homo sapiens

<400> 1660

```
Arg Ser Tyr Tyr Leu
1               5
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<210> 1661
<211> 10
<212> PRT
<213> Homo sapiens

<400> 1661

Arg Ala Ser Gln Val Arg Ser Asn Leu Ala
1   5   10

<210> 1662
<211> 6
<212> PRT
<213> Homo sapiens

<400> 1662

Asp Ala Ser Thr Ala Thr
1   5

<210> 1663
<211> 9
<212> PRT
<213> Homo sapiens

<400> 1663

Gln Gln Arg Ser Asn Trp Pro Pro Thr
1   5

<210> 1664
<211> 13
<212> PRT
<213> Homo sapiens

<400> 1664

Cys Leu Ser Ala Thr Cys Asp Cys Thr Leu Cys Gly Pro
1   5   10

<210> 1665
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial polynucleotide

<400> 1665
caggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcaatt atatcatttg atggaagtaa aaaatattat   180

```
gcaaactccg tgaagggccg atccaccatc tccagagaca attccaagaa cacgctgtct      240

ctgcaaatga acagcctggg acctgaggac acggctctat attactgtgc gaaactgccc      300

tccccgtatt actttgatag tcggttcgtg tgggtcgccg ccagcgcatt tcacttctgg      360

ggccagggaa tcctggtcac cgtctcttca                                       390


<210>  1666
<211>  330
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial nucleotide

<400>  1666
aattttatgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgctctg gaagcagctc caacatcgga ggtaatactg tacactggtt ccagcagctc      120

ccaggaacgg cccccaaact cctcatctat actaatagtc tgcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctaaa tggtcaggtg      300

ttcggcggag ggaccaagct gaccgtccta                                       330


<210>  1667
<211>  130
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Aritificial polynucleotide

<400>  1667

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


Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Gly Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Leu Pro Ser Pro Tyr Tyr Phe Asp Ser Arg Phe Val Trp Val
            100                 105                 110


Ala Ala Ser Ala Phe His Phe Trp Gly Gln Gly Ile Leu Val Thr Val
        115                 120                 125


Ser Ser
    130


<210>  1668
<211>  110
<212>  PRT
<213>  artificial sequence

<220>
<223>  Aritificial polynucleotide

<400>  1668

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
            20                  25                  30


Thr Val His Trp Phe Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Thr Asn Ser Leu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
```

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Gln Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1669
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1669
aattttatgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgctctg gaagcagctc caacatcgga ggtaatactg tacactggtt ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat actaatagtc tgcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggata acagcctaaa tggtcaggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 1670
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1670

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
20 25 30

Thr Val His Trp Phe Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

```
        35                  40                  45


Ile Tyr Thr Asn Ser Leu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asn Ser Leu
                85                  90                  95


Asn Gly Gln Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1671
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polynucleotide

<400>  1671

Gly Phe Thr Phe Ser Asn Tyr Gly
1               5


<210>  1672
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polynucleotide

<400>  1672

Ile Ser Phe Asp Gly Ser Lys Lys
1               5


<210>  1673
<211>  25
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> artificial polynucleotide

<400> 1673

Cys Ala Lys Leu Pro Ser Pro Tyr Tyr Phe Asp Ser Arg Phe Val Trp
1   5   10   15

Val Ala Ala Ser Ala Phe His Phe Trp
            20   25

<210> 1674
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1674

Ser Ser Asn Ile Gly Gly Asn Thr
1   5

<210> 1675
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> artifcial polynucleotide

<400> 1675

Thr Asn Ser
1

<210> 1676
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1676

Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Gln Val Phe

1   5   10

<210> 1677
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1677

Cys Ala Ala Trp Asp Asn Ser Leu Asn Gly Gln Val Phe
1   5   10

<210> 1678
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial nucleotide

<400> 1678
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg   60

agctgcaaag cgagcggcta tacctttgcg agcgcgtgga tgcattggat gcgccaggcg   120

ccgggccagg gcctggaatg gattggctgg attaacccgg gcaacgtgaa caccaaatat   180

aacgaaaaat ttaaaggccg cgcgaccctg accgtggata ccagcaccaa caccgcgtat   240

atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcagcacc   300

tattatcgcc cgctggatta ttggggccag ggcaccctgg tgaccgtgag cagc   354

<210> 1679
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1679
gatattgtga tgacccagag cccggatagc ctggcggtga gcctgggcga acgcgcgacc   60

attaactgca aaagcagcca gagcattctg tatagcagca accagaaaaa ctatctggcg   120 tggtatcagc agaaaccggg ccagagcccg aaactgctga tttattgggc gagcacccgc 180

gaaagcggcg tgccggatcg ctttagcggc agcggcagcg gcaccgattt taccctgacc 240

attagcagcc tgcaggcgga agatgtggcg gtgtattatt gccatcagta tatgagcagc 300

tatacctttg gccagggcac caaactggaa attaaa 336

<210> 1680
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1680
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg 60

tcctgcaagg ccagcggcta caccttcgcc agccaatgga tgcactggat gcggcaggca 120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac 180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc 300

tggtaccggc cgctggacta ctggggccag ggcaccctgg tgaccgtgag cagc 354

<210> 1681
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1681
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc 60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg 180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc 240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta catcagcagc 300

tacaccttcg gccagggcac aaagctggaa atcaag 336

<210> 1682
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1682
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg 60

tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca 120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac 180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacg 300

tggtatcggc cgaatgacta ctggggccag ggcaccctgg tgaccgtgag cagc 354

<210> 1683
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1683
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc 60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg 180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc 240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta caaaagcagc 300

tacaccttcg gccagggcac aaagctggaa atcaag 336

<210> 1684
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1684
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg   60

tcctgcaagg ccagcggcta caccttcgcc agcagctgga tgcactggat gcggcaggca   120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac   180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac   240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaaccacc   300

cgttatcggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc   354

<210> 1685
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1685
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc   60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc   120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg   180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc   240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta ccgtagcagc   300

tacaccttcg gccagggcac aaagctggaa atcaag   336

<210> 1686
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1686
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg   60

tcctgcaagg ccagcggcta caccttcgcc agccaatata tgcactggat gcggcaggca   120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac   180

```
aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagactgacc      300

tattatcggc cgccggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1687
<211>  336
<212>  DNA
<213>  artificial sequence

<220>
<223>  artificial polynucleotide

<400>  1687
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccact       60

atagcagcta caccttcggc cagggcacaa agctggaaat caagccatca actgcaagag      120

cagccagagc atcctgtaca gcagcaacca gaagaactac ctggcctggt atcagcagaa      180

gcccggccag agccccaagc tgctgatcta ctgggccagc acccgggaga gcggcgtgcc      240

cgaccggttt agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca      300

ggccgaggac gtggccgtgt actactgcca ccagta                                336


<210>  1688
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial polynucleotide

<400>  1688
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ctggagcttc cgtcaaggtg       60

tcctgcaagg ccagcggcta caccttcgcc agctactaca tgcactggat gcggcaggca      120

cctggacagg gcctcgaatg gatcggctgg atcaaccccg gcaacgtgaa caccaagtac      180

aacgagaagt tcaagggcag ggccaccctg accgtggaca ccagcaccaa caccgcctac      240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaagcacc      300

tactaccggc ccctggacta ctggggccag ggcaccctgg tgaccgtgag cagc            354


<210>  1689
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```
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial polynucleotide

<400>  1689
gacatcgtga tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc       60

atcaactgca agagcagcca gagcatcctg tacagcagca accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagagcccc aagctgctga tctactgggc cagcacccgg      180

gagagcggcg tgcccgaccg gtttagcggc agcggctccg gcaccgactt caccctgacc      240

atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccaccagta cctgagcagc      300

tacaccttcg gccagggcac aaagctggaa atcaag                                336


<210>  1690
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1690

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 Ala Ser Ala
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1691
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1691

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Met Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1692
<211>  118
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1692

```
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 Ala Ser Gln
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

<210> 1693
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1693

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Ile Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1694
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1694

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 Ala Ser Ser
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Trp Tyr Arg Pro Asn Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 1695
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1695

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 Ile Leu Tyr Ser
            20   25   30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 His Gln
                85   90   95

Tyr Lys Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

```
<210>  1696
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1696

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 Ala Ser Ser
            20                  25                  30


Trp Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Thr Arg Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1697
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artifcial polypeptide

<400>  1697
```

```
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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Arg Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1698
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1698

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 Ala Ser Gln
            20                  25                  30


Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
```

```
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1699
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1699

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95
```

```
Tyr Tyr Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1700
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1700

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 Ala Ser Tyr
            20                  25                  30


Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asn Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Asn 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 Thr Tyr Tyr Arg Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1701
<211>  112
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  artificial polypeptide

<400>  1701

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 Ile Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 His Gln
                85                  90                  95


Tyr Leu Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  1702
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1702

Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  1703
<211>  8
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> artificial polypeptide

<400> 1703

Ile Asn Pro Gly Asn Val Asn Thr
1   5

<210> 1704
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1704

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
1   5

<210> 1705
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1705

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1   5   10

<210> 1706
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1706

Trp Ala Ser Thr Arg Glu
1   5

<210> 1707

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<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1707

His Gln Tyr Leu Ser Ser Tyr Thr
1               5


<210>  1708
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1708

Gly Tyr Thr Phe Ala Ser Tyr Tyr
1               5


<210>  1709
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1709

Ile Asn Pro Gly Asn Val Asn Thr
1               5


<210>  1710
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1710

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
```

```
1               5


<210>  1711
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1711

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1712
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1712

Trp Ala Ser Thr Arg Glu
1               5


<210>  1713
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1713

His Gln Tyr Leu Ser Ser Tyr Thr
1               5


<210>  1714
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide
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<400>  1714

Gly Tyr Thr Phe Ala Ser Gln Trp
1               5


<210>  1715
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1715

Ile Asn Pro Gly Asn Val Asn Thr
1               5


<210>  1716
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1716

Ser Thr Trp Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1717
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1717

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1718
<211>  6
<212>  PRT
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<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1718

Trp Ala Ser Thr Arg Glu
1               5


<210>  1719
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1719

His Gln Tyr Ile Ser Ser Tyr Thr
1               5


<210>  1720
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1720

Gly Tyr Thr Phe Ala Ser Ser Trp
1               5


<210>  1721
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1721

Ile Asn Pro Gly Asn Val Asn Thr
1               5
```

<210> 1722
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1722

```
Ser Thr Trp Tyr Arg Pro Asn Asp Tyr
1               5
```

<210> 1723
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1723

```
Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10
```

<210> 1724
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1724

```
Trp Ala Ser Thr Arg Glu
1               5
```

<210> 1725
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1725

```
His Gln Tyr Lys Ser Ser Tyr Thr
1               5


<210>  1726
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1726

Gly Tyr Thr Phe Ala Ser Ser Trp
1               5


<210>  1727
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1727

Ile Asn Pro Gly Asn Val Asn Thr
1               5


<210>  1728
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1728

Thr Ile Arg Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1729
<211>  12
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  artificial polypeptide

<400>  1729

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1730
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1730

Trp Ala Ser Thr Arg Glu
1               5


<210>  1731
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1731

His Gln Tyr Arg Ser Ser Tyr Thr
1               5


<210>  1732
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1732

Gly Tyr Thr Phe Ala Ser Ser Trp
1               5


<210>  1733
```

```
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1733

Ile Asn Pro Gly Asn Val Asn Thr
1               5


<210>  1734
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1734

Leu Thr Tyr Tyr Arg Pro Pro Asp Tyr
1               5


<210>  1735
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1735

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1736
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1736

Trp Ala Ser Thr Arg Glu
```

```
1               5


<210>  1737
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1737

His Gln Tyr Tyr Ser Ser Tyr Thr
1               5


<210>  1738
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1738

Gly Tyr Thr Phe Ala Ser Ala Trp
1               5


<210>  1739
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1739

Ile Asn Pro Gly Asn Val Asn Thr
1               5


<210>  1740
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide
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```
<400>  1740

Ser Thr Tyr Tyr Arg Pro Leu Asp Tyr
1               5


<210>  1741
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1741

Gln Ser Ile Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1               5                   10


<210>  1742
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1742

Trp Ala Ser Thr Arg Glu
1               5


<210>  1743
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1743

His Gln Tyr Met Ser Ser Tyr Thr
1               5


<210>  1744
<211>  354
<212>  DNA
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<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1744
caggtccagc tcgtccagtc cggcgctgaa gtggtgaaac ccggggcatc cgtcaaagtc   60

tcttgtaagg ctagtggcta caccttcaca tcctactgga tgcattgggt gaaacaggca   120

cctggccagg gactcgaatg gatcggagcc gtgtctcctg gaaattccga cacctcctac   180

aacgaaaaat tcaagggcaa ggcaaccctc actgtggaca aatctgcctc taccgcctac   240

atggaactct catctctccg ctctgaggat actgctgtgt actactgtac ccggtcacga   300

tacggcaata acgccctcga ttactggggg cagggaactc tggtcactgt gtct   354

<210> 1745
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1745
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc   60

atcacctgca gagccagcca gggcatcagc agcaacatcg tgtggtacca gcagaagccc   120

ggcaaggccc ccaagggcct gatctaccac ggcaccaacc tggagagcgg cgtgcccagc   180

agattcagcg gcagcggcag cggcaccgac tacaccctga ccatcagcag cctgcagccc   240

gaggacttcg ccacctacta ctgcgtgcag tacagccagt tcccccccac cttcggccag   300

ggcaccaagc tggagatcaa g   321

<210> 1746
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1746
caggtccagc tcgtccagtc cggcgctgaa gtggtgaaac ccggggcatc cgtcaaagtc   60

tcttgtaagg ctagtggcta caccttcaca tcctactgga tgcattgggt gaaacaggca 120

cctggccagg gactcgaatg gatcggagcc gtgtctcctg gaaattccga cacctcctac 180

aacgaaaaat tcaagggcaa ggcaaccctc actgtggata ctagtgcttc taccgcctac 240

atggaactct catctctccg ctctgaggac actgccgtct actactgtac tcggtcacga 300

tacgggaaca acgctctcga ttactgggga cagggcacac tggtcactgt ctct 354

<210> 1747
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1747
gatattcagc tcacacagag cccatcttct ctgtctgctt ctgtgggcga tcgagtgaca 60

atcacttgtc gggctagtca gggcatttct agcaacattg tgtggctcca gcagaaacct 120

ggcaaagccc caaaaggcct catctaccac ggaaccaacc tggaatctgg cgtgccatct 180

cggtttagtg gatctggatc cgggaccgat tacacactca ccatctcttc actggaacct 240

gaggatttcg ccacctacta ctgtgtccag tactcccagt ttccacccac ttttggacag 300

ggaaccaaac tcgagatcaa a 321

<210> 1748
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1748
caggtccagc tcgtccagtc cggcgctgaa gtggtgaaac ccggggcatc cgtcaaagtc 60

tcttgtaagg ctagtggcta caccttcaca tcctactgga tgcattgggt gaaacaggca 120

cctggccagg gactcgaatg gatcggagcc gtgtctcctg gaaattccga cacctcctac 180

aacgaaaaat tcaagggcaa ggcaaccctc actgtggaca aatctgcctc taccgcctac 240

atggaactct catctctccg ctctgaggat actgctgtgt actactgtac ccggtcacga 300

```
tacggcaata acgccctcga ttactggggg cagggaactc tggtcactgt gtct            354


<210>  1749
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial polynucleotide

<400>  1749
gatattcagc tcacacagag cccatcttct ctgtctgctt ctgtgggcga tcgagtgaca       60

atcacttgtc gggctagtca gggcatttct agcaacattg tgtggctcca gcagaaacct      120

ggcaaagccc caaaaggcct catctaccac ggaaccaacc tggaatctgg cgtgccatct      180

cggtttagtg gatctggatc cgggaccgat tacacactca ccatctcttc actggaacct      240

gaggatttcg ccacctacta ctgtgtccag tactcccagt ttccacccac ttttggacag      300

ggaaccaaac tcgagatcaa a                                                321


<210>  1750
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1750

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


Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu 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

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser
115

<210> 1751
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1751

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
20 25 30

Ile Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Gly Leu Ile
35 40 45

Tyr His Gly Thr Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105

<210> 1752
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1752

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


Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr 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


Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser
        115
```

<210> 1753
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1753

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
            20                  25                  30


Ile Val Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Gly Leu Ile
        35                  40                  45


Tyr His Gly Thr Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  1754
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1754

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


Gly Ala Val Ser Pro Gly Asn Ser Asp Thr Ser Tyr Asn Glu Lys Phe
```

```
    50                  55                  60

Lys Gly Lys Ala Thr Leu 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

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser
        115


<210>  1755
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1755

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Asn
            20                  25                  30

Ile Val Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Gly Leu Ile
        35                  40                  45

Tyr His Gly Thr Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Ser Gln Phe Pro Pro
                85                  90                  95
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```
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  1756
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1756

Gly Tyr Thr Phe Thr Ser Tyr Trp
1               5


<210>  1757
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1757

Val Ser Pro Gly Asn Ser Asp Thr
1               5


<210>  1758
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1758

Thr Arg Ser Arg Tyr Gly Asn Asn Ala Leu Asp Tyr
1               5                   10


<210>  1759
<211>  9
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> artificial polypeptide

<400> 1759

Gln Gly Ile Ser Ser Asn Ile Val Trp
1   5

<210> 1760
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1760

His Gly Thr
1

<210> 1761
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1761

Val Gln Tyr Ser Gln Phe Pro Pro Thr
1   5

<210> 1762
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1762
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaagtc   60

tcctgcaagg cttctggata caccttcagc ggctactcta cacactggct gcgacaggtc   120

cctggacagg gacttgagtg gattggatgg gacaacccta gtagtggtga cacgacctat   180 gcagagaatt ttcggggcag ggtcaccctg accagggaca cgtccatcac cacagattac 240

ttggaagtga ggggtctaag atctgacgac acggccgtct attattgtgc cagaggcgga 300

gatgactaca gctttgacca ttggggtcag ggcaccctgg tcaccgtctc ctca 354

<210> 1763
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial polynucleotide

<400> 1763
tcttctgagc tgactcagga cccagctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccgag gagacagcct cagaagttat tatgcaagct ggtaccaaca gaagccagga 120

caggcccctg tacttgtcat ctatggtgaa aacaaccgac cctcagggat cccagaccga 180

ttctctggct ccagctcagg agacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgg gacagcagtg atcaccttct cctattcggt 300

ggagggacca agttgaccgt cctaggt 327

<210> 1764
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1764

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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 Gly Tyr
            20                  25                  30


Ser Thr His Trp Leu Arg Gln Val Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr Tyr Ala Glu Asn Phe
```

```
    50                  55                  60


Arg Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Thr Thr Asp Tyr
65                  70                  75                  80


Leu Glu Val Arg Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gly Asp Asp Tyr Ser Phe Asp His Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  1765
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1765

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


Thr Val Arg Ile Thr Cys Arg Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Glu Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ser Ser Gly Asp Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Asp His Leu
                85                  90                  95
```

```
Leu Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>  1766
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1766

Gly Tyr Ser Thr His
1               5


<210>  1767
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1767

Trp Asp Asn Pro Ser Ser Gly Asp Thr Thr Tyr Ala Glu Asn Phe Arg
1               5                   10                  15


Gly



<210>  1768
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1768

Gly Gly Asp Asp Tyr Ser Phe Asp His
1               5


<210>  1769
```

```
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1769

Arg Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1               5                   10


<210>  1770
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1770

Gly Glu Asn Asn Arg Pro Ser
1               5


<210>  1771
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  artificial polypeptide

<400>  1771

Asn Ser Arg Asp Ser Ser Asp His Leu Leu Leu
1               5                   10


<210>  1772
<211>  364
<212>  DNA
<213>  Homo sapiens

<400>  1772
caggtgcagc tggtgcagtc tgggggaggc gtggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct      120

ccagggaagg gcctggagtg ggtctcaagt cttagttgga atactggtcg agtagcctat      180
```

```
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ttccctgtat      240

ctgcaaatga acagtctgag acctgaggac acggccttct attactgtgc aaaaggctcc      300

gcccttggct tagttggctg gttcgacgcc tggggccagg gcaccctggt caccgtctcc      360

tcag                                                                   364


<210>  1798
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  1798

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Leu Ser Trp Asn Thr Gly Arg Val Ala Tyr Ala 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 Pro Glu Asp Thr Ala Phe Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Ser Ala Leu Gly Leu Val Gly Trp Phe Asp Ala Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1773
<211>  322
<212>  DNA
```

```
<213>  Homo sapiens

<400>  1773
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc       60

acatgccaag gagacagtct cagaacctat tatggaagtt ggtaccagca gaagccagga      120

caggcccctc tacttgtctt ctatggcaaa gagagtcggc cctcagggat cccagaccga      180

ttctctggct ccacctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa      240

gatgaggctg actattactg taactcccag gacagcagtg gtgacttatt attcggcgga      300

gggaccaagc tgaccgtcct ag                                               322


<210>  1799
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1799

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Thr Tyr Tyr Gly
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Leu Leu Val Phe Tyr
        35                  40                  45


Gly Lys Glu Ser Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Thr Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Gln Asp Ser Ser Gly Asp Leu
                85                  90                  95


Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1774
```

```
<211>  352
<212>  DNA
<213>  Homo sapiens

<400>  1774
caggtgcagc tggtgcaatc tgggggaggc ttggtccagt ctgggaagtc cgtgagactc       60

tcttgtgcag cctctggatt cacatttggt gattatgcca tgcactgggt ccggcaagct      120

ccaggaaagg gcctggagtg ggtcgcaggc attactagga atagtggtcg catagcctat      180

gcggactttg tgaagggccg attcatcatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagcgaaatg      300

actggggctt atgatatttg ggggccaaggg accacggtca ccgtctcctc ag             352


<210>  1800
<211>  117
<212>  PRT
<213>  Homo sapiens

<400>  1800

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Ser Gly Lys
1               5                   10                  15


Ser Val Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


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


Lys Gly Arg Phe Ile 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 Ser Glu Met Thr Gly Ala Tyr Asp Ile Trp Gly Gln Gly Thr Thr
            100                 105                 110
```

Val Thr Val Ser Ser
        115

<210> 1775
<211> 325
<212> DNA
<213> Homo sapiens

<400> 1775
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc   60

acatgccaag gagacggcct cagatactat tatgcaagct ggtaccagca gaagccagga   120

caggcccctа tacttgtcct ctttggtaaa aacaaccggc cctcagggat cccagaccga   180

ttctctggct ccagctcagg aaatacagct tccttgacca tcactggggc tcaggcggaa   240

gatgaggctg actattactg taactcgcgg gacagcagtg gtaaccatcg attcttcgga   300

actgggacca aggtcaccgt cctaa   325

<210> 1801
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1801

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

Thr Val Arg Ile Thr Cys Gln Gly Asp Gly Leu Arg Tyr Tyr Tyr Ala
            20   25   30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Leu Phe
        35   40   45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50   55   60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65   70   75   80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His

```
                85                  90                  95


Arg Phe Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  1776
<211>  361
<212>  DNA
<213>  Homo sapiens

<400>  1776
caggtgcagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agctgaggac acggctgtat attactgtgc gaaagaggat      300

tactatgata gtagtggttc gaactactgg ggccagggaa ccctggtcac cgtctcctca      360

g                                                                      361


<210>  1802
<211>  120
<212>  PRT
<213>  Homo sapiens

<400>  1802

Gln Val Gln Leu Val Gln 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 Ser Tyr
            20                  25                  30


Ala 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 Asn 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 Glu Asp Tyr Tyr Asp Ser Ser Gly Ser Asn Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1777
<211>  331
<212>  DNA
<213>  Homo sapiens

<400>  1777
ctgcctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc       60

tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc      120

ccaggaacgg cccccaaact cctcacctat aggaatgatc agcggccctc aggggtccct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg      240

tccgaggatg aggctgatta tttctgttca gcttgggatg acagcctggg tggcgaggtc      300

ttcggaactg ggaccaaggt caacgtccta g                                     331


<210>  1803
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1803

Leu Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30


Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45
```

```
Thr Tyr Arg Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ser Ala Trp Asp Asp Ser Leu
                85                  90                  95


Gly Gly Glu Val Phe Gly Thr Gly Thr Lys Val Asn Val Leu
            100                 105                 110


<210>  1778
<211>  355
<212>  DNA
<213>  Homo sapiens

<400>  1778
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agccatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaatcggt      300

acggcggatg cttttgatat ctggggccaa gggaccacgg tcaccgtctc ctcag           355


<210>  1804
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  1804

Gln Val Gln Leu Val Gln Ser Gly Gly 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 His
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

```
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Ile Gly Thr Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser
        115


<210>  1779
<211>  331
<212>  DNA
<213>  Homo sapiens

<400>  1779
cagtctgccc tgactcagcc accctcagtg tctgggaccc ccggacagag ggtcaccatc       60

tcttgttctg gaggcgtccc caacatcgga agtaatcctg taaactggta cctccaccgc      120

ccaggaacgg cccccaaact cctcatctat aatagcaatc agtggccctc aggggtccct      180

gaccgatttt ctggctccag gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgga tggtctggtt      300

ttcggcggag ggaccaagtt gaccgtccta g                                     331


<210>  1805
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  1805

Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Ser Gly Gly Val Pro Asn Ile Gly Ser Asn
            20                  25                  30


Pro Val Asn Trp Tyr Leu His Arg Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Asn Ser Asn Gln Trp Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asp Gly Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1780
<211>  373
<212>  DNA
<213>  Homo sapiens

<400>  1780
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt       60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac      180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaaaaa      300

agcagcagct ggtacggggg ggacaactgg ttcgacccct ggggccaggg caccctggtc      360

accgtctcct cag                                                         373


<210>  1806
<211>  124
<212>  PRT
<213>  Homo sapiens

<400>  1806
```

```
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 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser 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 Glu Lys Ser Ser Ser Trp Tyr Gly Gly Asp Asn Trp Phe Asp
            100                 105                 110


Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1781
<211>  331
<212>  DNA
<213>  Homo sapiens

<400>  1781
cagtctgccc tgactcagcc tcgctcagtg tccgggtctc ctggacagtc agtcaccatc       60

tcctgcactg gaagcagcag tgatgttggt ggttatcatt atgtctcctg gtaccaacaa      120

tacccaggca aagtccccaa actgatgatt tatgatgtct ctaggcggcc ctcaggggtt      180

tctgatcgct tctctggctc caagtctggc agcacggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cactgtggtc      300

ttcggcggag ggaccaagct gaccgtccta c                                     331
```

<210> 1807
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1807

```
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


His Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Val Pro Lys Leu
        35                  40                  45


Met Ile Tyr Asp Val Ser Arg Arg Pro Ser Gly Val Ser Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Ser Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95


Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 1782
<211> 390
<212> DNA
<213> Homo sapiens

<400> 1782

```
caggtgcagc tggtgcaatc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc        60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc       120

cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat       180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac       240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatgta       300

cacccccttag atatagcagt ggctgccgac gattactact actacggtat ggacgtctgg       360
```

```
ggccaaggca ccctggtcac cgtctcctca                                        390


<210>  1808
<211>  130
<212>  PRT
<213>  Homo sapiens

<400>  1808

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


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60


Gln 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 Asp Val His Pro Leu Asp Ile Ala Val Ala Ala Asp Asp Tyr
            100                 105                 110


Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        115                 120                 125


Ser Ser
    130


<210>  1783
<211>  325
<212>  DNA
<213>  Homo sapiens
```

```
<400>  1783
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc        60

acatgccaag gagacagcct cacaaccaat tatgcaagct ggtaccagca gaagccagga       120

caggcccctg ttcttgtcat ctatggtaaa aacaagcggc cctcagggat cccagaccga       180

ttctctggct ccatctcagg gaacacagct tccttgacca tcactggggc tcaggcggag       240

gatgaggctg actattactg taactcccgg gacagcagtg gtaagcatta tgtcttcgga       300

actgggacca aggtcaccgt cctag                                             325


<210>  1809
<211>  108
<212>  PRT
<213>  Homo sapiens

<400>  1809

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


Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Thr Thr Asn Tyr Ala
            20                  25                  30


Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Gly Lys Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60


Ile Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Lys His
                85                  90                  95


Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  1784
<211>  367
<212>  DNA
```

<213> Homo sapiens

<400> 1784

```
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc        60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct       120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac       180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagattgg       300

ggcctagtac aactggaatc cggctatgac tactggggcc agggaaccct ggtcaccgtc       360

tcctcag                                                                 367
```

<210> 1810
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1810

```
Glu 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 Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Trp Gly Leu Val Gln Leu Glu Ser Gly Tyr Asp Tyr Trp
            100                 105                 110
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1785
<211>  334
<212>  DNA
<213>  Homo sapiens

<400>  1785
cagtctgtgc tgactcagcc accctcagtg tctggggccc cagggcagag ggtcaccatc       60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccaacag      120

cttccaggaa aagcccccaa actcctcatc tatgataata ccaatcggcc ctcgggggtc      180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cagtgggctc      240

cagtctgagg atgaggctga ttattactgt gcagcatggg atgaaagcct gaatggtcag      300

gtcttcggaa ctgggaccaa ggtcaccgtc ctag                                  334


<210>  1811
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  1811

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30


Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Asp Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80


Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Glu Ser
```

                85   90   95

Leu Asn Gly Gln Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 1786
<211> 367
<212> DNA
<213> Homo sapiens

<400> 1786
caggtacagc tgcagcagtc aggcccagga ctggtgaagc cttcggggac cctgtccctc   60

acctgcgctg tctctggtgg ctccatcagc agtagtgact ggtggagttg ggtccgccag   120

gtcccaggga aggggctgga gtggattggg gaaatctatc acagtggcag tcccaactac   180

aacccgtccc tcaggggtcg agtcaccata tcagtagaca agtcgaagaa ccagttctcc   240

ctgaagctga gctctgtgac cgccgcggac acggccgtct attactgtgc gagagaaaga   300

gttgctccta cagtagacgg tgcttttgat gtctggggcc aagggacaat ggtcaccgtc   360

tcctcag   367

<210> 1812
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1812

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1   5   10   15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20   25   30

Asp Trp Trp Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp
        35   40   45

Ile Gly Glu Ile Tyr His Ser Gly Ser Pro Asn Tyr Asn Pro Ser Leu
    50   55   60

Arg Gly Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser

```
65                  70                  75                  80


Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Arg Val Ala Pro Thr Val Asp Gly Ala Phe Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  1787
<211>  322
<212>  DNA
<213>  Homo sapiens

<400>  1787
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggcaagtca gagcattacc acctatttaa attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180

aggttcagtg gcagtggatc tgggacagaa ttcactctca ctatcagcag cctgcagcct      240

gaagattttg caacttatta ttgtcaacag gccagcagtt tccctctcac tttcggcgga      300

gggaccaagg tggatctcaa ac                                               322


<210>  1813
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1813

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Thr Thr Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

Tyr Ala Ala Ser Ser Leu Gln 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 Ala Ser Ser Phe Pro Leu
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Asp Leu Lys
            100   105

<210> 1788
<211> 364
<212> DNA
<213> Homo sapiens

<400> 1788
gaggtgcagc tggtgcagtc tggagctgag gtgaaaaagc ccggggagtc tctgaagatc   60

tcctgtaagg gttcgggata cagctttacc aactactgga tcggctgggt gcgccagatg   120

cccgggaaag gcctggagtg gattgggatc atctatcctg gtgactctga taccagatac   180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccaccag cactgcctac   240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaggataaag   300

agttactatg atagtagtgg ttattacctc tggggccagg gaaccctggt caccgtctcc   360

tcag   364

<210> 1814
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1814

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 Ser Phe Thr Asn Tyr
            20   25   30

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


Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60


Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Thr 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 Ile Lys Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1789
<211>  322
<212>  DNA
<213>  Homo sapiens

<400>  1789
cagtctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccagcata       60

acctgtgggg gaaacaacat tgggagtaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tcctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgaagaggt attcggcgga      300

gggaccaagc tgaccgtcct ag                                               322


<210>  1815
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1815

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
```

```
1               5                   10                  15

Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Glu Glu
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1790
<211>  346
<212>  DNA
<213>  Homo sapiens

<400>  1790
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc        60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct       120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac       180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat       240

ctgcaaatga acagcctgag agccgacgac acggctgtct attactgtgc gagaaggggg       300

ttcatggacg tctggggcaa aggcaccctg gtcaccgtct cctcag                      346


<210>  1816
<211>  115
<212>  PRT
<213>  Homo sapiens

<400>  1816
```

```
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Arg Gly Phe Met Asp Val Trp Gly Lys Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115


<210>  1791
<211>  325
<212>  DNA
<213>  Homo sapiens

<400>  1791
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaccatc        60

acatgccaag gagacatcct cgaagcctat tatgcaagtt ggtaccagca gaggccagga       120

caggcccctg tccttgtcat ctatggcgaa aacaaccggc cctcagggat cccagaccgg       180

ttctctggct ccaggtcagg aaacacagcc tccttgacca tcactggggc tcaggcggaa       240

gatgaggctg actattattg taactctcgg gacagcagtg gtagccatgt ggtattcggc       300

ggagggacca agatgaccgt cctgg                                             325
```

<210> 1817
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1817

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

Thr Val Thr Ile Thr Cys Gln Gly Asp Ile Leu Glu Ala Tyr Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Glu Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Ser His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Met Thr Val Leu
100 105

<210> 1792
<211> 346
<212> DNA
<213> Homo sapiens

<400> 1792
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttaac agctttgcca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggcac 300

gcttttgata tctggggcca agggaccacg gtcaccgtct cctcag 346

<210> 1818
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1818

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Phe
            20                  25                  30


Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly His Ala Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr
            100                 105                 110


Val Ser Ser
        115
```

<210> 1793
<211> 337
<212> DNA
<213> Homo sapiens

<400> 1793

```
gacatcgtga tgacccagtc tccactctct ctgtccgtca cccctgggca gccggcctcc       60

atctcctgca agtctagtca gagcctcctg catagtgatg gaaagaccta tttgtattgg      120

tacctgcaga agccaggcca gcctccacaa ctcctgatct atgaagtttc caaccggttc      180
```

```
tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc      240

agccgggtgg aggctgagga tgttggggtt tattactgca tgcaaagtat acagcttcct      300

ctcactttcg gcggagggac caaggtggag atcaaac                               337


<210>  1819
<211>  112
<212>  PRT
<213>  Homo sapiens

<400>  1819

Asp Ile Val Met Thr Gln Ser 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 Tyr 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 Met Gln Ser
                85                  90                  95


Ile Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210>  1794
<211>  352
<212>  DNA
<213>  Homo sapiens

<400>  1794
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120
```

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaaagataaa   300

ggtggggggt tcgacccctg gggccaggga accctggtca ccgtctcctc ag   352

<210> 1820
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1820

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Lys Gly Gly Gly Phe Asp Pro Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115
```

<210> 1795
<211> 331
<212> DNA

<213> Homo sapiens

<400> 1795
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc   60

tcctgcaccc gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc   120

ccgggcagtt cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtccct   180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga   240

ctgaagactg aggacgaggc tgactactac tgtcagtctt atgatagtac ctctcatgtc   300

ttcggaactg ggacccaggt caccgtccta g   331

<210> 1821
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1821

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
            20   25   30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
        35   40   45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85   90   95

Thr Ser His Val Phe Gly Thr Gly Thr Gln Val Thr Val Leu
            100   105   110

<210> 1796

```
<211>  373
<212>  DNA
<213>  Homo sapiens

<400>  1796
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc       60

tcctgtaagg gttctggata cagctttacc aactactgga tcggctgggt gcgccagatg      120

cccgggaaag gcctggagtg ggtggggatc atctatcctg gtgactctga taccagatac      180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac      240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaccaggg      300

tattactatg gttcggggag ttattataac gttgactact ggggccaggg caccctggtc      360

accgtctcct cag                                                         373


<210>  1822
<211>  124
<212>  PRT
<213>  Homo sapiens

<400>  1822

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 Ser Phe Thr Asn Tyr
            20                  25                  30


Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60


Gln 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 Pro Gly Tyr Tyr Tyr Gly Ser Gly Ser Tyr Tyr Asn Val Asp
```

```
        100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120



<210>  1797
<211>  322
<212>  DNA
<213>  Homo sapiens

<400>  1797
cagcctgggc tgactcagcc accctcagtg tccgtgtccc caggacagac agccagcatc       60

acctgctctg gagatgaatt gggggataaa tttgctttct ggtatcaaca aaagccaggc      120

cagtcccctg tgctggtcat ctatcaagat agtaagaggc cctcagggat ccctgagcga      180

ttctctggct ccatctctgg gaacacggcc accctgacta tcagcagggt cgaggccgga      240

gatgaggccg actatttctg tcaggtgtgg gatagcaatg gtggtccccc attcgggaga      300

gggaccaagc tgaccgtcct ag                                               322



<210>  1823
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  1823

Gln Pro Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15


Thr Ala Ser Ile Thr Cys Ser Gly Asp Glu Leu Gly Asp Lys Phe Ala
            20                  25                  30


Phe Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45


Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Ile Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80
```

```
Asp Glu Ala Asp Tyr Phe Cys Gln Val Trp Asp Ser Asn Gly Gly Pro
                85                  90                  95


Pro Phe Gly Arg Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1824
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1824

Gly Phe Thr Phe Asp Asp Tyr Ala
1               5


<210>  1825
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1825

Leu Ser Trp Asn Thr Gly Arg Val
1               5


<210>  1826
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  1826

Ala Lys Gly Ser Ala Leu Gly Leu Val Gly Trp Phe Asp Ala
1               5                   10


<210>  1827
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1827

Ser Leu Arg Thr Tyr Tyr
1               5
```

<210> 1828
<211> 3
<212> PRT
<213> Homo sapiens

<400> 1828

Gly Lys Glu
1

<210> 1829
<211> 10
<212> PRT
<213> Homo sapiens

<400> 1829

Asn Ser Gln Asp Ser Ser Gly Asp Leu Leu
1 5 10

<210> 1830
<211> 8
<212> PRT
<213> Homo sapiens

<400> 1830

Gly Phe Thr Phe Gly Asp Tyr Ala
1 5

<210> 1831
<211> 8
<212> PRT
<213> Homo sapiens

<400> 1831

Ile Thr Arg Asn Ser Gly Arg Ile
1 5

<210> 1832
<211> 10
<212> PRT
<213> Homo sapiens

<400> 1832

```
Ala Ser Glu Met Thr Gly Ala Tyr Asp Ile
1               5                   10


<210>  1833
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1833

Gly Leu Arg Tyr Tyr Tyr
1               5


<210>  1834
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1834

Gly Lys Asn
1


<210>  1835
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1835

Asn Ser Arg Asp Ser Ser Gly Asn His Arg Phe
1               5                   10


<210>  1836
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1836

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  1860
<211>  8
<212>  PRT
<213>  Homo sapiens
```

```
<400>  1860

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  1878
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1878

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  1890
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1890

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  1837
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1837

Ile Ser Tyr Asp Gly Ser Asn Lys
1               5


<210>  1838
<211>  13
<212>  PRT
<213>  Homo sapiens

<400>  1838

Ala Lys Glu Asp Tyr Tyr Asp Ser Ser Gly Ser Asn Tyr
1               5                   10


<210>  1839
```

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

<400> 1839

```
Ser Ser Asn Ile Gly Ser Asn Tyr
1               5
```

<210> 1840
<211> 3
<212> PRT
<213> Homo sapiens

<400> 1840

```
Arg Asn Asp
1
```

<210> 1841
<211> 11
<212> PRT
<213> Homo sapiens

<400> 1841

```
Ser Ala Trp Asp Asp Ser Leu Gly Gly Glu Val
1               5                   10
```

<210> 1842
<211> 8
<212> PRT
<213> Homo sapiens

<400> 1842

```
Gly Phe Thr Phe Ser Ser His Ala
1               5
```

<210> 1843
<211> 8
<212> PRT
<213> Homo sapiens

<400> 1843

```
Ile Ser Gly Ser Gly Gly Ser Thr
1               5
```

```
<210>  1861
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1861

Ile Ser Gly Ser Gly Gly Ser Thr
1               5


<210>  1879
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1879

Ile Ser Gly Ser Gly Gly Ser Thr
1               5


<210>  1885
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1885

Ile Ser Gly Ser Gly Gly Ser Thr
1               5


<210>  1891
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1891

Ile Ser Gly Ser Gly Gly Ser Thr
1               5


<210>  1844
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1844
```

```
Ala Lys Ile Gly Thr Ala Asp Ala Phe Asp Ile
1               5                   10


<210>  1845
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1845

Val Pro Asn Ile Gly Ser Asn Pro
1               5


<210>  1846
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1846

Asn Ser Asn
1


<210>  1847
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1847

Ala Ala Trp Asp Asp Ser Leu Asp Gly Leu Val
1               5                   10


<210>  1848
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1848

Gly Tyr Thr Phe Thr Ser Tyr Tyr
1               5


<210>  1849
<211>  8
<212>  PRT
```

```
<213>  Homo sapiens

<400>  1849

Ile Asn Pro Ser Gly Gly Ser Thr
1               5


<210>  1850
<211>  17
<212>  PRT
<213>  Homo sapiens

<400>  1850

Ala Arg Glu Lys Ser Ser Ser Trp Tyr Gly Gly Asp Asn Trp Phe Asp
1               5                   10                  15


Pro



<210>  1851
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1851

Ser Ser Asp Val Gly Gly Tyr His Tyr
1               5


<210>  1852
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1852

Asp Val Ser
1


<210>  1853
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1853
Ser Ser Tyr Thr Ser Ser Ser Thr Val Val
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1               5                   10


<210>  1854
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1854

Gly Tyr Thr Phe Thr Ser Tyr Gly
1               5


<210>  1855
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1855

Ile Ser Ala Tyr Asn Gly Asn Thr
1               5


<210>  1856
<211>  23
<212>  PRT
<213>  Homo sapiens

<400>  1856

Ala Arg Asp Val His Pro Leu Asp Ile Ala Val Ala Ala Asp Asp Tyr
1               5                   10                  15


Tyr Tyr Tyr Gly Met Asp Val
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<210>  1857
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1857

Ser Leu Thr Thr Asn Tyr
1               5


<210>  1858
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<211> 3
<212> PRT
<213> Homo sapiens

<400> 1858

Gly Lys Asn
1

<210> 1859
<211> 11
<212> PRT
<213> Homo sapiens

<400> 1859

```
Asn Ser Arg Asp Ser Ser Gly Lys His Tyr Val
1               5                   10
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<210> 1862
<211> 15
<212> PRT
<213> Homo sapiens

<400> 1862

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Ala Lys Asp Trp Gly Leu Val Gln Leu Glu Ser Gly Tyr Asp Tyr
1               5                   10                  15
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<210> 1863
<211> 9
<212> PRT
<213> Homo sapiens

<400> 1863

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Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1               5
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<210> 1864
<211> 3
<212> PRT
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<400> 1864

Asp Asn Thr
1

<210> 1865
<211> 11
<212> PRT
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<400> 1865

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Ala Ala Trp Asp Glu Ser Leu Asn Gly Gln Val
1               5                   10
```

<210> 1866
<211> 9
<212> PRT
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<400> 1866

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Gly Gly Ser Ile Ser Ser Ser Asp Trp
1               5
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<210> 1867
<211> 7
<212> PRT
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<400> 1867

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Ile Tyr His Ser Gly Ser Pro
1               5
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<210> 1868
<211> 15
<212> PRT
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<400> 1868

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Ala Arg Glu Arg Val Ala Pro Thr Val Asp Gly Ala Phe Asp Val
1               5                   10                  15
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<210> 1869
<211> 6
<212> PRT
<213> Homo sapiens

<400> 1869

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Gln Ser Ile Thr Thr Tyr
1               5


<210>  1870
<211>  3
<212>  PRT
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<400>  1870

Ala Ala Ser
1


<210>  1871
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1871

Gln Gln Ala Ser Ser Phe Pro Leu Thr
1               5


<210>  1872
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1872

Gly Tyr Ser Phe Thr Asn Tyr Trp
1               5


<210>  1873
<211>  8
<212>  PRT
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<400>  1873

Ile Tyr Pro Gly Asp Ser Asp Thr
1               5


<210>  1874
<211>  14
<212>  PRT
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<213>  Homo sapiens

<400>  1874

Ala Arg Ile Lys Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu
1               5                   10


<210>  1896
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  1896

Ala Arg Ile Lys Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu
1               5                   10


<210>  1875
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1875

Asn Ile Gly Ser Lys Ser
1               5


<210>  1876
<211>  3
<212>  PRT
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<400>  1876

Asp Asp Ser
1


<210>  1877
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1877

Gln Val Trp Asp Ser Ser Ser Glu Glu Val
1               5                   10
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<210>  1880
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1880

Ala Arg Arg Gly Phe Met Asp Val
1               5


<210>  1881
<211>  6
<212>  PRT
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<400>  1881

Ile Leu Glu Ala Tyr Tyr
1               5


<210>  1882
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1882

Gly Glu Asn
1


<210>  1883
<211>  11
<212>  PRT
<213>  Homo sapiens

<400>  1883

Asn Ser Arg Asp Ser Ser Gly Ser His Val Val
1               5                   10


<210>  1884
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1884

Gly Phe Thr Phe Asn Ser Phe Ala
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1               5


<210>  1886
<211>  8
<212>  PRT
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<400>  1886

Ala Lys Gly His Ala Phe Asp Ile
1               5


<210>  1887
<211>  11
<212>  PRT
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<400>  1887

Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr
1               5                   10


<210>  1888
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1888

Glu Val Ser
1


<210>  1889
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1889

Met Gln Ser Ile Gln Leu Pro Leu Thr
1               5


<210>  1892
<211>  10
<212>  PRT
<213>  Homo sapiens
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```
<400>  1892

Ala Lys Asp Lys Gly Gly Gly Phe Asp Pro
1               5                   10


<210>  1893
<211>  8
<212>  PRT
<213>  Homo sapiens

<400>  1893

Ser Gly Ser Ile Ala Ser Asn Tyr
1               5


<210>  1894
<211>  3
<212>  PRT
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<400>  1894

Glu Asp Asn
1


<210>  1895
<211>  9
<212>  PRT
<213>  Homo sapiens

<400>  1895

Gln Ser Tyr Asp Ser Thr Ser His Val
1               5


<210>  1897
<211>  8
<212>  PRT
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<400>  1897

Ile Tyr Pro Gly Asp Ser Asp Thr
1               5


<210>  1898
<211>  17
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<212>  PRT
<213>  Homo sapiens

<400>  1898

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


Tyr




<210>  1899
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  1899

Glu Leu Gly Asp Lys Phe
1               5


<210>  1900
<211>  3
<212>  PRT
<213>  Homo sapiens

<400>  1900

Gln Asp Ser
1


<210>  1901
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  1901

Gln Val Trp Asp Ser Asn Gly Gly Pro Pro
1               5                   10


<210>  1902
<211>  15
<212>  PRT
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<220>
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<223> artificial polypeptide

<400> 1902

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 1903
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1903

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1   5   10

<210> 1904
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial polypeptide

<400> 1904

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1   5   10

<210> 1905
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Polypeptide

<400> 1905

Ala Pro Glu Leu Leu Gly Gly Pro Asp Val Phe Leu Phe
1   5   10